Phyre^2

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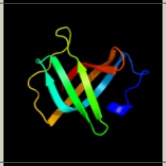
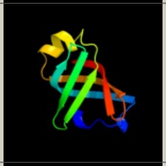
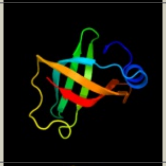
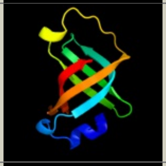
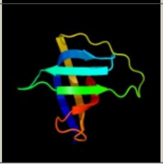
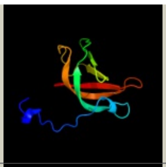
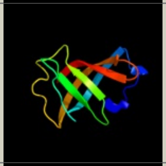
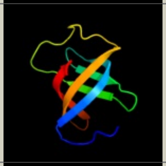
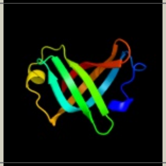
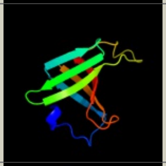
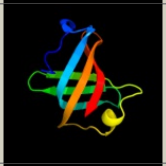
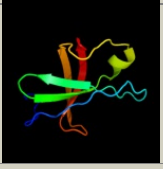
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nnxa_	Alignment		100.0	35	**Fold:**OB-fold **Superfamily:**Hypothetical protein YgiW **Family:**Hypothetical protein YgiW
2	d1b8aa1	Alignment		96.1	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
3	d1l0wa1	Alignment		96.1	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
4	c1b8aB_	Alignment		96.1	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
5	c1wydB_	Alignment		96.1	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
6	d2pi2a1	Alignment		96.0	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
7	d1n9wa1	Alignment		95.8	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
8	c2pi2A_	Alignment		95.4	16	**PDB header:**replication, dna binding protein **Chain:** A: **PDB Molecule:**replication protein a 32 kda subunit; **PDBTitle:** full-length replication protein a subunits rpa14 and rpa32
9	c3mxnB_	Alignment		95.3	19	**PDB header:**replication **Chain:** B: **PDB Molecule:**recq-mediated genome instability protein 2; **PDBTitle:** crystal structure of the rmi core complex
10	d1c0aa1	Alignment		95.2	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
11	c3kf6A_	Alignment		95.0	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein stn1; **PDBTitle:** crystal structure of s. pombe stn1-ten1 complex

12	c3i7fA_	Alignment		94.7	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
13	c1eqrC_	Alignment		94.6	22	**PDB header:**ligase **Chain:** C: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of free aspartyl-trna synthetase from2 escherichia coli
14	c3bjuB_	Alignment		93.6	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of tetrameric form of human lysyl-trna2 synthetase
15	c3m4qA_	Alignment		93.5	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, putative; **PDBTitle:** entamoeba histolytica asparaginyl-trna synthetase (asnrs)
16	c1x55A_	Alignment		93.4	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase; **PDBTitle:** crystal structure of asparaginyl-trna synthetase from pyrococcus2 horikoshii complexed with asparaginyl-adenylate analogue
17	c3e9hB_	Alignment		93.4	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
18	d1eova1	Alignment		93.0	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
19	c1efwA_	Alignment		91.3	19	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from thermus2 thermophilus complexed to trnaasp from escherichia coli
20	c3e0eA_	Alignment		91.0	14	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication protein a; **PDBTitle:** crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 targe mrr110b
21	d1bbua1	Alignment	not modelled	90.9	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
22	d1e1oa1	Alignment	not modelled	90.9	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
23	c1n9wA_	Alignment	not modelled	90.5	26	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase 2; **PDBTitle:** crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus
24	d2oq0a1	Alignment	not modelled	90.3	16	**Fold:**OB-fold **Superfamily:**HIN-2000 domain-like **Family:**HIN-200/IF120x domain
25	c2xgtB_	Alignment	not modelled	89.1	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**asparaginyl-trna synthetase, cytoplasmic; **PDBTitle:** asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate
26	c1e22A_	Alignment	not modelled	86.4	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-pcp
27	c3dm3A_	Alignment	not modelled	86.3	19	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication factor a; **PDBTitle:** crystal structure of a domain of a replication factor a2 protein, from methanocaldococcus jannaschii. northeast3 structural genomics target mjr118e
28	d1gm5a2	Alignment	not modelled	85.1	8	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins

						Family: RecG "wedge" domain
29	c3b6yB_	Alignment	not modelled	83.3	16	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**gamma-interferon-inducible protein ifi-16; **PDBTitle:** crystal structure of the second hin-200 domain of interferon-inducible2 protein 16
30	c3kf8C_	Alignment	not modelled	83.2	16	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**protein stn1; **PDBTitle:** crystal structure of c. tropicalis stn1-ten1 complex
31	d1krta_	Alignment	not modelled	80.9	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
32	d1sr3a_	Alignment	not modelled	77.0	13	**Fold:**OB-fold **Superfamily:**Heme chaperone CcmE **Family:**Heme chaperone CcmE
33	c1asyA_	Alignment	not modelled	72.0	14	**PDB header:**complex (aminoacyl-trna synthase/trna) **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp
34	c3e0jG_	Alignment	not modelled	70.5	16	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna polymerase subunit delta-2; **PDBTitle:** x-ray structure of the complex of regulatory subunits of2 human dna polymerase delta
35	c2k75A_	Alignment	not modelled	68.6	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein ta0387; **PDBTitle:** solution nmr structure of the ob domain of ta0387 from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar80b.
36	c3hbcA_	Alignment	not modelled	63.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**choloylglycine hydrolase; **PDBTitle:** crystal structure of choloylglycine hydrolase from bacteroides2 thetaiotaomicron vpi
37	c2oq0D_	Alignment	not modelled	62.7	15	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**gamma-interferon-inducible protein ifi-16; **PDBTitle:** crystal structure of the first hin-200 domain of interferon-inducible2 protein 16
38	d1t9ha1	Alignment	not modelled	49.6	11	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
39	c1gm5A_	Alignment	not modelled	46.1	8	**PDB header:**helicase **Chain:** A: **PDB Molecule:**recg; **PDBTitle:** structure of recg bound to three-way dna junction
40	d1j6qa_	Alignment	not modelled	44.4	21	**Fold:**OB-fold **Superfamily:**Heme chaperone CcmE **Family:**Heme chaperone CcmE
41	c1j6qA_	Alignment	not modelled	44.4	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**cytochrome c maturation protein e; **PDBTitle:** solution structure and characterization of the heme2 chaperone ccme
42	c2hezB_	Alignment	not modelled	38.2	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**bile salt hydrolase; **PDBTitle:** bifidobacterium longum bile salt hydrolase
43	d1cz5a1	Alignment	not modelled	36.2	10	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
44	c2kenA_	Alignment	not modelled	35.7	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of the ob domain (residues 67-166)2 of mm0293 from methanosarcina mazei. northeast structural3 genomics consortium target mar214a.
45	c3cp0A_	Alignment	not modelled	35.5	8	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**membrane protein implicated in regulation of membrane **PDBTitle:** crystal structure of the soluble domain of membrane protein implicated2 in regulation of membrane protease activity from corynebacterium3 glutamicum
46	d2pi2e1	Alignment	not modelled	34.3	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
47	d1jt8a_	Alignment	not modelled	31.8	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
48	c3obyB_	Alignment	not modelled	31.5	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeoglobus fulgidus pelota reveals inter-2 domain structural plasticity
49	c3ka5A_	Alignment	not modelled	31.2	32	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**ribosome-associated protein y (psrp-1); **PDBTitle:** crystal structure of ribosome-associated protein y (psrp-1)2 from clostridium acetobutylicum. northeast structural3 genomics consortium target id car123a
50	d2vgna1	Alignment	not modelled	27.0	13	**Fold:**Sm-like fold **Superfamily:**Dom34/Pelota N-terminal domain-like **Family:**Dom34/Pelota N-terminal domain-like
51	d2cs7a1	Alignment	not modelled	26.9	13	**Fold:**IL8-like **Superfamily:**PhtA domain-like **Family:**PhtA domain-like
52	c2bx6A_	Alignment	not modelled	26.6	21	**PDB header:**transduction protein **Chain:** A: **PDB Molecule:**xrp2 protein; **PDBTitle:** crystal structure of the human retinitis pigmentosa2 protein 2 (rp2)
						PDB header:structural genomics, unknown function

53	c2k5hA_	Alignment	not modelled	26.5	13	**Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of protein encoded by mth693 from2 methanobacterium thermoautotrophicum: northeast structural3 genomics consortium target tt824a
54	d2pvaa_	Alignment	not modelled	25.5	35	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Penicillin V acylase
55	c3k2tA_	Alignment	not modelled	23.9	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo2511 protein; **PDBTitle:** crystal structure of lmo2511 protein from listeria2 monocytogenes, northeast structural genomics consortium3 target lkr84a
56	d1qcsa1	Alignment	not modelled	23.9	10	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
57	d2heqa1	Alignment	not modelled	23.8	30	**Fold:**SH3-like barrel **Superfamily:**YorP-like **Family:**YorP-like
58	c2pqaB_	Alignment	not modelled	23.8	11	**PDB header:**replication **Chain:** B: **PDB Molecule:**replication protein a 14 kda subunit; **PDBTitle:** crystal structure of full-length human rpa 14/32 heterodimer
59	d1u0la1	Alignment	not modelled	22.9	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
60	c2bjgB_	Alignment	not modelled	22.7	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**choloylglycine hydrolase; **PDBTitle:** crystal structure of conjugated bile acid hydrolase from2 clostridium perfringens in complex with reaction products3 taurine and deoxycholate
61	c2oqkA_	Alignment	not modelled	22.5	17	**PDB header:**translation **Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a; **PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
62	d2exda1	Alignment	not modelled	22.3	10	**Fold:**OB-fold **Superfamily:**NfeD domain-like **Family:**NfeD domain-like
63	c3h43F_	Alignment	not modelled	21.8	19	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**proteasome-activating nucleotidase; **PDBTitle:** n-terminal domain of the proteasome-activating nucleotidase2 of methanocaldococcus jannaschii
64	c2vgmA_	Alignment	not modelled	21.7	9	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dom34; **PDBTitle:** structure of yeast dom34 : a protein related to translation2 termination factor erf1 and involved in no-go decay.
65	c1cz5A_	Alignment	not modelled	21.3	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**vcp-like atpase; **PDBTitle:** nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
66	d2do3a1	Alignment	not modelled	20.7	18	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**SPT5 KOW domain-like
67	d2cu3a1	Alignment	not modelled	20.5	5	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
68	c2k50A_	Alignment	not modelled	19.3	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**replication factor a related protein; **PDBTitle:** solution nmr structure of the replication factor a related2 protein from methanobacterium thermoautotrophicum.3 northeast structural genomics target tr91a.
69	c2kl0A_	Alignment	not modelled	19.1	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thiamin biosynthesis this; **PDBTitle:** solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
70	d1tygb_	Alignment	not modelled	18.7	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
71	c3cl5A_	Alignment	not modelled	18.6	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hemagglutinin-esterase; **PDBTitle:** structure of coronavirus hemagglutinin-esterase in complex with 4,9-o-2 diacetyl sialic acid
72	d1hr0w_	Alignment	not modelled	18.3	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
73	d1vr3a1	Alignment	not modelled	18.2	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
74	c1tygG_	Alignment	not modelled	17.8	21	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
75	c2wg6L_	Alignment	not modelled	17.7	17	**PDB header:**transcription,hydrolase **Chain:** L: **PDB Molecule:**general control protein gcn4, **PDBTitle:** proteasome-activating nucleotidase (pan) n-domain (57-134)2 from archaeoglobus fulgidus fused to gcn4, p61a mutant
76	d1qkia2	Alignment	not modelled	16.6	13	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
77	c3e0dA_	Alignment	not modelled	15.9	25	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase iii subunit alpha; **PDBTitle:** insights into the replisome from the crystral structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit

78	c2oqcB_	Alignment	not modelled	15.5	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**penicillin v acylase; **PDBTitle:** crystal structure of penicillin v acylase from bacillus subtilis
79	c3cwiA_	Alignment	not modelled	15.4	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**thiamine-biosynthesis protein this; **PDBTitle:** crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
80	d1h9aa2	Alignment	not modelled	15.3	7	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
81	d1t44g_	Alignment	not modelled	14.9	24	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
82	d1o7ia_	Alignment	not modelled	14.7	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
83	d1zud21	Alignment	not modelled	13.7	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
84	c1h9aA_	Alignment	not modelled	13.0	7	**PDB header:**oxidoreductase (choh(d) - nad(p)) **Chain:** A: **PDB Molecule:**glucose 6-phosphate 1-dehydrogenase; **PDBTitle:** complex of active mutant (q365->c) of glucose 6-phosphate2 dehydrogenase from l. mesenteroides with coenzyme nadp
85	d1ytfc_	Alignment	not modelled	12.9	16	**Fold:**Transcription factor IIA (TFIIA), beta-barrel domain **Superfamily:**Transcription factor IIA (TFIIA), beta-barrel domain **Family:**Transcription factor IIA (TFIIA), beta-barrel domain
86	d1v1qa_	Alignment	not modelled	12.9	9	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
87	c3i4oA_	Alignment	not modelled	12.6	8	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-1; **PDBTitle:** crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
88	c2yk5A_	Alignment	not modelled	12.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cmp-n-acetylneuraminate-beta-galactosamide-alpha-2,3- **PDBTitle:** structure of neisseria los-specific sialyltransferase (nst),2 in complex with cmp.
89	d1ah9a_	Alignment	not modelled	12.2	6	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
90	c2bhlB_	Alignment	not modelled	12.0	13	**PDB header:**oxidoreductase (choh(d)-nadp) **Chain:** B: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose-6-phosphate dehydrogenase2 (deletion variant) complexed with glucose-6-phosphate
91	d1nvpc_	Alignment	not modelled	11.9	21	**Fold:**Transcription factor IIA (TFIIA), beta-barrel domain **Superfamily:**Transcription factor IIA (TFIIA), beta-barrel domain **Family:**Transcription factor IIA (TFIIA), beta-barrel domain
92	c1nvpC_	Alignment	not modelled	11.9	21	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**transcription initiation factor iia beta chain; **PDBTitle:** human tfiia/tbp/dna complex
93	c3f6hA_	Alignment	not modelled	11.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-isopropylmalate synthase; **PDBTitle:** crystal structure of the regulatory domain of licms in2 complexed with isoleucine - type iii
94	d1umua_	Alignment	not modelled	11.4	3	**Fold:**LexA/Signal peptidase **Superfamily:**LexA/Signal peptidase **Family:**LexA-related
95	d1nh2c_	Alignment	not modelled	11.2	16	**Fold:**Transcription factor IIA (TFIIA), beta-barrel domain **Superfamily:**Transcription factor IIA (TFIIA), beta-barrel domain **Family:**Transcription factor IIA (TFIIA), beta-barrel domain
96	c1nh2C_	Alignment	not modelled	11.2	16	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**transcription initiation factor iia large chain; **PDBTitle:** crystal structure of a yeast tfiia/tbp/dna complex
97	c1qkiE_	Alignment	not modelled	11.1	13	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose 6-phosphate dehydrogenase2 (variant canton r459l) complexed with structural nadp+
98	d1g4ma2	Alignment	not modelled	11.0	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Arrestin/Vps26-like
99	c2pjhB_	Alignment	not modelled	10.9	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** strctural model of the p97 n domain- npl4 ubd complex