

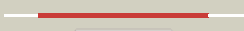


























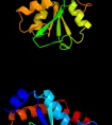
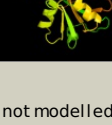


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ylnA_	 Alignment		100.0	35	PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter, periplasmic binding protein, PDBTitle: crystal structure of the l-cystine solute receptor of2 neisseria gonorrhoeae in the closed conformation
2	c3hv1A_	 Alignment		100.0	25	PDB header: transport protein Chain: A: PDB Molecule: polar amino acid abc uptake transporter substrate PDBTitle: crystal structure of a polar amino acid abc uptake2 transporter substrate binding protein from streptococcus3 thermophilus
3	c3k4uA_	 Alignment		100.0	31	PDB header: transport protein Chain: A: PDB Molecule: binding component of abc transporter; PDBTitle: crystal structure of putative binding component of abc transporter2 from wolinnella succinogenes dsm 1740 complexed with lysine
4	c2ieeB_	 Alignment		100.0	32	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: probable abc transporter extracellular-binding PDBTitle: crystal structure of yckb_bacsu from bacillus subtilis.2 northeast structural genomics consortium target sr574.
5	c3g41A_	 Alignment		100.0	21	PDB header: transport protein Chain: A: PDB Molecule: amino acid abc transporter, periplasmic amino acid-binding PDBTitle: the structure of cpn0482, the arginine binding protein from the2 periplasm of chlamydia pneumoniae
6	c3kbrA_	 Alignment		100.0	26	PDB header: lyase Chain: A: PDB Molecule: cyclohexadienyl dehydratase; PDBTitle: the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01
7	c2o1mB_	 Alignment		100.0	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: probable amino-acid abc transporter PDBTitle: crystal structure of the probable amino-acid abc2 transporter extracellular-binding protein ytmk from3 bacillus subtilis. northeast structural genomics4 consortium target sr572
8	c2vhaB_	 Alignment		100.0	22	PDB header: transport protein Chain: B: PDB Molecule: periplasmic binding transport protein; PDBTitle: debp
9	d1hsla_	 Alignment		100.0	27	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
10	c3r39A_	 Alignment		100.0	24	PDB header: transport protein Chain: A: PDB Molecule: putative periplasmic binding protein; PDBTitle: crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica
11	c3i6vA_	 Alignment		100.0	28	PDB header: transport protein Chain: A: PDB Molecule: periplasmic his/glu/gln/arg/opine family-binding protein; PDBTitle: crystal structure of a periplasmic his/glu/gln/arg/opine family-2 binding protein from silicibacter pomeroyi in complex with lysine

12	dl1sta_	Alignment		100.0	27	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
13	c1xt8B_	Alignment		100.0	21	PDB header: transport protein Chain: B: PDB Molecule: putative amino-acid transporter periplasmic solute-binding PDBTitle: crystal structure of cysteine-binding protein from campylobacter2 jejuni at 2.0 a resolution
14	c3h7mA_	Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of a histidine kinase sensor domain with2 similarity to periplasmic binding proteins
15	d1wdna_	Alignment		100.0	32	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
16	c3delC_	Alignment		100.0	21	PDB header: protein binding, transport protein Chain: C: PDB Molecule: arginine binding protein; PDBTitle: the structure of ct381, the arginine binding protein from the2 periplasm chlamydia trachomatis
17	c2yjpB_	Alignment		100.0	28	PDB header: transport protein Chain: B: PDB Molecule: putative abc transporter, periplasmic binding protein, PDBTitle: crystal structure of the solute receptors for l-cysteine of2 neisseria gonorrhoeae
18	c2q89A_	Alignment		100.0	29	PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter amino acid-binding protein; PDBTitle: crystal structure of ehuh in complex with hydroxyectoine
19	c2y7iB_	Alignment		100.0	29	PDB header: arginine-binding protein Chain: B: PDB Molecule: stm4351; PDBTitle: structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
20	d1xt8a1	Alignment		100.0	22	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
21	c2q2aD_	Alignment	not modelled	100.0	26	PDB header: transport protein Chain: D: PDB Molecule: artj; PDBTitle: crystal structures of the arginine-, lysine-, histidine-2 binding protein artj from the thermophilic bacterium3 geobacillus stearothermophilus
22	c3kzgB_	Alignment	not modelled	100.0	27	PDB header: transport protein Chain: B: PDB Molecule: arginine 3rd transport system periplasmic binding PDBTitle: crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila
23	c2v25B_	Alignment	not modelled	100.0	28	PDB header: receptor Chain: B: PDB Molecule: major cell-binding factor; PDBTitle: structure of the campylobacter jejuni antigen peb1a, an2 aspartate and glutamate receptor with bound aspartate
24	c3mplA_	Alignment	not modelled	100.0	16	PDB header: signaling protein Chain: A: PDB Molecule: virulence sensor protein bvgs; PDBTitle: crystal structure of bordetella pertussis bvgs vft2 domain (double2 mutant f375e/q461e)
25	d1mqia_	Alignment	not modelled	100.0	22	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
26	d2a5sa1	Alignment	not modelled	100.0	21	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
27	c2xx7B_	Alignment	not modelled	100.0	22	PDB header: transport protein Chain: B: PDB Molecule: glutamate receptor 2; PDBTitle: crystal structure of 1-(4-(1-pyrrolidinylcarbonyl)phenyl)-3-2 (trifluoromethyl)-4,5,6,7-tetrahydro-1h-indazole in complex with3 the ligand binding domain of the rat glua2 receptor and glutamate4 at 2.2a resolution.
						Fold: Periplasmic binding protein-like II

28	dlii5a_	Alignment	not modelled	100.0	18	Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
29	d1pb7a_	Alignment	not modelled	100.0	24	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
30	d1s50a1	Alignment	not modelled	99.9	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
31	c2ppyB_	Alignment	not modelled	99.9	21	PDB header: transport protein Chain: B: PDB Molecule: ionotropic glutamate receptor bacterial homologue; PDBTitle: crystal structure of the glur0 ligand-binding core from nostoc2 punctiforme in complex with (l)-glutamate
32	c1yaeB_	Alignment	not modelled	99.9	20	PDB header: membrane protein Chain: B: PDB Molecule: glutamate receptor, ionotropic kainate 2; PDBTitle: structure of the kainate receptor subunit glur6 agonist binding domain2 complexed with domoic acid
33	c2rc9A_	Alignment	not modelled	99.9	20	PDB header: membrane protein Chain: A: PDB Molecule: glutamate [nmda] receptor subunit 3a; PDBTitle: crystal structure of the nr3a ligand binding core complex with acpc at2 1.96 angstrom resolution
34	c2v3tA_	Alignment	not modelled	99.9	20	PDB header: receptor Chain: A: PDB Molecule: glutamate receptor delta-2 subunit synonym PDBTitle: structure of the ligand-binding core of the ionotropic2 glutamate receptor-like glurdelta2 in the apo form
35	d2f34a1	Alignment	not modelled	99.9	20	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
36	c3kg2A_	Alignment	not modelled	99.8	27	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: glutamate receptor 2; PDBTitle: ampa subtype ionotropic glutamate receptor in complex with competitive2 antagonist zk 200775
37	c3n5lA_	Alignment	not modelled	98.3	10	PDB header: transport protein Chain: A: PDB Molecule: binding protein component of abc phosphonate transporter; PDBTitle: crystal structure of a binding protein component of abc phosphonate2 transporter (pa3383) from pseudomonas aeruginosa at 1.97 a resolution
38	c3e4rA_	Alignment	not modelled	97.7	13	PDB header: transport protein Chain: A: PDB Molecule: nitrate transport protein; PDBTitle: crystal structure of the alkanesulfonate binding protein2 (ssua) from the phytopathogenic bacteria xanthomonas3 axonopodis pv. citri bound to hepes
39	d1xs5a_	Alignment	not modelled	97.7	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
40	c2x26A_	Alignment	not modelled	97.7	18	PDB header: transport protein Chain: A: PDB Molecule: periplasmic aliphatic sulphonates-binding protein; PDBTitle: crystal structure of the periplasmic aliphatic sulphonate2 binding protein ssua from escherichia coli
41	c3k2dA_	Alignment	not modelled	97.5	13	PDB header: immune system Chain: A: PDB Molecule: abc-type metal ion transport system, periplasmic component; PDBTitle: crystal structure of immunogenic lipoprotein a from vibrio vulnificus
42	c3tqwA_	Alignment	not modelled	97.3	15	PDB header: transport protein Chain: A: PDB Molecule: methionine-binding protein; PDBTitle: structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
43	c3l6gA_	Alignment	not modelled	97.2	11	PDB header: glycine betaine-binding protein Chain: A: PDB Molecule: betaine abc transporter permease and substrate binding PDBTitle: crystal structure of lactococcal opuac in its open conformation
44	c2x7pA_	Alignment	not modelled	97.0	11	PDB header: unknown function Chain: A: PDB Molecule: possible thiamine biosynthesis enzyme; PDBTitle: the conserved candida albicans ca3427 gene product defines a new2 family of proteins exhibiting the generic periplasmic binding3 protein structural fold
45	c3gxaA_	Alignment	not modelled	96.8	15	PDB header: protein binding Chain: A: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946
46	c3uifA_	Alignment	not modelled	96.8	17	PDB header: transport protein Chain: A: PDB Molecule: sulfonate abc transporter, periplasmic sulfonate-binding PDBTitle: crystal structure of putative sulfonate abc transporter, periplasmic2 sulfonate-binding protein ssua from methylobacillus flagellatus kt
47	c3ix1B_	Alignment	not modelled	96.5	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding PDBTitle: periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
48	c3ix1A_	Alignment	not modelled	96.5	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding PDBTitle: periplasmic n-formyl-4-amino-5-aminomethyl-2-methylpyrimidine binding2 protein from bacillus halodurans
49	c3ir1F_	Alignment	not modelled	96.5	15	PDB header: protein binding Chain: F: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
50	c3qslA_	Alignment	not modelled	95.8	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of cae31940 from bordetella bronchiseptica rb50
						PDB header: unknown function

51	c3un6A_	Alignment	not modelled	95.7	12	Chain: A: PDB Molecule: hypothetical protein saouhsc_00137; PDBTitle: 2.0 angstrom crystal structure of ligand binding component of abc-type2 import system from staphylococcus aureus with zinc bound
52	c3tmgA_	Alignment	not modelled	95.1	14	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine, l-proline abc transporter, PDBTitle: crystal structure of glycine betaine, l-proline abc transporter,2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi
53	c2g29A_	Alignment	not modelled	94.7	15	PDB header: transport protein Chain: A: PDB Molecule: nitrate transport protein nrtA; PDBTitle: crystal structure of the periplasmic nitrate-binding2 protein nrtA from synechocystis pcc 6803
54	d1zbma1	Alignment	not modelled	94.5	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
55	c3ho7A_	Alignment	not modelled	93.8	16	PDB header: transcription Chain: A: PDB Molecule: oxyr; PDBTitle: crystal structure of oxyr from porphyromonas gingivalis
56	d1p99a_	Alignment	not modelled	93.8	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
57	c1p99A_	Alignment	not modelled	93.8	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pg110; PDBTitle: 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
58	c2ql3G_	Alignment	not modelled	92.3	11	PDB header: transcription Chain: G: PDB Molecule: probable transcriptional regulator, lysr family protein; PDBTitle: crystal structure of the c-terminal domain of a probable lysr family2 transcriptional regulator from rhodococcus sp. rha1
59	c2i4cA_	Alignment	not modelled	92.1	13	PDB header: transport protein Chain: A: PDB Molecule: bicarbonate transporter; PDBTitle: crystal structure of bicarbonate transport protein cmpA from2 synechocystis sp. pcc 6803 in complex with bicarbonate and calcium
60	c3n6uA_	Alignment	not modelled	91.6	9	PDB header: transcription regulator Chain: A: PDB Molecule: lysr type regulator of tsambcd; PDBTitle: effector binding domain of tsar in complex with its inducer p-2 toluenesulfonate
61	d1i6aa_	Alignment	not modelled	90.4	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
62	d1al3a_	Alignment	not modelled	90.4	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
63	c1al3A_	Alignment	not modelled	90.4	12	PDB header: transcription regulation Chain: A: PDB Molecule: cys regulon transcriptional activator cysb; PDBTitle: cofactor binding fragment of cysb from klebsiella aerogenes
64	c3lr1A_	Alignment	not modelled	88.1	12	PDB header: transport protein Chain: A: PDB Molecule: tungstate abc transporter, periplasmic tungstate- PDBTitle: the crystal structure of the tungstate abc transporter from2 geobacter sulfurreducens
65	c3jv9B_	Alignment	not modelled	88.0	12	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: the structure of a reduced form of oxyr from n. meningitidis
66	d2czla1	Alignment	not modelled	83.5	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
67	c3muqB_	Alignment	not modelled	82.4	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved functionally unknown protein from2 vibrio parahaemolyticus rimd 2210633
68	c2rejA_	Alignment	not modelled	81.5	18	PDB header: choline-binding protein Chain: A: PDB Molecule: putative glycine betaine abc transporter protein; PDBTitle: abc-transporter choline binding protein in unliganded semi-2 closed conformation
69	c3fd3A_	Alignment	not modelled	78.8	7	PDB header: transcription regulator Chain: A: PDB Molecule: chromosome replication initiation inhibitor protein; PDBTitle: structure of the c-terminal domains of a lysr family protein from2 agrobacterium tumefaciens str. c58.
70	c3hn0A_	Alignment	not modelled	77.7	12	PDB header: transport protein Chain: A: PDB Molecule: nitrate transport protein; PDBTitle: crystal structure of an abc transporter (bdi_1369) from2 parabacteroides distasonis at 1.75 a resolution
71	c2de4B_	Alignment	not modelled	76.1	16	PDB header: hydrolase Chain: B: PDB Molecule: dibenzothiophene desulfurization enzyme b; PDBTitle: crystal structure of dszb c27s mutant in complex with biphenyl-2-2 sulfinic acid
72	d1amfa_	Alignment	not modelled	74.8	13	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
73	c3fj7A_	Alignment	not modelled	68.7	16	PDB header: protein binding Chain: A: PDB Molecule: major antigenic peptide peb3; PDBTitle: crystal structure of l-phospholactate bound peb3
74	c3chgB_	Alignment	not modelled	68.4	12	PDB header: ligand binding protein Chain: B: PDB Molecule: glycine betaine-binding protein; PDBTitle: the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa

75	d2nxoa1	Alignment	not modelled	63.4	10	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
76	d2esna2	Alignment	not modelled	62.9	10	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
77	c2vd3B	Alignment	not modelled	60.1	12	PDB header: transferase Chain: B: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum
78	c2uyeA	Alignment	not modelled	58.0	7	PDB header: transcription Chain: A: PDB Molecule: regulatory protein; PDBTitle: double mutant y110s,f111v dntf from burkholderia sp. strain2 dntf in complex with thiocyanate
79	c2h5yC	Alignment	not modelled	54.1	9	PDB header: metal transport Chain: C: PDB Molecule: molybdate-binding periplasmic protein; PDBTitle: crystallographic structure of the molybdate-binding protein of2 xanthomonas citri at 1.7 ang resolution bound to molybdate
80	d1atga	Alignment	not modelled	54.0	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
81	c3b50A	Alignment	not modelled	53.8	16	PDB header: transport protein Chain: A: PDB Molecule: sialic acid-binding periplasmic protein siap; PDBTitle: structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
82	c2f78A	Alignment	not modelled	52.0	10	PDB header: gene regulation Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: benm effector binding domain with its effector benzoate
83	c3hhfB	Alignment	not modelled	39.9	10	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: structure of crga regulatory domain, a lysr-type transcriptional2 regulator from neisseria meningitidis.
84	c2h9qC	Alignment	not modelled	38.3	10	PDB header: transcription Chain: C: PDB Molecule: hth-type transcriptional regulator catm; PDBTitle: crystal structure of the effector binding domain of a catm2 variant (r156h)
85	d2ozza1	Alignment	not modelled	38.0	9	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
86	c2dvzA	Alignment	not modelled	37.9	14	PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: structure of a periplasmic transporter
87	d1ixca2	Alignment	not modelled	37.6	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
88	c2f7cA	Alignment	not modelled	37.3	10	PDB header: gene regulation Chain: A: PDB Molecule: hth-type transcriptional regulator catm; PDBTitle: catm effector binding domain with its effector cis,cis-muconate
89	c2f5xC	Alignment	not modelled	33.7	10	PDB header: transport protein Chain: C: PDB Molecule: bugd; PDBTitle: structure of periplasmic binding protein bugd
90	c3kn3C	Alignment	not modelled	32.5	13	PDB header: transcription Chain: C: PDB Molecule: putative periplasmic protein; PDBTitle: crystal structure of lysr substrate binding domain (25-263) of2 putative periplasmic protein from wolinnella succinogenes
91	d1us5a	Alignment	not modelled	29.3	21	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
92	d2fyia1	Alignment	not modelled	28.9	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
93	c3fxbB	Alignment	not modelled	27.6	14	PDB header: transport protein Chain: B: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of the ectoine-binding protein ueha
94	c2hxrA	Alignment	not modelled	26.6	10	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator cynr; PDBTitle: structure of the ligand binding domain of e. coli cynr, a2 transcriptional regulator controlling cyanate metabolism
95	c2h9bB	Alignment	not modelled	26.2	11	PDB header: transcription Chain: B: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of the effector binding domain of a benm variant2 (benm r156h/t157s)
96	c1jvnB	Alignment	not modelled	25.8	11	PDB header: transferase Chain: B: PDB Molecule: bifunctional histidine biosynthesis protein hishf; PDBTitle: crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
97	c1twyG	Alignment	not modelled	24.2	12	PDB header: structural genomics, unknown function Chain: G: PDB Molecule: abc transporter, periplasmic substrate-binding protein; PDBTitle: crystal structure of an abc-type phosphate transport receptor from2 vibrio cholerae
98	d1twya	Alignment	not modelled	24.2	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
99	d2o38a1	Alignment	not modelled	23.6	30	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
						PDB header: structural genomics, unknown function

100	c2o38A_	Alignment	not modelled	23.6	30	Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
101	c3kosA_	Alignment	not modelled	22.2	8	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator ampr; PDBTitle: structure of the ampr effector binding domain from citrobacter2 freundii
102	c2qpqC_	Alignment	not modelled	21.8	12	PDB header: transport protein Chain: C: PDB Molecule: protein bug27; PDBTitle: structure of bug27 from bordetella pertussis
103	c3mz1D_	Alignment	not modelled	20.8	6	PDB header: transcription regulator Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: the crystal structure of a possible transcription regulator protein2 from sinorhizobium meliloti 1021