
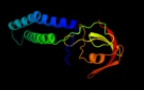




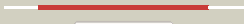
















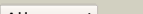



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2p4vA_	 Alignment		100.0	99	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor greb; PDBTitle: crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
2	c1grjA_	 Alignment		100.0	34	PDB header: transcription regulation Chain: A: PDB Molecule: greA protein; PDBTitle: greA transcript cleavage factor from escherichia coli
3	c2etnA_	 Alignment		100.0	27	PDB header: transcription Chain: A: PDB Molecule: anti-cleavage anti-greA transcription factor PDBTitle: crystal structure of thermus aquaticus gfh1
4	c3bmbB_	 Alignment		100.0	20	PDB header: rna binding protein Chain: B: PDB Molecule: regulator of nucleoside diphosphate kinase; PDBTitle: crystal structure of a new rna polymerase interacting2 protein
5	c2pn0D_	 Alignment		100.0	24	PDB header: transcription Chain: D: PDB Molecule: prokaryotic transcription elongation factor PDBTitle: prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea
6	d1grja1	 Alignment		99.9	29	Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain
7	d2f23a1	 Alignment		99.9	26	Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain
8	d2f23a2	 Alignment		99.9	32	Fold: FKBP-like Superfamily: FKBP-like Family: GreA transcript cleavage factor, C-terminal domain
9	d2etna2	 Alignment		99.8	33	Fold: FKBP-like Superfamily: FKBP-like Family: GreA transcript cleavage factor, C-terminal domain
10	d1grja2	 Alignment		99.8	39	Fold: FKBP-like Superfamily: FKBP-like Family: GreA transcript cleavage factor, C-terminal domain
11	c3gtyX_	 Alignment		95.5	17	PDB header: chaperone/ribosomal protein Chain: X: PDB Molecule: trigger factor; PDBTitle: promiscuous substrate recognition in folding and assembly activities2 of the trigger factor chaperone

12	c1w26B_	Alignment		93.2	16	PDB header: chaperone Chain: B: PDB Molecule: trigger factor; PDBTitle: trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
13	d1w26a3	Alignment		91.1	14	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
14	d1t11a3	Alignment		89.9	18	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
15	c1t11A_	Alignment		83.6	16	PDB header: chaperone Chain: A: PDB Molecule: trigger factor; PDBTitle: trigger factor
16	c3o0pA_	Alignment		68.8	26	PDB header: transferase , hydrolase Chain: A: PDB Molecule: sortase family protein; PDBTitle: pilus-related sortase c of group b streptococcus
17	d1ndha1	Alignment		68.5	14	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
18	c1cz5A_	Alignment		67.9	22	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)
19	c2kw8A_	Alignment		67.7	19	PDB header: protein binding Chain: A: PDB Molecule: lpxtg-site transpeptidase family protein; PDBTitle: solution structure of bacillus anthracis sortase a (srta)2 transpeptidase
20	d1t2wa_	Alignment		66.5	19	Fold: Sortase Superfamily: Sortase Family: Sortase
21	d1krha1	Alignment	not modelled	66.1	15	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
22	d1umka1	Alignment	not modelled	65.9	16	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
23	d2cnda1	Alignment	not modelled	65.8	14	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
24	d1qx4a1	Alignment	not modelled	65.1	16	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
25	c3re9A_	Alignment	not modelled	62.2	23	PDB header: transferase Chain: A: PDB Molecule: sortase-like protein; PDBTitle: crystal structure of sortasec1 from streptococcus suis
26	c3fn5B_	Alignment	not modelled	61.5	13	PDB header: hydrolase Chain: B: PDB Molecule: sortase a; PDBTitle: crystal structure of sortase a (spy1154) from streptococcus2 pyogenes serotype m1 strain sf370
27	d2piaa1	Alignment	not modelled	60.8	14	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
28	c3g66A_	Alignment	not modelled	60.5	26	PDB header: transferase Chain: A: PDB Molecule: sortase c; PDBTitle: the crystal structure of streptococcus pneumoniae sortase c2 provides novel insights into catalysis as well as pilin3 substrate specificity
						PDB header: hydrolase

29	c2xwgA	Alignment	not modelled	59.9	32	Chain: A: PDB Molecule: sortase; PDBTitle: crystal structure of sortase c-1 from actinomyces oris (formerly2 actinomyces naeslundii)
30	c2w1kB	Alignment	not modelled	59.2	19	PDB header: transferase Chain: B: PDB Molecule: putative sortase; PDBTitle: crystal structure of sortase c-3 (srtc-3) from2 streptococcus pneumoniae
31	d1fdra1	Alignment	not modelled	52.5	19	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
32	c3rccl	Alignment	not modelled	52.4	16	PDB header: hydrolase Chain: I: PDB Molecule: sortase srta; PDBTitle: crystal structure of the streptococcus agalactiae sortase a
33	d1e32a3	Alignment	not modelled	50.8	15	Fold: Cdc48 domain 2-like Superfamily: Cdc48 domain 2-like Family: Cdc48 domain 2-like
34	d1l1pa	Alignment	not modelled	49.9	5	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
35	c1zeqX	Alignment	not modelled	49.4	13	PDB header: metal binding protein Chain: X: PDB Molecule: cation efflux system protein cusf; PDBTitle: 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
36	c2kfwA	Alignment	not modelled	47.8	40	PDB header: isomerase Chain: A: PDB Molecule: fkbp-type peptidyl-prolyl cis-trans isomerase PDBTitle: solution structure of full-length slyd from e.coli
37	c3rbjB	Alignment	not modelled	47.5	29	PDB header: hydrolase Chain: B: PDB Molecule: sortase family protein; PDBTitle: crystal structure of the lid-mutant of streptococcus agalactiae2 sortase c1
38	c2pjhB	Alignment	not modelled	44.8	19	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: strctural model of the p97 n domain- npl4 ubd complex
39	c2w1jB	Alignment	not modelled	42.8	26	PDB header: transferase Chain: B: PDB Molecule: putative sortase; PDBTitle: crystal structure of sortase c-1 (srtc-1) from2 streptococcus pneumoniae
40	c2dq0A	Alignment	not modelled	41.4	28	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of seryl-trna synthetase from pyrococcus2 horikoshii complexed with a seryl-adenylate analog
41	c2k8iA	Alignment	not modelled	39.8	38	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: solution structure of e.coli slyd
42	c2l66B	Alignment	not modelled	39.2	17	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, abrb family; PDBTitle: the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
43	c3cgnA	Alignment	not modelled	38.8	22	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of thermophilic slyd
44	c3pr9A	Alignment	not modelled	38.7	25	PDB header: chaperone Chain: A: PDB Molecule: fkbp-type peptidyl-prolyl cis-trans isomerase; PDBTitle: structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
45	c3shuB	Alignment	not modelled	38.3	22	PDB header: cell adhesion Chain: B: PDB Molecule: tight junction protein zo-1; PDBTitle: crystal structure of zo-1 pdz3
46	d1hxva	Alignment	not modelled	38.2	11	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
47	c1hxvA	Alignment	not modelled	38.2	11	PDB header: chaperone Chain: A: PDB Molecule: trigger factor; PDBTitle: ppiase domain of the mycoplasma genitalium trigger factor
48	c2kr7A	Alignment	not modelled	37.4	26	PDB header: isomerase Chain: A: PDB Molecule: fkbp-type peptidyl-prolyl cis-trans isomerase slyd; PDBTitle: solution structure of helicobacter pylori slyd
49	c2l55A	Alignment	not modelled	35.8	7	PDB header: metal binding protein Chain: A: PDB Molecule: silb,silver efflux protein, mfp component of the three PDBTitle: solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
50	d1qfja1	Alignment	not modelled	32.1	20	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
51	c3g5oA	Alignment	not modelled	32.0	16	PDB header: toxin/antitoxin Chain: A: PDB Molecule: uncharacterized protein rv2865; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
52	c3u5cG	Alignment	not modelled	31.4	18	PDB header: ribosome Chain: G: PDB Molecule: 40s ribosomal protein s6-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution
53	c3prdA	Alignment	not modelled	29.6	25	PDB header: chaperone, isomerase Chain: A: PDB Molecule: fkbp-type peptidyl-prolyl cis-trans isomerase; PDBTitle: structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
54	d1kwaa	Alignment	not modelled	29.4	13	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain

55	c2gpiA	 Alignment	not modelled	29.3	17	PDB header: fad-binding protein Chain: A: PDB Molecule: siderophore-interacting protein; PDBTitle: crystal structure of a siderophore-interacting protein (spu3cn32_0076)2 from shewanella putrefaciens cn-32 at 2.20 a resolution
56	d2iv2x1	 Alignment	not modelled	29.0	14	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
57	c2z17A	 Alignment	not modelled	28.4	35	PDB header: protein binding Chain: A: PDB Molecule: pleckstrin homology sec7 and coiled-coil domains- PDBTitle: crystal struncture of pdz domain from human pleckstrin2 homology, sec7
58	c3shwA	 Alignment	not modelled	28.3	27	PDB header: cell adhesion Chain: A: PDB Molecule: tight junction protein zo-1; PDBTitle: crystal structure of zo-1 pdz3-sh3-guk supramodule complex with2 connexin-45 peptide
59	c2xznY	 Alignment	not modelled	27.9	18	PDB header: ribosome Chain: Y: PDB Molecule: rps6e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
60	d1gvha2	 Alignment	not modelled	27.8	19	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
61	c3k1rA	 Alignment	not modelled	27.5	13	PDB header: structural protein Chain: A: PDB Molecule: harmonin; PDBTitle: structure of harmonin npd21 in complex with the sam- pbm of2 sans
62	c1e0tD	 Alignment	not modelled	27.4	16	PDB header: phosphotransferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: r292d mutant of e. coli pyruvate kinase
63	d2gp4a1	 Alignment	not modelled	27.3	26	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: IlvD/EDD C-terminal domain-like
64	c2eehA	 Alignment	not modelled	27.2	24	PDB header: metal binding protein Chain: A: PDB Molecule: pdz domain-containing protein 7; PDBTitle: solution structure of first pdz domain of pdz domain2 containing protein 7
65	d1pina2	 Alignment	not modelled	26.9	18	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
66	c3lssA	 Alignment	not modelled	26.6	7	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: trypanosoma brucei seryl-trna synthetase in complex with atp
67	d1dm9a	 Alignment	not modelled	26.2	23	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Heat shock protein 15 kD
68	c1dm9A	 Alignment	not modelled	26.2	23	PDB header: structural genomics Chain: A: PDB Molecule: hypothetical 15.5 kd protein in mrca-pcka PDBTitle: heat shock protein 15 kd
69	d1ix5a	 Alignment	not modelled	26.1	33	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
70	d2jioa1	 Alignment	not modelled	26.0	16	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
71	c2krqA	 Alignment	not modelled	24.5	11	PDB header: signaling protein Chain: A: PDB Molecule: na(+)/h(+) exchange regulatory cofactor nhe-rf1; PDBTitle: solution structure of human sodium/ hydrogen exchange2 regulatory factor 1(150-358)
72	c1w9qb	 Alignment	not modelled	24.4	18	PDB header: cell adhesion Chain: B: PDB Molecule: syntenin 1; PDBTitle: crystal structure of the pdz tandem of human syntenin in2 complex with tnefap peptide
73	d1tvca1	 Alignment	not modelled	24.3	17	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
74	d1vlfm1	 Alignment	not modelled	24.1	16	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
75	d1st6a4	 Alignment	not modelled	23.4	22	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
76	d1h0ha1	 Alignment	not modelled	22.7	19	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
77	c2gzvA	Alignment	not modelled	22.1	17	PDB header: signaling protein Chain: A: PDB Molecule: prkca-binding protein; PDBTitle: the cystal structure of the pdz domain of human pick1 (casp target)
78	d1ep3b1	Alignment	not modelled	21.7	20	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
79	d1nbwa1	Alignment	not modelled	21.4	41	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Swiveling domain of dehydratase reactivase alpha subunit Family: Swiveling domain of dehydratase reactivase alpha subunit
80	c2nivA	Alignment	not modelled	21.1	13	PDB header: membrane protein Chain: A: PDB Molecule: 55 kda erythrocyte membrane protein;

80	c2ejyA	Alignment	not modelled	21.1	15	PDBTitle: solution structure of the p55 pdz t85c domain complexed2 with the glycophorin c f127c peptide
81	d1st6a3	Alignment	not modelled	20.0	23	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
82	d2a6qa1	Alignment	not modelled	19.5	18	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
83	d1logya1	Alignment	not modelled	19.3	17	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
84	c3e0vB	Alignment	not modelled	18.5	21	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
85	d2d0oa1	Alignment	not modelled	18.4	50	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Swiveling domain of dehydratase reactivase alpha subunit Family: Swiveling domain of dehydratase reactivase alpha subunit
86	d1wi2a	Alignment	not modelled	18.0	24	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
87	d1gawa1	Alignment	not modelled	17.9	28	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
88	d1kqfa1	Alignment	not modelled	17.7	22	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
89	c2ki8A	Alignment	not modelled	17.3	21	PDB header: oxidoreductase Chain: A: PDB Molecule: tungsten formylmethanofuran dehydrogenase, PDBTitle: solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7
90	d2bmwa1	Alignment	not modelled	17.2	25	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
91	d2f5ya1	Alignment	not modelled	17.1	23	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
92	d1seta1	Alignment	not modelled	17.0	22	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Seryl-tRNA synthetase (SerRS)
93	d1eu1a1	Alignment	not modelled	16.7	21	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
94	c2piaA	Alignment	not modelled	16.5	20	PDB header: reductase Chain: A: PDB Molecule: phthalate dioxygenase reductase; PDBTitle: phthalate dioxygenase reductase: a modular structure for2 electron transfer from pyridine nucleotides to [2fe-2s]
95	d1vloa1	Alignment	not modelled	16.5	20	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
96	c2gp4A	Alignment	not modelled	16.1	26	PDB header: lyase Chain: A: PDB Molecule: 6-phosphogluconate dehydratase; PDBTitle: structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
97	d1qwza	Alignment	not modelled	15.8	10	Fold: Sortase Superfamily: Sortase Family: Sortase
98	c2g16A	Alignment	not modelled	15.7	28	PDB header: luminescent protein Chain: A: PDB Molecule: green fluorescent protein; PDBTitle: structure of s65a y66s gfp variant after backbone2 fragmentation
99	c2fug4	Alignment	not modelled	15.6	12	PDB header: oxidoreductase Chain: 4: PDB Molecule: nadh-quinone oxidoreductase chain 4; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus