



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 06:59 AM UTC

PDB ID : 3KYH / pdb_00003kyh
Title : Saccharomyces cerevisiae Cet1-Ceg1 capping apparatus
Authors : Lima, C.D.
Deposited on : 2009-12-06
Resolution : 3.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

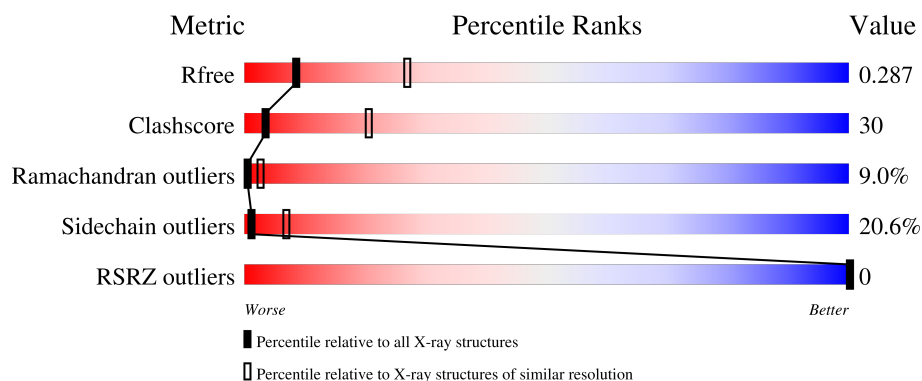
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	310	
1	B	310	
2	C	461	
2	D	461	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10696 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called mRNA-capping enzyme subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	0	0
			2212	1407	375	426	4			
1	B	276	Total	C	N	O	S	0	0	0
			2212	1407	375	426	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	240	MET	-	initiating methionine	UNP O13297
B	240	MET	-	initiating methionine	UNP O13297

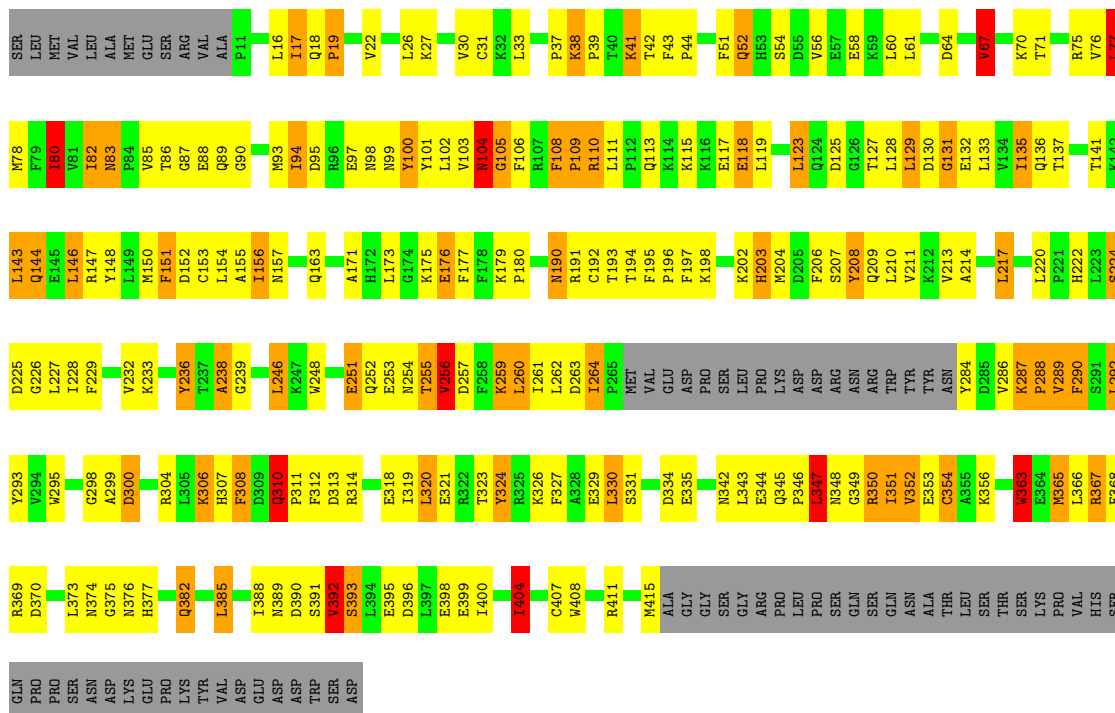
- Molecule 2 is a protein called mRNA-capping enzyme subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	387	Total	C	N	O	S	0	0	0
			3136	2007	528	583	18			
2	D	387	Total	C	N	O	S	0	0	0
			3136	2007	528	583	18			

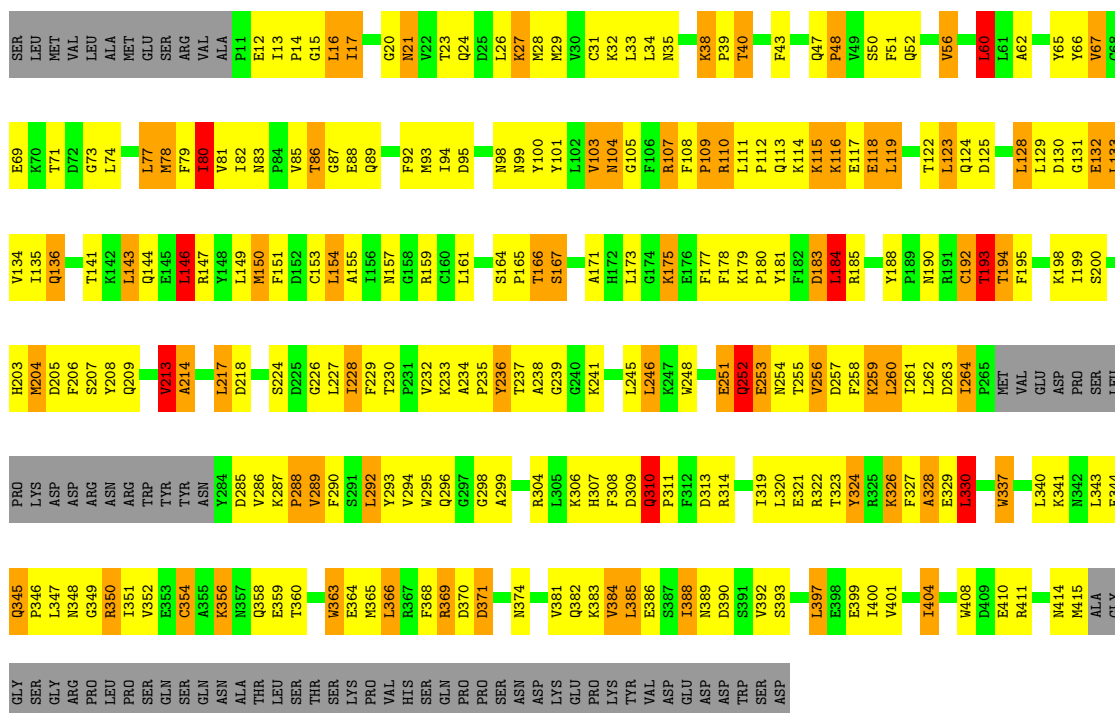
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	SER	-	expression tag	UNP Q01159
C	0	LEU	-	expression tag	UNP Q01159
D	-1	SER	-	expression tag	UNP Q01159
D	0	LEU	-	expression tag	UNP Q01159

Chain C: 35% 34% 12% • 16%



Chain D: 30% 38% 15% 1% 16%



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	165.99Å 165.99Å 172.35Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.98 – 3.00 19.98 – 3.00	Depositor EDS
% Data completeness (in resolution range)	95.2 (19.98-3.00) 95.3 (19.98-3.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 2.98Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.249 , 0.298 0.244 , 0.287	Depositor DCC
R_{free} test set	2580 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	63.7	Xtriage
Anisotropy	0.505	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 29.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.458 for h,-h-k,-l	Xtriage
Reported twinning fraction	0.514 for H, K, L 0.486 for h+k,-k,-l	Depositor
Outliers	0 of 50992 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	10696	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.12	1/2256 (0.0%)	1.59	26/3058 (0.9%)
1	B	1.19	3/2256 (0.1%)	1.63	31/3058 (1.0%)
2	C	0.81	0/3207	1.41	38/4334 (0.9%)
2	D	0.79	0/3207	1.37	30/4334 (0.7%)
All	All	0.96	4/10926 (0.0%)	1.49	125/14784 (0.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
2	C	0	1
All	All	0	3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	275	ILE	CA-C	6.21	1.59	1.52
1	B	324	PRO	CA-C	5.96	1.57	1.52
1	B	312	VAL	CA-CB	5.43	1.61	1.54
1	B	334	GLU	CA-C	5.12	1.58	1.52

The worst 5 of 125 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	426	VAL	N-CA-C	10.16	122.81	107.77
2	C	131	GLY	N-CA-C	9.94	125.65	111.14
1	B	441	PRO	N-CA-C	9.03	121.72	110.70
1	A	274	ASN	CB-CA-C	8.88	118.63	109.83
1	A	246	ILE	N-CA-C	8.51	119.32	110.72

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	465	ASP	Peptide
1	B	465	ASP	Peptide
2	C	310	GLN	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2212	0	2218	159	0
1	B	2212	0	2218	150	0
2	C	3136	0	3126	157	0
2	D	3136	0	3126	199	0
All	All	10696	0	10688	638	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 30.

The worst 5 of 638 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:446:LYS:HA	1:B:446:LYS:NZ	1.64	1.13
2:D:109:PRO:HD2	2:D:180:PRO:HB2	1.24	1.13
1:B:497:ILE:HD11	1:B:519:LEU:HD11	1.32	1.12
2:C:390:ASP:O	2:C:392:VAL:HG23	1.55	1.07
1:A:499:THR:HG22	1:A:503:LEU:HD12	1.37	1.07

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	268/310 (86%)	195 (73%)	46 (17%)	27 (10%)	0	2
1	B	268/310 (86%)	192 (72%)	48 (18%)	28 (10%)	0	2
2	C	383/461 (83%)	287 (75%)	68 (18%)	28 (7%)	1	4
2	D	383/461 (83%)	280 (73%)	69 (18%)	34 (9%)	0	3
All	All	1302/1542 (84%)	954 (73%)	231 (18%)	117 (9%)	0	3

5 of 117 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	279	ASP
1	A	286	GLN
1	A	336	ASP
1	A	342	ASN
1	B	279	ASP

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	254/290 (88%)	200 (79%)	54 (21%)	1	6
1	B	254/290 (88%)	206 (81%)	48 (19%)	1	9
2	C	352/421 (84%)	278 (79%)	74 (21%)	1	6
2	D	352/421 (84%)	278 (79%)	74 (21%)	1	6
All	All	1212/1422 (85%)	962 (79%)	250 (21%)	1	7

5 of 250 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	103	VAL
2	D	252	GLN
2	C	256	VAL
2	D	237	THR
2	D	350	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	382	GLN
2	D	163	GLN
2	D	21	ASN
2	D	98	ASN
2	D	339	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	276/310 (89%)	-1.27	0 100 100	24, 55, 112, 145	0
1	B	276/310 (89%)	-1.28	0 100 100	19, 53, 100, 156	0
2	C	387/461 (83%)	-1.20	0 100 100	46, 92, 123, 154	0
2	D	387/461 (83%)	-1.18	0 100 100	50, 91, 124, 155	0
All	All	1326/1542 (85%)	-1.22	0 100 100	19, 80, 121, 156	0

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.