



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 05:02 AM UTC

PDB ID : 5L3T / pdb_00005l3t
Title : Structure of the *Saccharomyces cerevisiae* TREX-2 complex
Authors : Stewart, M.; Aibara, S.
Deposited on : 2016-05-24
Resolution : 4.93 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

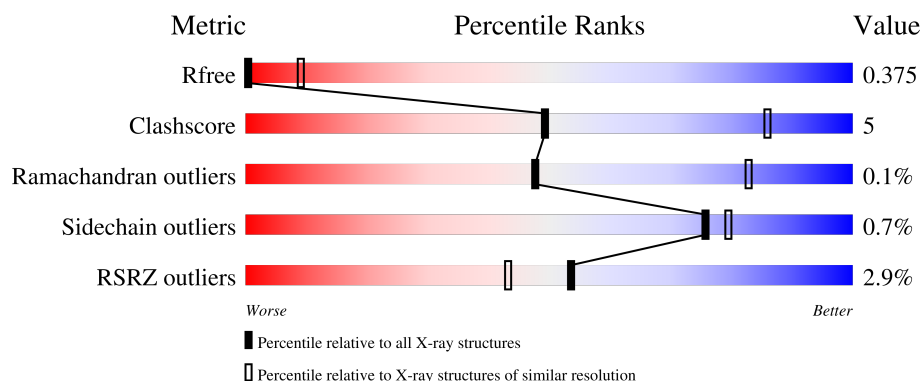
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.93 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	1008 (5.88-3.96)
Clashscore	190562	1020 (5.82-3.98)
Ramachandran outliers	187476	1125 (5.94-3.90)
Sidechain outliers	187428	1105 (5.94-3.90)
RSRZ outliers	180081	1003 (5.88-3.96)

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	1301	19% 77%
2	B	455	2% 88% 11%
3	C	89	2% 48% 6% 46%
4	D	24	71% 29%
4	E	24	92% 8%

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Mol	Chain	Length	Quality of chain
5	F	12	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: a green segment representing 83%, a yellow segment representing 8%, and a grey segment representing 8%. The percentages are labeled below the corresponding segments.

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6831 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 Nuclear mRNA export protein SAC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	294	Total	C	N	O	S	0	0	0
			2438	1564	420	441	13			

- Molecule 2 is a protein called Nuclear mRNA export protein THP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	455	Total	C	N	O	S	0	0	0
			3714	2392	645	659	18			

- Molecule 3 is a protein called 26S proteasome complex subunit SEM1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	48	Total	C	N	O	0	0	0
			419	258	64	97			

- Molecule 4 is a protein called Sac3polyAla.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	17	Total	C	N	O	0	0	0
			85	51	17	17			
4	E	24	Total	C	N	O	0	0	0
			120	72	24	24			

- Molecule 5 is a protein called Sac3polyAla.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	F	11	Total	C	N	O	0	0	0
			55	33	11	11			

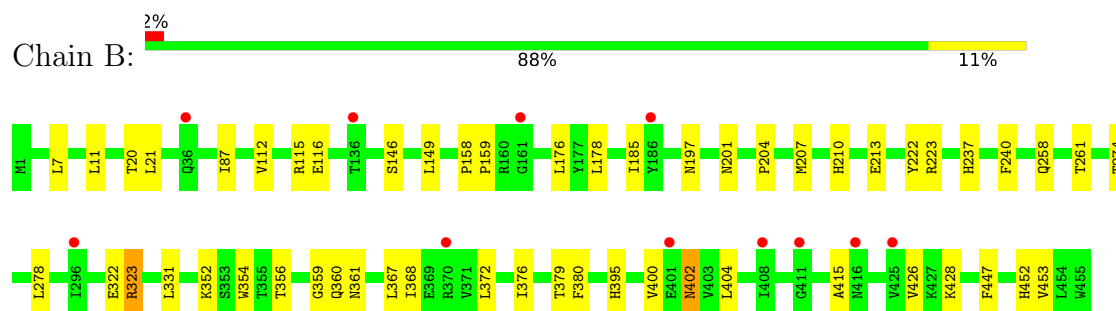
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Chain A:**

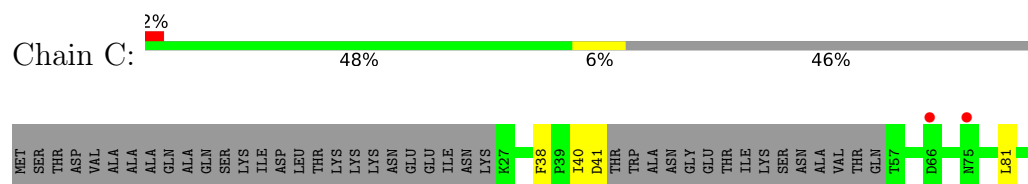
Amino Acid	Percentage (%)
MET	~1%
ASN	~2%
THR	~3%
LEU	~4%
PHE	~5%
GLY	~6%
SER	~7%
VAL	~8%
ASP	~9%
PRO	~10%
HIS	~11%
LYS	~12%
CYS	~13%
TRP	~14%
ARG	~15%
ILE	~16%
ALA	~17%
GLN	~18%

ASN	VAL	ALA	TYR	LEU	PHE
PRO	LEU	SER	ASP	SER	SER
VAL	PRO	PRO	LYS	GLU	VAL
THR	VAL	ARG	THR	THR	THR
PRO	SER	SER	LEU	SER	GLN
VAL	THR	LYS	ARG	ILE	LEU
LEU	PRO	LYS	GLN	LYS	LYS
ASP	SER	ARG	LYS	HIS	ILE
GLY	HIS	LYS	ARG	LEU	PHE
ALA	SER	LEU	SER	LEU	ASN
ASP	ASN	PRO	LEU	LYS	THR
GLN	ASN	ILE	ALA	LEU	GLY
GLY	ILE	LEU	GLY	ASN	VAL
LYS	GLU	LEU	ILE	ARG	THR
GLU	ALA	SER	HIS	ASN	ASN
ASP	ALA	THR	SER	SER	PRO
ILE	SER	THR	ARG	LYS	ASP
PRO	PHE	HIS	SER	ASN	PHE
SER	SER	SER	THR	THR	ASP
SER	GLY	SER	GLN	SER	ASP
ILE	ASN	GLN	LEU	LEU	LEU
LEU	ASN	PHE	GLN	VAL	GLU
GLU	THR	LYS	THR	ILE	MET
LEU	THR	THR	THR	GLU	LYS
LYS	ASP	PRO	LYS	ARG	LEU
ILE	ILE	ILE	ASP	ILE	LYS
LEU	GLN	ALA	ILE	ASP	ASP
ILE	GLN	SER	ASP	LEU	ASP
ASP	GLN	ARG	GLN	MET	GLY
SER	GLN	LEU	LYS	ASN	GLU
VAL	LEU	ASN	MET	LEU	GLY
LYS	ILE	THR	LYS	THR	LEU
LYS	GLU	LYS	LYS	THR	LEU
LYS	ASN	GLY	MET	GLU	LYS
VAL	GLN	SER	LEU	SER	LYS
ASN	LYS	SER	GLU	LEU	LEU
ASN	SER	THR	THR	PRO	ILE
ASP	THR	PRO	ASN	ASN	THR
	VAL	LEU	LYS	GLU	LEU
	THR	THR	TYR	ASP	ASN
	ASN	SER	GLN	LYS	THR
	VAL	HIS	GLN	LEU	ASN
	SER	ALA	ILE	GLU	CYS
	GLU	MET	ILE	ILE	PHE
	ILE	LYS	GLU	SER	SER
	LEU	ARG	ASN	HIS	LEU
	GLY	ASN	THR	THR	ILE
	ASN	ASN	TYR	VAL	ILE
	GLN	SER	ALA	THR	TYR
	GLU	ARG	HIS	LYS	TRP
	ILE	VAL	LEU	THR	GLU
	CYS	THR	GLU	THR	SER
	GLN	SER	SER	ALA	GLU
	THR	LEU	HIS	ARG	ASN
	PRO	HIS	ILE	GLY	ASN

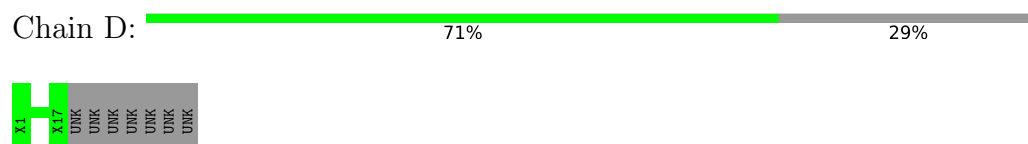
• Molecule 2: Nuclear mRNA export protein THP1



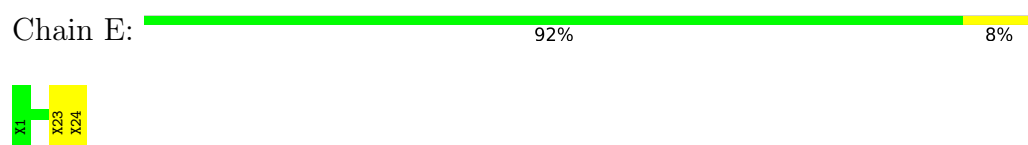
• Molecule 3: 26S proteasome complex subunit SEM1



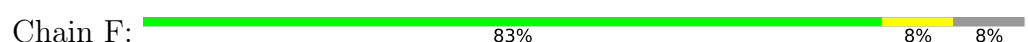
• Molecule 4: Sac3polyAla



• Molecule 4: Sac3polyAla



• Molecule 5: Sac3polyAla





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	78.17Å 84.09Å 165.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.08 – 4.93 47.08 – 4.93	Depositor EDS
% Data completeness (in resolution range)	57.1 (47.08-4.93) 50.8 (47.08-4.93)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.91 (at 4.85Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.338 , 0.370 0.339 , 0.375	Depositor DCC
R_{free} test set	174 reflections (3.24%)	wwPDB-VP
Wilson B-factor (Å ²)	68.5	Xtriage
Anisotropy	0.208	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 842.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.80	EDS
Total number of atoms	6831	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.08% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.15	0/2492	0.39	0/3368
2	B	0.16	0/3804	0.35	1/5168 (0.0%)
3	C	0.16	0/426	0.43	0/575
All	All	0.16	0/6722	0.37	1/9111 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	323	ARG	N-CA-C	6.14	117.98	111.28

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	2438	0	2449	38	2
2	B	3714	0	3754	32	1
3	C	419	0	355	4	0
4	D	85	0	19	0	0
4	E	120	0	26	1	0
5	F	55	0	13	1	0
All	All	6831	0	6616	72	2

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 5.

The worst 5 of 72 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:A:276:LEU:HB3	1:A:277:PRO:HD3	1.73	0.70
3:C:38:PHE:HE1	3:C:40:ILE:HD13	1.57	0.69
1:A:266:ASP:OD1	1:A:310:ARG:NH2	2.28	0.67
1:A:256:ARG:HG2	5:F:1:UNK:N	2.10	0.66
1:A:326:ASN:O	1:A:329:PHE:CZ	2.48	0.66

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:288:ARG:NH2	2:B:213:GLU:OE2[4_545]	2.11	0.09
1:A:271:ASN:OD1	1:A:486:ARG:NH2[3_654]	2.16	0.04

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	292/1301 (22%)	290 (99%)	1 (0%)	1 (0%)	36	71
2	B	453/455 (100%)	444 (98%)	9 (2%)	0	100	100
3	C	44/89 (49%)	44 (100%)	0	0	100	100
All	All	789/1845 (43%)	778 (99%)	10 (1%)	1 (0%)	48	83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	276	LEU

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	274/1212 (23%)	271 (99%)	3 (1%)	65	74
2	B	419/419 (100%)	417 (100%)	2 (0%)	81	82
3	C	47/81 (58%)	47 (100%)	0	100	100
All	All	740/1712 (43%)	735 (99%)	5 (1%)	76	79

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	276	LEU
1	A	374	ILE
1	A	475	ILE
2	B	323	ARG
2	B	402	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	242	GLN
2	B	386	GLN
3	C	88	ASN
2	B	420	GLN
2	B	452	HIS

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 [i](#)

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	294/1301 (22%)	0.11	10 (3%) 48 40	30, 76, 101, 134	0
2	B	455/455 (100%)	0.18	11 (2%) 59 49	44, 82, 117, 144	0
3	C	48/89 (53%)	0.37	2 (4%) 40 36	61, 93, 114, 123	0
4	D	0/24	-	-	-	-
4	E	0/24	-	-	-	-
5	F	0/12	-	-	-	-
All	All	797/1905 (41%)	0.17	23 (2%) 53 43	30, 80, 114, 144	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	401	GLU	5.2
3	C	75	ASN	4.6
2	B	411	GLY	4.4
2	B	161	GLY	3.7
1	A	401	CYS	3.0

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.