



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 01:32 PM UTC

PDB ID : 3N7N / pdb_00003n7n
Title : Structure of Csm1/Lrs4 complex
Authors : Corbett, K.D.; Harrison, S.C.
Deposited on : 2010-05-27
Resolution : 3.90 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

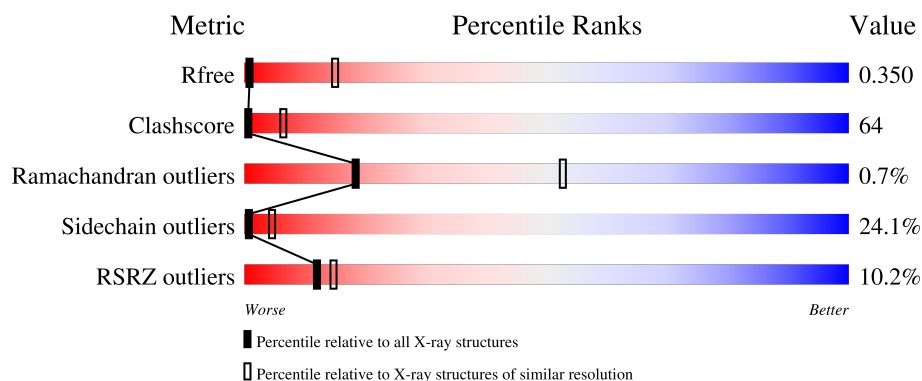
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.90 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	1270 (4.10-3.70)
Clashscore	190562	1034 (4.08-3.72)
Ramachandran outliers	187476	1251 (4.10-3.70)
Sidechain outliers	187428	1243 (4.10-3.70)
RSRZ outliers	180081	1269 (4.10-3.70)

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	190	13% 24% 46% 16% 14%
1	B	190	7% 25% 48% 13% 14%
1	C	190	8% 22% 44% 17% 17%
1	D	190	9% 21% 44% 18% 17%
2	E	95	% 28% 67%

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Mol	Chain	Length	Quality of chain
2	F	95	%21%11%68%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5496 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 Monopolin complex subunit CSM1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	163	Total	C	N	O	S	0	0	0
			1313	840	208	263	2			
1	B	164	Total	C	N	O	S	0	0	0
			1326	847	212	265	2			
1	C	158	Total	C	N	O	S	0	0	0
			1271	810	203	256	2			
1	D	158	Total	C	N	O	S	0	0	0
			1281	821	202	256	2			

- Molecule 2 is a protein called Monopolin complex subunit LRS4.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	31	Total	C	N	O	0	0	0
			155	93	31	31			
2	F	30	Total	C	N	O	0	0	0
			150	90	30	30			

There are 14 discrepancies between the modelled and reference sequences:

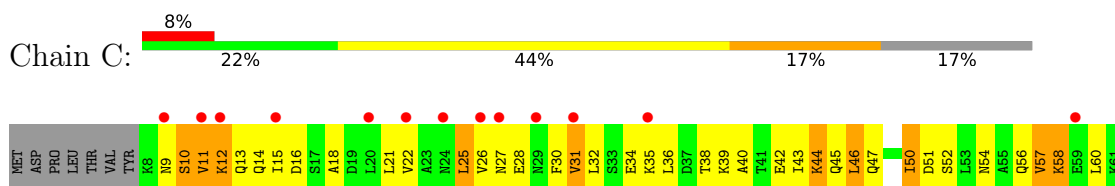
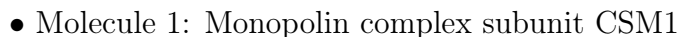
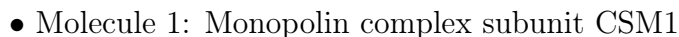
Chain	Residue	Modelled	Actual	Comment	Reference
E	?	-	LEU	deletion	UNP Q04087
E	?	-	ASN	deletion	UNP Q04087
E	?	-	ASN	deletion	UNP Q04087
E	?	-	ASN	deletion	UNP Q04087
E	?	-	LYS	deletion	UNP Q04087
E	?	-	GLY	deletion	UNP Q04087
E	?	-	ASP	deletion	UNP Q04087
F	?	-	LEU	deletion	UNP Q04087
F	?	-	ASN	deletion	UNP Q04087
F	?	-	ASN	deletion	UNP Q04087
F	?	-	ASN	deletion	UNP Q04087
F	?	-	LYS	deletion	UNP Q04087

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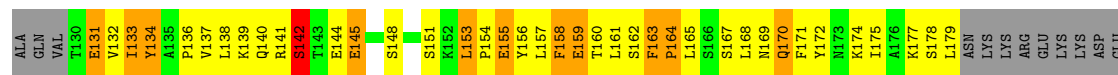
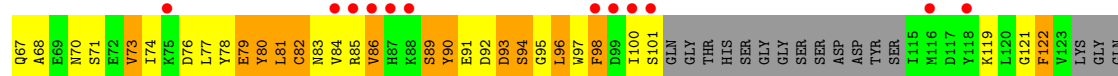
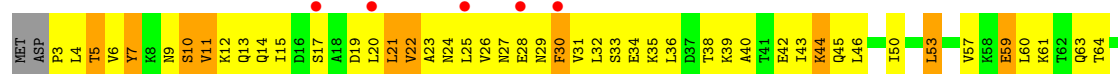
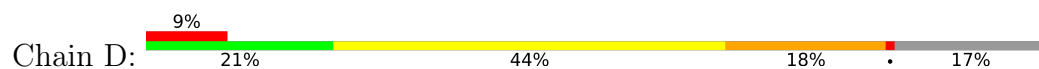
Chain	Residue	Modelled	Actual	Comment	Reference
F	?	-	GLY	deletion	UNP Q04087
F	?	-	ASP	deletion	UNP Q04087

- Molecule 1: Monopolin complex subunit CSM1

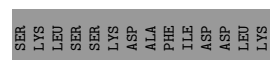
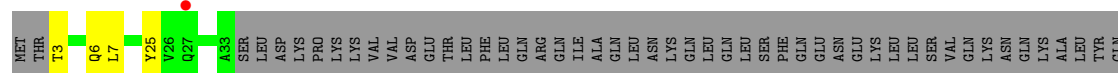




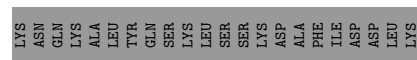
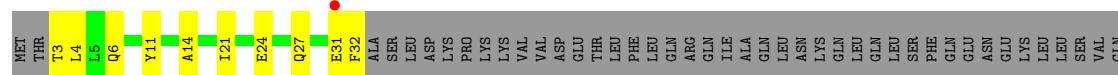
● Molecule 1: Monopolin complex subunit CSM1



● Molecule 2: Monopolin complex subunit LRS4



● Molecule 2: Monopolin complex subunit LRS4



4 Data and refinement statistics

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	152.62Å 152.62Å 118.79Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 3.90 50.00 – 3.91	Depositor EDS
% Data completeness (in resolution range)	44.5 (50.00-3.90) 44.7 (50.00-3.91)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.82 (at 3.88Å)	Xtriage
Refinement program	CNS 1.3, PHENIX (phenix.refine: 1.6.1_357)	Depositor
R, R_{free}	0.333 , 0.355 0.328 , 0.350	Depositor DCC
R_{free} test set	321 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	65.7	Xtriage
Anisotropy	1.103	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 329.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.056 for -h,-k,l	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	5496	wwPDB-VP
Average B, all atoms (Å ²)	358.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.60% 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	0.83	1/1332 (0.1%)	1.12	9/1800 (0.5%)
1	B	0.70	1/1345 (0.1%)	1.11	3/1817 (0.2%)
1	C	0.85	2/1288 (0.2%)	1.15	8/1738 (0.5%)
1	D	0.72	2/1300 (0.2%)	1.04	2/1756 (0.1%)
2	E	0.41	0/154	0.88	0/214
2	F	0.35	0/149	0.77	0/207
All	All	0.76	6/5568 (0.1%)	1.09	22/7532 (0.3%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	118	TYR	CA-CB	-6.02	1.45	1.53
1	C	118	TYR	CA-CB	-5.99	1.45	1.53
1	D	133	ILE	CA-CB	-5.62	1.46	1.54
1	B	89	SER	CA-C	5.32	1.58	1.52
1	C	81	LEU	C-N	-5.28	1.25	1.33

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	156	TYR	N-CA-C	7.96	119.96	111.28
1	A	36	LEU	N-CA-C	7.59	119.56	111.28
1	B	156	TYR	N-CA-C	6.09	118.71	111.71
1	B	135	ALA	N-CA-C	-5.80	100.12	109.58
1	A	87	HIS	N-CA-C	5.78	117.27	110.97

There are no chirality outliers.

There are no planarity outliers.

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	1313	0	1310	161	0
1	B	1326	0	1328	183	0
1	C	1271	0	1265	219	1
1	D	1281	0	1281	223	1
2	E	155	0	67	14	0
2	F	150	0	62	21	0
All	All	5496	0	5313	691	1

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 64.

The worst 5 of 691 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:C:26:VAL:HG12	1:C:30:PHE:CE2	1.24	1.69
1:A:7:TYR:CD1	1:B:7:TYR:CE1	2.02	1.47
1:D:14:GLN:HB3	2:F:14:ALA:CB	1.46	1.43
1:C:36:LEU:CD1	1:D:36:LEU:HD12	1.54	1.36
1:D:14:GLN:CB	2:F:14:ALA:HB1	1.53	1.35

All (1) 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:C:39:LYS:CE	1:D:30:PHE:CD2[2_545]	1.98	0.22

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	157/190 (83%)	143 (91%)	14 (9%)	0	100	100
1	B	160/190 (84%)	148 (92%)	11 (7%)	1 (1%)	21	55
1	C	152/190 (80%)	139 (91%)	12 (8%)	1 (1%)	18	53
1	D	152/190 (80%)	132 (87%)	17 (11%)	3 (2%)	6	32
2	E	29/95 (30%)	29 (100%)	0	0	100	100
2	F	28/95 (30%)	27 (96%)	1 (4%)	0	100	100
All	All	678/950 (71%)	618 (91%)	55 (8%)	5 (1%)	18	53

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	33	SER
1	D	80	TYR
1	B	136	PRO
1	C	136	PRO
1	D	158	PHE

5.3.2 Protein sidechains ⓘ

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	151/176 (86%)	116 (77%)	35 (23%)	1	5
1	B	152/176 (86%)	119 (78%)	33 (22%)	1	6
1	C	146/176 (83%)	115 (79%)	31 (21%)	1	7
1	D	148/176 (84%)	103 (70%)	45 (30%)	0	2
All	All	597/704 (85%)	453 (76%)	144 (24%)	1	4

5 of 144 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	63	GLN
1	D	170	GLN
1	D	79	GLU
1	D	122	PHE
1	B	71	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	83	ASN
1	D	67	GLN
1	D	169	ASN
1	D	83	ASN
1	A	102	GLN

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	163/190 (85%)	0.72	24 (14%) 6 9	195, 331, 461, 500	0
1	B	164/190 (86%)	0.59	14 (8%) 16 17	149, 319, 447, 500	0
1	C	158/190 (83%)	0.42	15 (9%) 14 16	182, 398, 500, 500	0
1	D	158/190 (83%)	0.60	17 (10%) 11 14	142, 400, 500, 500	0
2	E	31/95 (32%)	0.50	1 (3%) 50 35	107, 270, 426, 483	0
2	F	30/95 (31%)	0.30	1 (3%) 49 34	201, 272, 384, 500	0
All	All	704/950 (74%)	0.57	72 (10%) 12 15	107, 349, 500, 500	0

The worst 5 of 72 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	86	VAL	17.6
1	D	84	VAL	8.8
1	D	75	LYS	7.7
1	D	20	LEU	6.4
1	A	171	PHE	5.7

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.