



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 01:41 AM UTC

PDB ID : 8KBC / pdb\_00008kbc  
Title : Structure of CmTad1 complexed with cAAA  
Authors : Xiao, Y.; Feng, Y.  
Deposited on : 2023-08-04  
Resolution : 2.80 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](mailto: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>.

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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

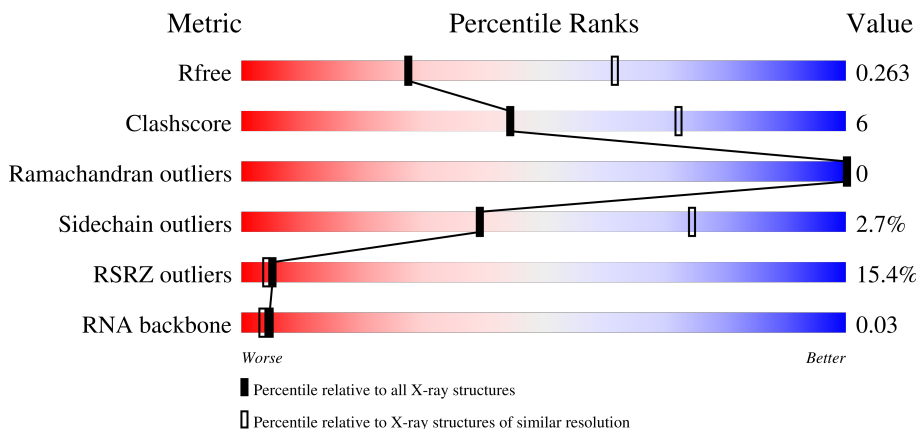
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)
RNA backbone	3983	1114 (3.00-2.60)

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  $\geq 3$ , 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	132	
1	B	132	
1	C	132	
1	D	132	

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Mol	Chain	Length	Quality of chain
1	E	132	 7% 79% 20% .
1	F	132	 11% 81% 17% .
1	G	132	 9% 77% 21% ..
1	H	132	 14% 85% 12% ..
1	I	132	 24% 71% 24% ..
1	J	132	 31% 75% 17% 6% .
1	K	132	 19% 78% 20% .
1	L	132	 25% 75% 18% . 5%
2	N	3	 33% 33% 33%
2	O	3	 33% 67%
2	P	3	 67% 33%
2	Q	3	 67% 33%

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 12833 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 Thoeris anti-defense 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	125	1017	647	172	190	8	0	0	0
1	B	132	1064	673	179	204	8	0	0	0
1	G	131	1058	670	178	202	8	0	0	0
1	H	129	1040	659	176	197	8	0	0	0
1	I	128	1034	656	175	195	8	0	0	0
1	J	129	1043	661	176	198	8	0	0	0
1	K	130	1052	667	177	200	8	0	0	0
1	L	126	1021	649	173	191	8	0	0	0
1	C	132	1064	673	179	204	8	0	0	0
1	D	131	1058	670	178	202	8	0	0	0
1	E	130	1052	667	177	200	8	0	0	0
1	F	132	1064	673	179	204	8	0	0	0

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	SER	-	expression tag	UNP P0DW61
A	-8	SER	-	expression tag	UNP P0DW61
A	-7	GLY	-	expression tag	UNP P0DW61
A	-6	LEU	-	expression tag	UNP P0DW61
A	-5	VAL	-	expression tag	UNP P0DW61

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	PRO	-	expression tag	UNP P0DW61
A	-3	ARG	-	expression tag	UNP P0DW61
A	-2	GLY	-	expression tag	UNP P0DW61
A	-1	SER	-	expression tag	UNP P0DW61
A	0	HIS	-	expression tag	UNP P0DW61
B	-9	SER	-	expression tag	UNP P0DW61
B	-8	SER	-	expression tag	UNP P0DW61
B	-7	GLY	-	expression tag	UNP P0DW61
B	-6	LEU	-	expression tag	UNP P0DW61
B	-5	VAL	-	expression tag	UNP P0DW61
B	-4	PRO	-	expression tag	UNP P0DW61
B	-3	ARG	-	expression tag	UNP P0DW61
B	-2	GLY	-	expression tag	UNP P0DW61
B	-1	SER	-	expression tag	UNP P0DW61
B	0	HIS	-	expression tag	UNP P0DW61
G	-9	SER	-	expression tag	UNP P0DW61
G	-8	SER	-	expression tag	UNP P0DW61
G	-7	GLY	-	expression tag	UNP P0DW61
G	-6	LEU	-	expression tag	UNP P0DW61
G	-5	VAL	-	expression tag	UNP P0DW61
G	-4	PRO	-	expression tag	UNP P0DW61
G	-3	ARG	-	expression tag	UNP P0DW61
G	-2	GLY	-	expression tag	UNP P0DW61
G	-1	SER	-	expression tag	UNP P0DW61
G	0	HIS	-	expression tag	UNP P0DW61
H	-9	SER	-	expression tag	UNP P0DW61
H	-8	SER	-	expression tag	UNP P0DW61
H	-7	GLY	-	expression tag	UNP P0DW61
H	-6	LEU	-	expression tag	UNP P0DW61
H	-5	VAL	-	expression tag	UNP P0DW61
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H	-1	SER	-	expression tag	UNP P0DW61
H	0	HIS	-	expression tag	UNP P0DW61
I	-9	SER	-	expression tag	UNP P0DW61
I	-8	SER	-	expression tag	UNP P0DW61
I	-7	GLY	-	expression tag	UNP P0DW61
I	-6	LEU	-	expression tag	UNP P0DW61
I	-5	VAL	-	expression tag	UNP P0DW61
I	-4	PRO	-	expression tag	UNP P0DW61
I	-3	ARG	-	expression tag	UNP P0DW61

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-2	GLY	-	expression tag	UNP P0DW61
I	-1	SER	-	expression tag	UNP P0DW61
I	0	HIS	-	expression tag	UNP P0DW61
J	-9	SER	-	expression tag	UNP P0DW61
J	-8	SER	-	expression tag	UNP P0DW61
J	-7	GLY	-	expression tag	UNP P0DW61
J	-6	LEU	-	expression tag	UNP P0DW61
J	-5	VAL	-	expression tag	UNP P0DW61
J	-4	PRO	-	expression tag	UNP P0DW61
J	-3	ARG	-	expression tag	UNP P0DW61
J	-2	GLY	-	expression tag	UNP P0DW61
J	-1	SER	-	expression tag	UNP P0DW61
J	0	HIS	-	expression tag	UNP P0DW61
K	-9	SER	-	expression tag	UNP P0DW61
K	-8	SER	-	expression tag	UNP P0DW61
K	-7	GLY	-	expression tag	UNP P0DW61
K	-6	LEU	-	expression tag	UNP P0DW61
K	-5	VAL	-	expression tag	UNP P0DW61
K	-4	PRO	-	expression tag	UNP P0DW61
K	-3	ARG	-	expression tag	UNP P0DW61
K	-2	GLY	-	expression tag	UNP P0DW61
K	-1	SER	-	expression tag	UNP P0DW61
K	0	HIS	-	expression tag	UNP P0DW61
L	-9	SER	-	expression tag	UNP P0DW61
L	-8	SER	-	expression tag	UNP P0DW61
L	-7	GLY	-	expression tag	UNP P0DW61
L	-6	LEU	-	expression tag	UNP P0DW61
L	-5	VAL	-	expression tag	UNP P0DW61
L	-4	PRO	-	expression tag	UNP P0DW61
L	-3	ARG	-	expression tag	UNP P0DW61
L	-2	GLY	-	expression tag	UNP P0DW61
L	-1	SER	-	expression tag	UNP P0DW61
L	0	HIS	-	expression tag	UNP P0DW61
C	-9	SER	-	expression tag	UNP P0DW61
C	-8	SER	-	expression tag	UNP P0DW61
C	-7	GLY	-	expression tag	UNP P0DW61
C	-6	LEU	-	expression tag	UNP P0DW61
C	-5	VAL	-	expression tag	UNP P0DW61
C	-4	PRO	-	expression tag	UNP P0DW61
C	-3	ARG	-	expression tag	UNP P0DW61
C	-2	GLY	-	expression tag	UNP P0DW61
C	-1	SER	-	expression tag	UNP P0DW61

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Chain	Residue	Modelled	Actual	Comment	Reference
C	0	HIS	-	expression tag	UNP P0DW61
D	-9	SER	-	expression tag	UNP P0DW61
D	-8	SER	-	expression tag	UNP P0DW61
D	-7	GLY	-	expression tag	UNP P0DW61
D	-6	LEU	-	expression tag	UNP P0DW61
D	-5	VAL	-	expression tag	UNP P0DW61
D	-4	PRO	-	expression tag	UNP P0DW61
D	-3	ARG	-	expression tag	UNP P0DW61
D	-2	GLY	-	expression tag	UNP P0DW61
D	-1	SER	-	expression tag	UNP P0DW61
D	0	HIS	-	expression tag	UNP P0DW61
E	-9	SER	-	expression tag	UNP P0DW61
E	-8	SER	-	expression tag	UNP P0DW61
E	-7	GLY	-	expression tag	UNP P0DW61
E	-6	LEU	-	expression tag	UNP P0DW61
E	-5	VAL	-	expression tag	UNP P0DW61
E	-4	PRO	-	expression tag	UNP P0DW61
E	-3	ARG	-	expression tag	UNP P0DW61
E	-2	GLY	-	expression tag	UNP P0DW61
E	-1	SER	-	expression tag	UNP P0DW61
E	0	HIS	-	expression tag	UNP P0DW61
F	-9	SER	-	expression tag	UNP P0DW61
F	-8	SER	-	expression tag	UNP P0DW61
F	-7	GLY	-	expression tag	UNP P0DW61
F	-6	LEU	-	expression tag	UNP P0DW61
F	-5	VAL	-	expression tag	UNP P0DW61
F	-4	PRO	-	expression tag	UNP P0DW61
F	-3	ARG	-	expression tag	UNP P0DW61
F	-2	GLY	-	expression tag	UNP P0DW61
F	-1	SER	-	expression tag	UNP P0DW61
F	0	HIS	-	expression tag	UNP P0DW61

- Molecule 2 is a RNA chain called (2-ACETYL-5-METHYLANILINO)(2,6-DIBROMOPHENYL)ACETAMIDE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	N	3	Total	C	N	O	P	0	0	0
			66	30	15	18	3			
2	O	3	Total	C	N	O	P	0	0	0
			66	30	15	18	3			
2	P	3	Total	C	N	O	P	0	0	0
			66	30	15	18	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	Q	3	66	30	15	18	3	0	0	0

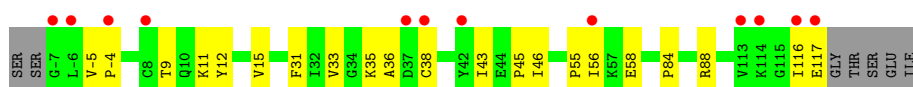
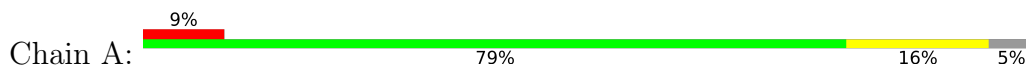
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		
3	F	1	Total	Zn	0	0
			1	1		

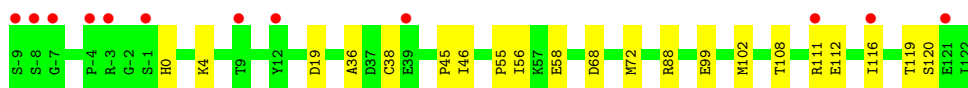
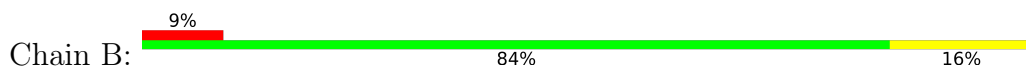
### 3 Residue-property plots [i](#)

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.

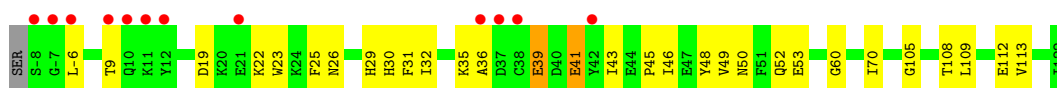
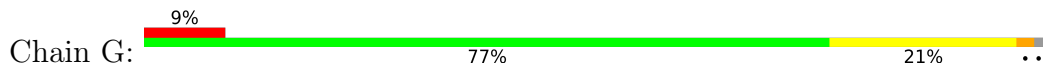
- Molecule 1: Thoeris anti-defense 1



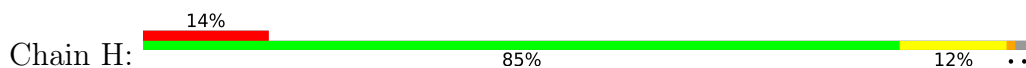
- Molecule 1: Thoeris anti-defense 1



- Molecule 1: Thoeris anti-defense 1



- Molecule 1: Thoeris anti-defense 1

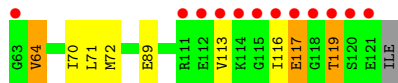
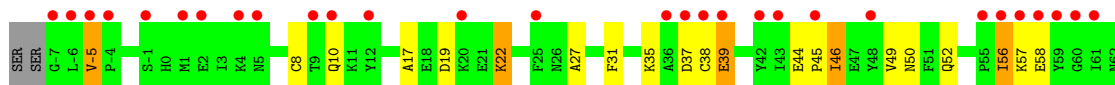
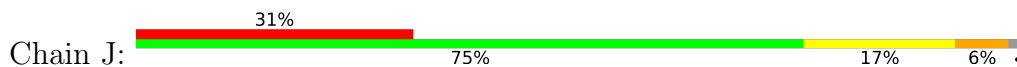


- Molecule 1: Thoeris anti-defense 1

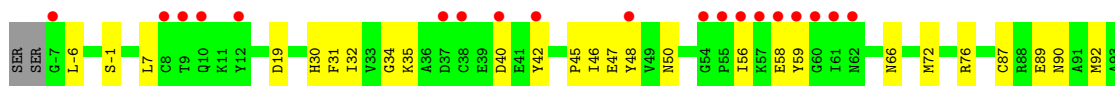
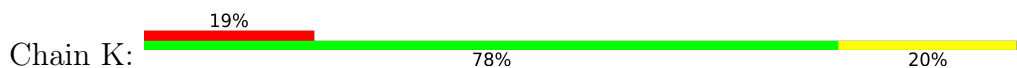




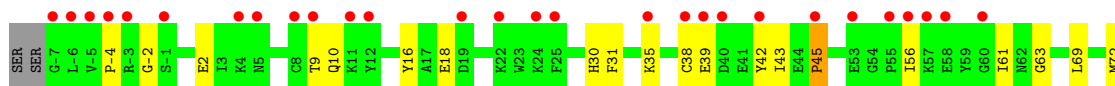
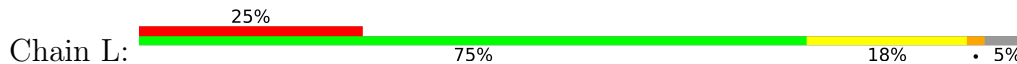
- Molecule 1: Thoeris anti-defense 1



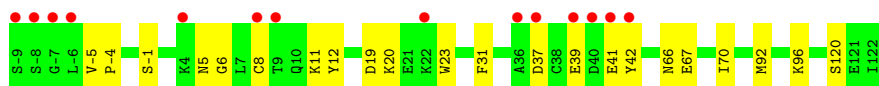
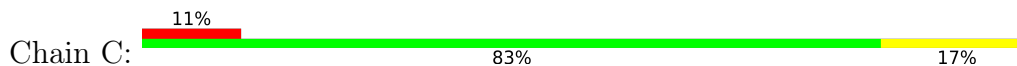
- Molecule 1: Thoeris anti-defense 1



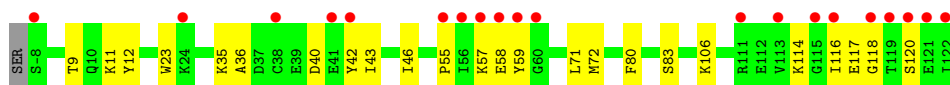
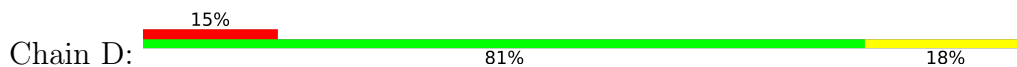
- Molecule 1: Thoeris anti-defense 1



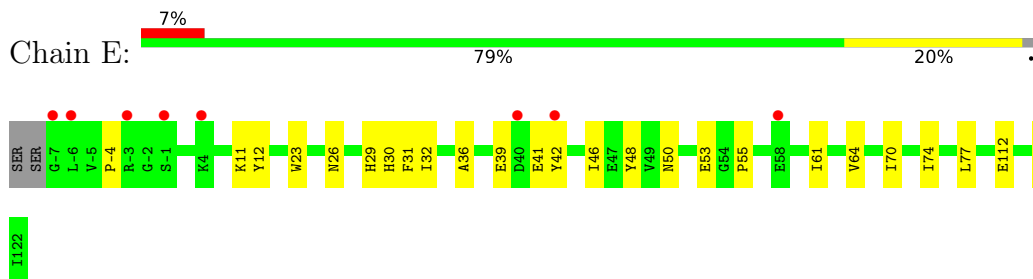
- Molecule 1: Thoeris anti-defense 1



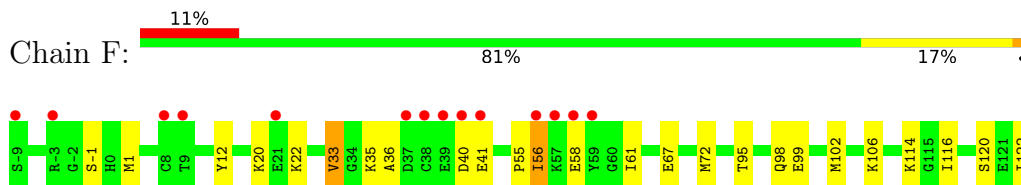
- Molecule 1: Thoeris anti-defense 1



- Molecule 1: Thoeris anti-defense 1



- Molecule 1: Thoeris anti-defense 1



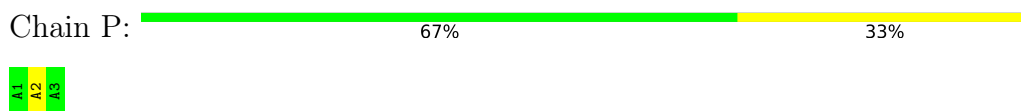
- Molecule 2: (2-ACETYL-5-METHYLANILINO)(2,6-DIBROMOPHENYL)ACETAMIDE



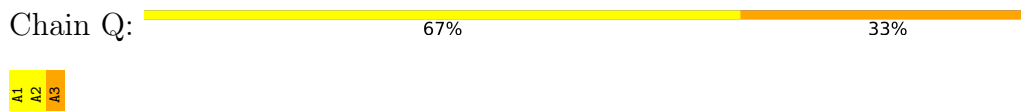
- Molecule 2: (2-ACETYL-5-METHYLANILINO)(2,6-DIBROMOPHENYL)ACETAMIDE



- Molecule 2: (2-ACETYL-5-METHYLANILINO)(2,6-DIBROMOPHENYL)ACETAMIDE



- Molecule 2: (2-ACETYL-5-METHYLANILINO)(2,6-DIBROMOPHENYL)ACETAMIDE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	138.94Å 145.73Å 150.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.27 – 2.80 44.27 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.9 (44.27-2.80) 98.9 (44.27-2.80)	Depositor EDS
$R_{merge}$	0.22	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.88 (at 2.81Å)	Xtrriage
Refinement program	PHENIX (1.18.2_3874: ???)	Depositor
R, $R_{free}$	0.226 , 0.268 0.230 , 0.263	Depositor DCC
$R_{free}$ test set	3793 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	54.5	Xtrriage
Anisotropy	0.184	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 60.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	0.000 for -h,l,k	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	12833	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	63.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.83% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

Bond lengths and bond angles in the following residue types are not validated in this section:  
ZN

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	0.54	0/1038	0.65	2/1397 (0.1%)
1	B	0.81	1/1085 (0.1%)	0.86	7/1459 (0.5%)
1	C	0.60	1/1085 (0.1%)	0.73	1/1459 (0.1%)
1	D	0.63	1/1079 (0.1%)	0.71	4/1451 (0.3%)
1	E	0.74	1/1073 (0.1%)	0.71	2/1443 (0.1%)
1	F	0.84	1/1085 (0.1%)	0.79	5/1459 (0.3%)
1	G	0.81	1/1079 (0.1%)	0.72	2/1451 (0.1%)
1	H	0.78	1/1061 (0.1%)	0.68	2/1428 (0.1%)
1	I	1.14	1/1055 (0.1%)	0.93	4/1420 (0.3%)
1	J	0.97	0/1064	1.10	14/1432 (1.0%)
1	K	0.70	0/1073	0.83	7/1443 (0.5%)
1	L	0.83	0/1042	0.91	5/1402 (0.4%)
2	N	1.62	0/74	1.32	0/113
2	O	1.67	0/74	1.67	0/113
2	P	1.65	0/74	1.36	0/113
2	Q	1.65	0/74	1.56	1/113 (0.9%)
All	All	0.83	8/13115 (0.1%)	0.84	56/17696 (0.3%)

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	23	TRP	CA-C	-5.57	1.45	1.52
1	G	23	TRP	CA-C	-5.39	1.45	1.52
1	H	52	GLN	CA-C	-5.31	1.45	1.52
1	F	106	LYS	CA-C	-5.23	1.46	1.52
1	C	37	ASP	CA-C	-5.20	1.46	1.53

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	39	GLU	N-CA-C	-9.51	93.11	108.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	27	ALA	N-CA-C	8.93	118.61	108.25
1	D	40	ASP	N-CA-C	8.47	120.52	111.28
1	J	37	ASP	N-CA-C	-8.40	97.58	110.10
1	G	9	THR	N-CA-C	8.34	120.00	111.07

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	1017	0	1009	11	0
1	B	1064	0	1051	11	0
1	C	1064	0	1051	15	0
1	D	1058	0	1046	15	0
1	E	1052	0	1041	17	0
1	F	1064	0	1051	14	0
1	G	1058	0	1046	18	0
1	H	1040	0	1029	11	0
1	I	1034	0	1024	22	0
1	J	1043	0	1030	15	0
1	K	1052	0	1041	19	0
1	L	1021	0	1012	15	0
2	N	66	0	33	1	0
2	O	66	0	33	4	0
2	P	66	0	33	0	0
2	Q	66	0	33	1	0
3	A	1	0	0	0	0
3	F	1	0	0	0	0
All	All	12833	0	12563	153	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 6.

The worst 5 of 153 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:K:32:ILE:HG12	1:K:48:TYR:CD2	1.98	0.99
1:K:32:ILE:HG12	1:K:48:TYR:HD2	1.29	0.97
1:C:20:LYS:HD3	1:C:23:TRP:CE3	2.22	0.74
1:B:99:GLU:HA	1:B:102:MET:HE2	1.75	0.67
1:A:11:LYS:HE2	1:A:12:TYR:CZ	2.31	0.66

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	123/132 (93%)	118 (96%)	5 (4%)	0	100	100
1	B	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
1	C	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
1	D	129/132 (98%)	125 (97%)	4 (3%)	0	100	100
1	E	128/132 (97%)	123 (96%)	5 (4%)	0	100	100
1	F	130/132 (98%)	126 (97%)	4 (3%)	0	100	100
1	G	129/132 (98%)	126 (98%)	3 (2%)	0	100	100
1	H	127/132 (96%)	123 (97%)	4 (3%)	0	100	100
1	I	126/132 (96%)	124 (98%)	2 (2%)	0	100	100
1	J	127/132 (96%)	126 (99%)	1 (1%)	0	100	100
1	K	128/132 (97%)	125 (98%)	3 (2%)	0	100	100
1	L	124/132 (94%)	122 (98%)	2 (2%)	0	100	100
All	All	1531/1584 (97%)	1492 (98%)	39 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	110/116 (95%)	108 (98%)	2 (2%)	51	82
1	B	116/116 (100%)	115 (99%)	1 (1%)	70	89
1	C	116/116 (100%)	116 (100%)	0	100	100
1	D	115/116 (99%)	115 (100%)	0	100	100
1	E	114/116 (98%)	112 (98%)	2 (2%)	51	82
1	F	116/116 (100%)	114 (98%)	2 (2%)	53	83
1	G	115/116 (99%)	110 (96%)	5 (4%)	26	60
1	H	113/116 (97%)	108 (96%)	5 (4%)	25	59
1	I	112/116 (97%)	106 (95%)	6 (5%)	20	51
1	J	113/116 (97%)	104 (92%)	9 (8%)	11	34
1	K	114/116 (98%)	113 (99%)	1 (1%)	70	89
1	L	110/116 (95%)	106 (96%)	4 (4%)	31	66
All	All	1364/1392 (98%)	1327 (97%)	37 (3%)	39	74

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	59	TYR
1	F	41	GLU
1	L	10	GLN
1	L	117	GLU
1	H	117	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	26	ASN
1	L	29	HIS
1	F	10	GLN
1	E	29	HIS

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Mol	Chain	Res	Type
1	I	26	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	N	2/3 (66%)	2 (100%)	0
2	O	2/3 (66%)	2 (100%)	0
2	P	2/3 (66%)	1 (50%)	0
2	Q	2/3 (66%)	2 (100%)	0
All	All	8/12 (66%)	7 (87%)	0

5 of 7 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	N	2	A
2	N	3	A
2	O	2	A
2	O	3	A
2	P	2	A

There are no RNA pucker outliers to report.

## 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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q < 0.9
1	A	125/132 (94%)	0.15	12 (9%) 13 10	26, 48, 103, 147	0
1	B	132/132 (100%)	0.40	12 (9%) 15 11	25, 57, 106, 139	0
1	C	132/132 (100%)	0.19	14 (10%) 11 8	28, 50, 100, 128	0
1	D	131/132 (99%)	0.33	20 (15%) 5 4	24, 49, 102, 117	0
1	E	130/132 (98%)	0.18	9 (6%) 23 16	25, 55, 97, 135	0
1	F	132/132 (100%)	0.24	14 (10%) 11 8	22, 49, 101, 121	0
1	G	131/132 (99%)	0.24	12 (9%) 14 10	24, 51, 99, 121	0
1	H	129/132 (97%)	0.39	18 (13%) 6 5	27, 49, 119, 144	0
1	I	128/132 (96%)	1.13	32 (25%) 2 1	35, 67, 124, 135	0
1	J	129/132 (97%)	1.35	41 (31%) 1 1	32, 81, 135, 161	0
1	K	130/132 (98%)	0.80	25 (19%) 3 2	31, 61, 114, 127	0
1	L	126/132 (95%)	1.02	33 (26%) 1 1	32, 73, 125, 144	0
2	N	3/3 (100%)	0.80	0 100 100	40, 40, 46, 55	3 (100%)
2	O	3/3 (100%)	0.72	0 100 100	40, 40, 44, 50	3 (100%)
2	P	3/3 (100%)	0.54	0 100 100	49, 49, 51, 52	3 (100%)
2	Q	3/3 (100%)	0.95	0 100 100	39, 39, 40, 49	3 (100%)
All	All	1567/1596 (98%)	0.53	242 (15%) 5 4	22, 56, 118, 161	12 (0%)

The worst 5 of 242 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	118	GLY	8.3
1	L	116	ILE	6.2
1	J	118	GLY	5.5
1	E	-7	GLY	5.3
1	J	119	THR	5.2

## 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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	ZN	F	201	1/1	0.98	0.09	69,69,69,69	0
3	ZN	A	201	1/1	0.99	0.10	67,67,67,67	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.