



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 29, 2020 – 01:58 am BST

PDB ID : 2Y1M  
Title : Structure of native c-Cbl  
Authors : Dou, H.; Sibbet, G.J.; Huang, D.T.  
Deposited on : 2010-12-08  
Resolution : 2.67 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.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

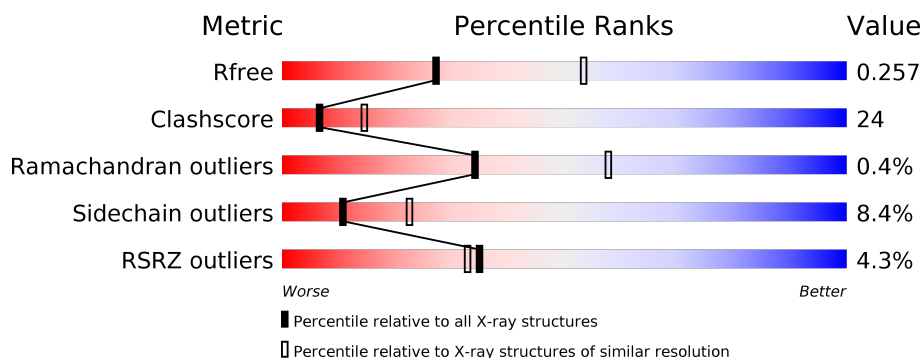
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.67 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))
$R_{free}$	130704	3863 (2.70-2.66)
Clashscore	141614	4210 (2.70-2.66)
Ramachandran outliers	138981	4141 (2.70-2.66)
Sidechain outliers	138945	4141 (2.70-2.66)
RSRZ outliers	127900	3780 (2.70-2.66)

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 on 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	389	<div> <div>2%</div> <div> <div></div> <div>65%</div> <div>31%</div> <div>• •</div> </div> </div>
1	B	389	<div> <div>3%</div> <div> <div></div> <div>60%</div> <div>35%</div> <div>• •</div> </div> </div>
1	C	389	<div> <div>4%</div> <div> <div></div> <div>60%</div> <div>34%</div> <div>5%</div> <div>•</div> </div> </div>
1	D	389	<div> <div>4%</div> <div> <div></div> <div>56%</div> <div>38%</div> <div>5%</div> <div>•</div> </div> </div>
1	E	389	<div> <div>5%</div> <div> <div></div> <div>56%</div> <div>38%</div> <div>5%</div> <div>•</div> </div> </div>
1	F	389	<div> <div>7%</div> <div> <div></div> <div>56%</div> <div>38%</div> <div>5%</div> <div>•</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 18832 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 E3 UBIQUITIN-PROTEIN LIGASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	384	Total	C	N	O	S	0	0	0
			3113	2000	523	565	25			
1	B	385	Total	C	N	O	S	0	0	0
			3121	2006	524	566	25			
1	C	385	Total	C	N	O	S	0	0	0
			3116	2002	524	565	25			
1	D	385	Total	C	N	O	S	0	0	0
			3123	2005	524	569	25			
1	E	383	Total	C	N	O	S	0	0	0
			3106	1996	522	563	25			
1	F	384	Total	C	N	O	S	0	0	0
			3114	2000	523	566	25			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	2	Total	Zn	0	0
			2	2		
2	E	2	Total	Zn	0	0
			2	2		
2	B	2	Total	Zn	0	0
			2	2		
2	C	2	Total	Zn	0	0
			2	2		
2	A	2	Total	Zn	0	0
			2	2		
2	F	2	Total	Zn	0	0
			2	2		

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	Total Ca 1 1	0	0
3	E	1	Total Ca 1 1	0	0
3	B	1	Total Ca 1 1	0	0
3	C	1	Total Ca 1 1	0	0
3	A	1	Total Ca 1 1	0	0
3	F	1	Total Ca 1 1	0	0

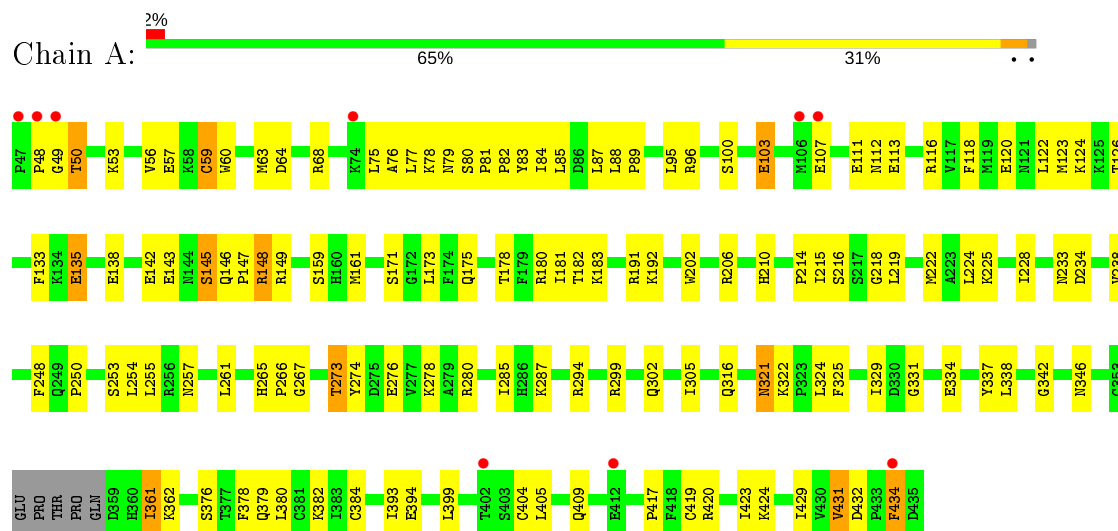
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	32	Total O 32 32	0	0
4	B	23	Total O 23 23	0	0
4	C	27	Total O 27 27	0	0
4	D	17	Total O 17 17	0	0
4	E	12	Total O 12 12	0	0
4	F	10	Total O 10 10	0	0

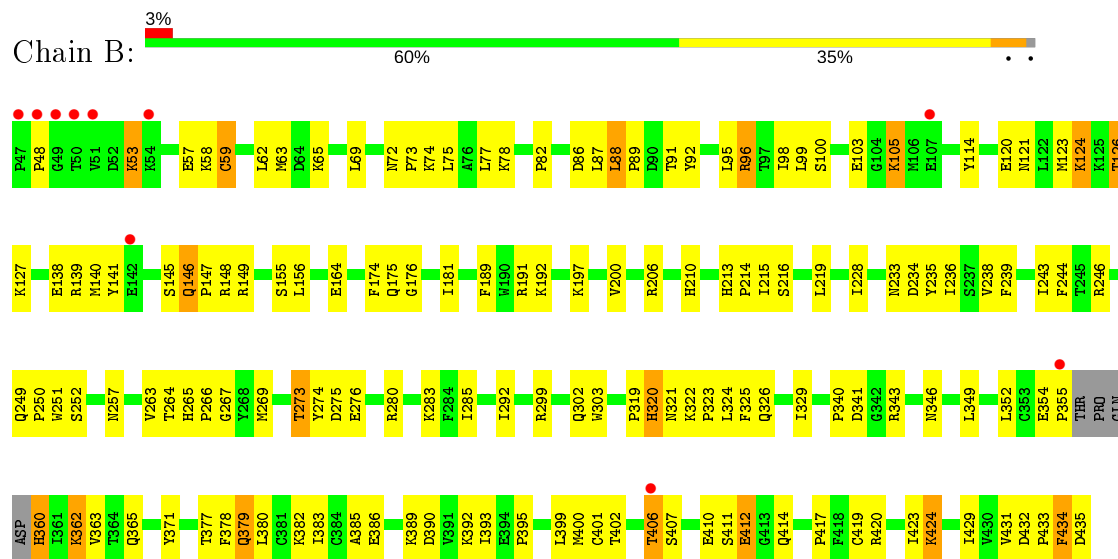
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: E3 UBIQUITIN-PROTEIN LIGASE

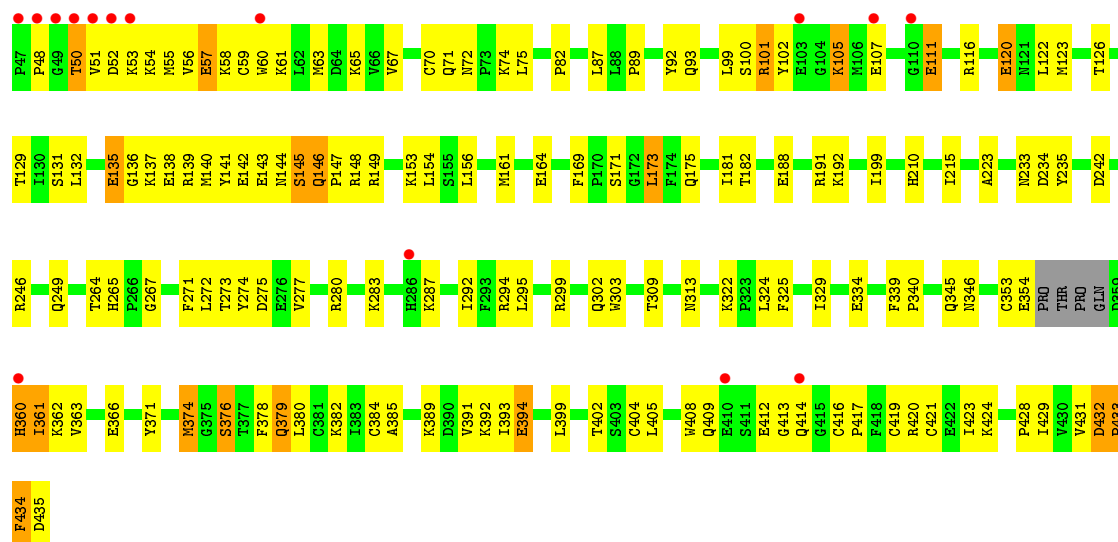


#### • Molecule 1: E3 UBIQUITIN-PROTEIN LIGASE

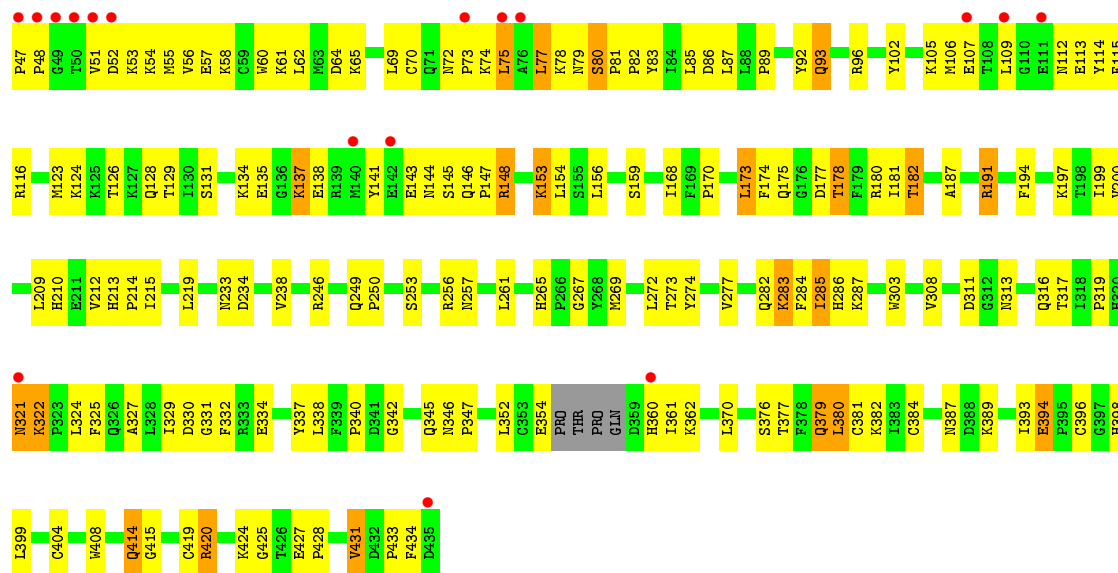


#### • Molecule 1: E3 UBIQUITIN-PROTEIN LIGASE

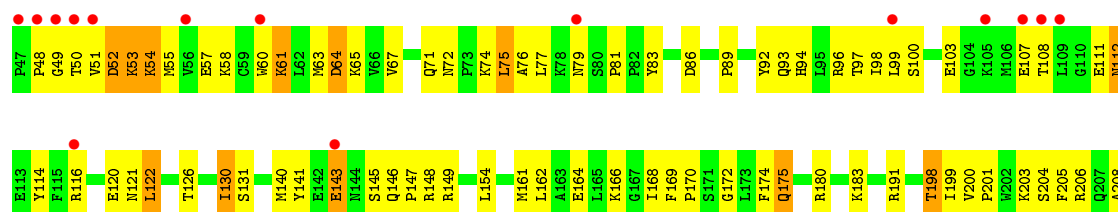


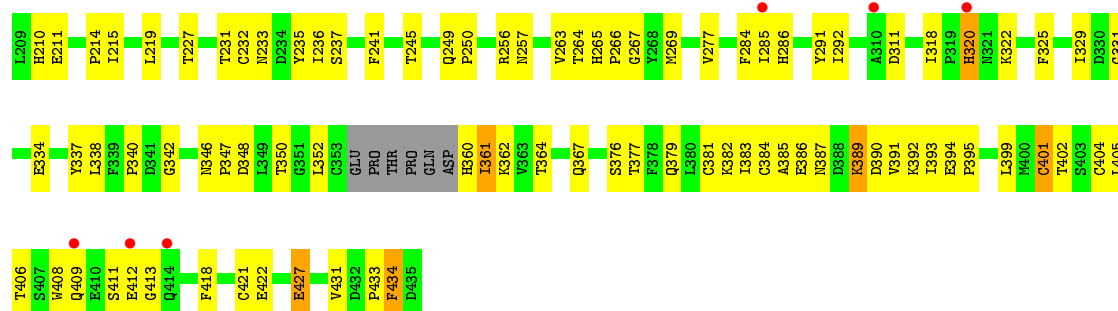


• Molecule 1: E3 UBIQUITIN-PROTEIN LIGASE

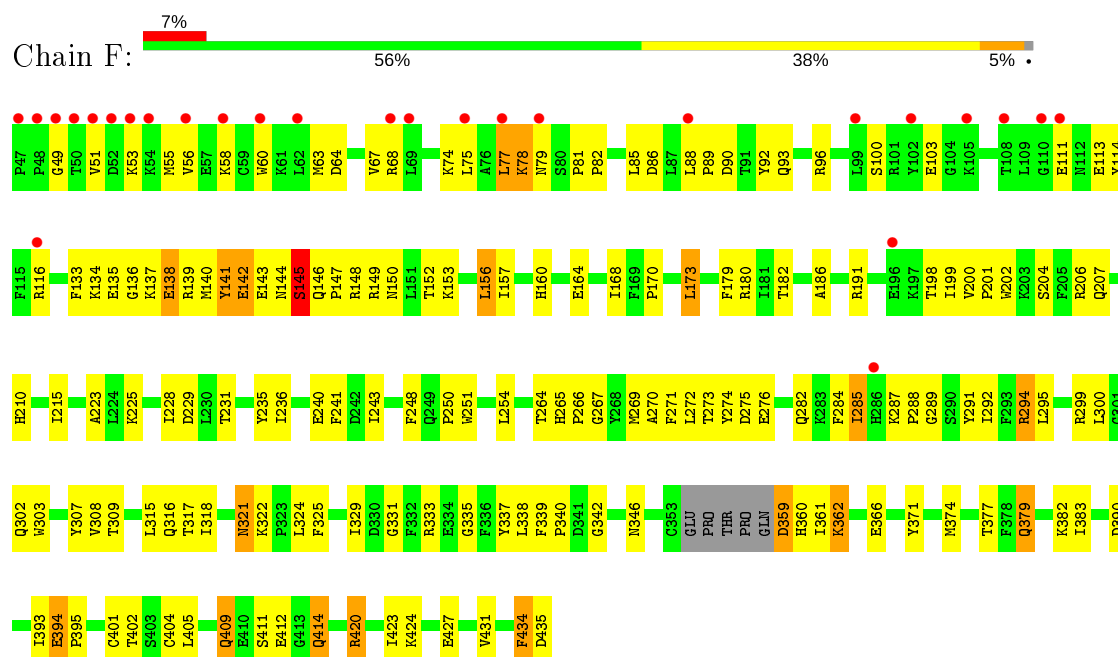


• Molecule 1: E3 UBIQUITIN-PROTEIN LIGASE





• Molecule 1: E3 UBIQUITIN-PROTEIN LIGASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	146.80Å 148.56Å 348.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.62 – 2.67 47.61 – 2.67	Depositor EDS
% Data completeness (in resolution range)	94.5 (47.62-2.67) 97.1 (47.61-2.67)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.08 (at 2.69Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.218 , 0.263 0.215 , 0.257	Depositor DCC
$R_{free}$ test set	5239 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	51.8	Xtriage
Anisotropy	0.577	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 50.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.035 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	18832	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.96% 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

### 5.1 Standard geometry

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

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	0.57	0/3192	0.68	0/4310
1	B	0.56	0/3201	0.65	0/4323
1	C	0.53	0/3195	0.65	0/4313
1	D	0.51	0/3202	0.65	0/4322
1	E	0.52	0/3185	0.66	0/4299
1	F	0.50	0/3193	0.65	1/4310 (0.0%)
All	All	0.53	0/19168	0.66	1/25877 (0.0%)

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	B	0	1
1	C	0	1
All	All	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	F	145	SER	N-CA-C	-5.12	97.17	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	321	ASN	Peptide

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Mol	Chain	Res	Type	Group
1	C	144	ASN	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	3113	0	3082	118	0
1	B	3121	0	3091	124	0
1	C	3116	0	3083	152	0
1	D	3123	0	3088	164	0
1	E	3106	0	3079	187	0
1	F	3114	0	3082	161	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	32	0	0	0	0
4	B	23	0	0	0	0
4	C	27	0	0	1	0
4	D	17	0	0	0	0
4	E	12	0	0	0	0
4	F	10	0	0	0	0
All	All	18832	0	18505	879	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 24.

The worst 5 of 879 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:F:143:GLU:HG2	1:F:144:ASN:ND2	1.36	1.38
1:E:145:SER:OG	1:E:147:PRO:HD2	1.43	1.17
1:C:361:ILE:O	1:C:361:ILE:HD12	1.45	1.16
1:D:282:GLN:HE22	1:D:285:ILE:HD11	1.08	1.12
1:C:101:ARG:HD3	1:C:173:LEU:HD23	1.31	1.11

There are no symmetry-related clashes.

## 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	380/389 (98%)	356 (94%)	23 (6%)	1 (0%)	41	64
1	B	381/389 (98%)	344 (90%)	37 (10%)	0	100	100
1	C	381/389 (98%)	346 (91%)	32 (8%)	3 (1%)	19	40
1	D	381/389 (98%)	341 (90%)	37 (10%)	3 (1%)	19	40
1	E	379/389 (97%)	339 (89%)	39 (10%)	1 (0%)	41	64
1	F	380/389 (98%)	337 (89%)	43 (11%)	0	100	100
All	All	2282/2334 (98%)	2063 (90%)	211 (9%)	8 (0%)	34	58

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	146	GLN
1	C	101	ARG
1	D	182	THR
1	E	285	ILE
1	D	285	ILE

### 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	345/350 (99%)	324 (94%)	21 (6%)	18	38
1	B	346/350 (99%)	315 (91%)	31 (9%)	9	20
1	C	344/350 (98%)	315 (92%)	29 (8%)	11	22
1	D	346/350 (99%)	318 (92%)	28 (8%)	11	25
1	E	344/350 (98%)	316 (92%)	28 (8%)	11	25
1	F	345/350 (99%)	308 (89%)	37 (11%)	6	14
All	All	2070/2100 (99%)	1896 (92%)	174 (8%)	11	22

5 of 174 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	421	CYS
1	D	311	ASP
1	F	359	ASP
1	D	64	ASP
1	D	113	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 64 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	265	HIS
1	D	175	GLN
1	F	265	HIS
1	C	346	ASN
1	D	144	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 18 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 [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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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	384/389 (98%)	0.01	9 (2%) 60 60	31, 46, 79, 109	0
1	B	385/389 (98%)	0.08	10 (2%) 56 55	32, 51, 85, 105	0
1	C	385/389 (98%)	0.14	15 (3%) 39 37	36, 54, 88, 110	0
1	D	385/389 (98%)	0.18	17 (4%) 34 32	36, 56, 89, 112	0
1	E	383/389 (98%)	0.27	21 (5%) 25 23	34, 58, 93, 126	0
1	F	384/389 (98%)	0.30	27 (7%) 16 14	35, 58, 92, 113	0
All	All	2306/2334 (98%)	0.16	99 (4%) 35 33	31, 54, 88, 126	0

The worst 5 of 99 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	49	GLY	5.4
1	F	51	VAL	5.1
1	E	51	VAL	4.8
1	A	47	PRO	4.8
1	E	47	PRO	4.7

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

### 6.3 Carbohydrates ⓘ

There are no carbohydrates 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	CA	F	1438	1/1	0.88	0.07	77,77,77,77	0
3	CA	B	1438	1/1	0.90	0.08	56,56,56,56	0
3	CA	D	1438	1/1	0.94	0.06	63,63,63,63	0
3	CA	E	1438	1/1	0.95	0.04	72,72,72,72	0
3	CA	A	1438	1/1	0.95	0.09	57,57,57,57	0
2	ZN	E	1436	1/1	0.96	0.13	70,70,70,70	0
3	CA	C	1438	1/1	0.96	0.05	66,66,66,66	0
2	ZN	C	1436	1/1	0.98	0.13	56,56,56,56	0
2	ZN	C	1437	1/1	0.99	0.14	50,50,50,50	0
2	ZN	F	1436	1/1	0.99	0.15	52,52,52,52	0
2	ZN	E	1437	1/1	0.99	0.12	56,56,56,56	0
2	ZN	A	1436	1/1	0.99	0.12	52,52,52,52	0
2	ZN	F	1437	1/1	0.99	0.17	41,41,41,41	0
2	ZN	A	1437	1/1	0.99	0.15	46,46,46,46	0
2	ZN	B	1437	1/1	0.99	0.17	49,49,49,49	0
2	ZN	D	1436	1/1	1.00	0.16	47,47,47,47	0
2	ZN	D	1437	1/1	1.00	0.18	46,46,46,46	0
2	ZN	B	1436	1/1	1.00	0.13	51,51,51,51	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.