



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 26, 2020 – 09:37 pm BST

PDB ID : 3LVG  
Title : Crystal structure of a clathrin heavy chain and clathrin light chain complex  
Authors : Wilbur, J.D.; Hwang, P.K.; Ybe, J.A.; Lane, M.; Sellers, B.D.; Jacobson, M.P.;  
Fletterick, R.J.; Brodsky, F.M.  
Deposited on : 2010-02-20  
Resolution : 7.94 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

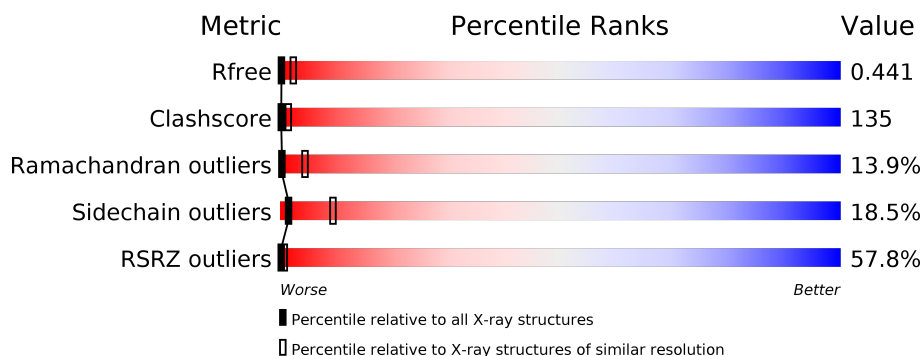
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 7.94 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	1005 (11.50-3.90)
Clashscore	141614	1070 (11.50-3.90)
Ramachandran outliers	138981	1003 (11.50-3.90)
Sidechain outliers	138945	1003 (11.50-3.86)
RSRZ outliers	127900	1004 (9.50-3.80)

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	624	<div> <div>57%</div> <div> <div>14%</div> <div>49%</div> <div>21%</div> <div>6%</div> <div>11%</div> </div> </div>
1	B	624	<div> <div>58%</div> <div> <div>12%</div> <div>52%</div> <div>20%</div> <div>5%</div> <div>11%</div> </div> </div>
1	C	624	<div> <div>39%</div> <div> <div>13%</div> <div>50%</div> <div>20%</div> <div>6%</div> <div>11%</div> </div> </div>
2	D	190	<div> <div>33%</div> <div> <div>35%</div> <div>46%</div> <div>12%</div> <div>5%</div> </div> </div>
2	E	190	<div> <div>16%</div> <div> <div>16%</div> <div>32%</div> <div>9%</div> <div>•</div> <div>39%</div> </div> </div>
2	F	190	<div> <div>19%</div> <div> <div>18%</div> <div>36%</div> <div>13%</div> <div>•</div> <div>31%</div> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 16504 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 Clathrin heavy chain 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	553	Total	C	N	O	S	0	0	0
			4543	2896	767	855	25			
1	B	553	Total	C	N	O	S	0	0	0
			4543	2896	767	855	25			
1	C	553	Total	C	N	O	S	0	0	0
			4543	2896	767	855	25			

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1052	MET	-	EXPRESSION TAG	UNP P49951
A	1053	GLY	-	EXPRESSION TAG	UNP P49951
A	1054	SER	-	EXPRESSION TAG	UNP P49951
A	1055	SER	-	EXPRESSION TAG	UNP P49951
A	1056	HIS	-	EXPRESSION TAG	UNP P49951
A	1057	HIS	-	EXPRESSION TAG	UNP P49951
A	1058	HIS	-	EXPRESSION TAG	UNP P49951
A	1059	HIS	-	EXPRESSION TAG	UNP P49951
A	1060	HIS	-	EXPRESSION TAG	UNP P49951
A	1061	HIS	-	EXPRESSION TAG	UNP P49951
A	1062	SER	-	EXPRESSION TAG	UNP P49951
A	1063	SER	-	EXPRESSION TAG	UNP P49951
A	1064	GLY	-	EXPRESSION TAG	UNP P49951
A	1065	LEU	-	EXPRESSION TAG	UNP P49951
A	1066	VAL	-	EXPRESSION TAG	UNP P49951
A	1067	PRO	-	EXPRESSION TAG	UNP P49951
A	1068	ARG	-	EXPRESSION TAG	UNP P49951
A	1069	GLY	-	EXPRESSION TAG	UNP P49951
A	1070	SER	-	EXPRESSION TAG	UNP P49951
A	1071	HIS	-	EXPRESSION TAG	UNP P49951
A	1072	MET	-	EXPRESSION TAG	UNP P49951
A	1073	LEU	-	EXPRESSION TAG	UNP P49951
B	1052	MET	-	EXPRESSION TAG	UNP P49951

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1053	GLY	-	EXPRESSION TAG	UNP P49951
B	1054	SER	-	EXPRESSION TAG	UNP P49951
B	1055	SER	-	EXPRESSION TAG	UNP P49951
B	1056	HIS	-	EXPRESSION TAG	UNP P49951
B	1057	HIS	-	EXPRESSION TAG	UNP P49951
B	1058	HIS	-	EXPRESSION TAG	UNP P49951
B	1059	HIS	-	EXPRESSION TAG	UNP P49951
B	1060	HIS	-	EXPRESSION TAG	UNP P49951
B	1061	HIS	-	EXPRESSION TAG	UNP P49951
B	1062	SER	-	EXPRESSION TAG	UNP P49951
B	1063	SER	-	EXPRESSION TAG	UNP P49951
B	1064	GLY	-	EXPRESSION TAG	UNP P49951
B	1065	LEU	-	EXPRESSION TAG	UNP P49951
B	1066	VAL	-	EXPRESSION TAG	UNP P49951
B	1067	PRO	-	EXPRESSION TAG	UNP P49951
B	1068	ARG	-	EXPRESSION TAG	UNP P49951
B	1069	GLY	-	EXPRESSION TAG	UNP P49951
B	1070	SER	-	EXPRESSION TAG	UNP P49951
B	1071	HIS	-	EXPRESSION TAG	UNP P49951
B	1072	MET	-	EXPRESSION TAG	UNP P49951
B	1073	LEU	-	EXPRESSION TAG	UNP P49951
C	1052	MET	-	EXPRESSION TAG	UNP P49951
C	1053	GLY	-	EXPRESSION TAG	UNP P49951
C	1054	SER	-	EXPRESSION TAG	UNP P49951
C	1055	SER	-	EXPRESSION TAG	UNP P49951
C	1056	HIS	-	EXPRESSION TAG	UNP P49951
C	1057	HIS	-	EXPRESSION TAG	UNP P49951
C	1058	HIS	-	EXPRESSION TAG	UNP P49951
C	1059	HIS	-	EXPRESSION TAG	UNP P49951
C	1060	HIS	-	EXPRESSION TAG	UNP P49951
C	1061	HIS	-	EXPRESSION TAG	UNP P49951
C	1062	SER	-	EXPRESSION TAG	UNP P49951
C	1063	SER	-	EXPRESSION TAG	UNP P49951
C	1064	GLY	-	EXPRESSION TAG	UNP P49951
C	1065	LEU	-	EXPRESSION TAG	UNP P49951
C	1066	VAL	-	EXPRESSION TAG	UNP P49951
C	1067	PRO	-	EXPRESSION TAG	UNP P49951
C	1068	ARG	-	EXPRESSION TAG	UNP P49951
C	1069	GLY	-	EXPRESSION TAG	UNP P49951
C	1070	SER	-	EXPRESSION TAG	UNP P49951
C	1071	HIS	-	EXPRESSION TAG	UNP P49951
C	1072	MET	-	EXPRESSION TAG	UNP P49951

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1073	LEU	-	EXPRESSION TAG	UNP P49951

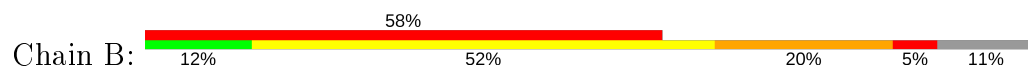
- Molecule 2 is a protein called Clathrin light chain B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	180	Total	C	N	O	S	0	0	0
			1146	690	227	228	1			
2	E	116	Total	C	N	O	S	0	0	0
			823	497	163	162	1			
2	F	132	Total	C	N	O	S	0	0	0
			906	546	179	180	1			



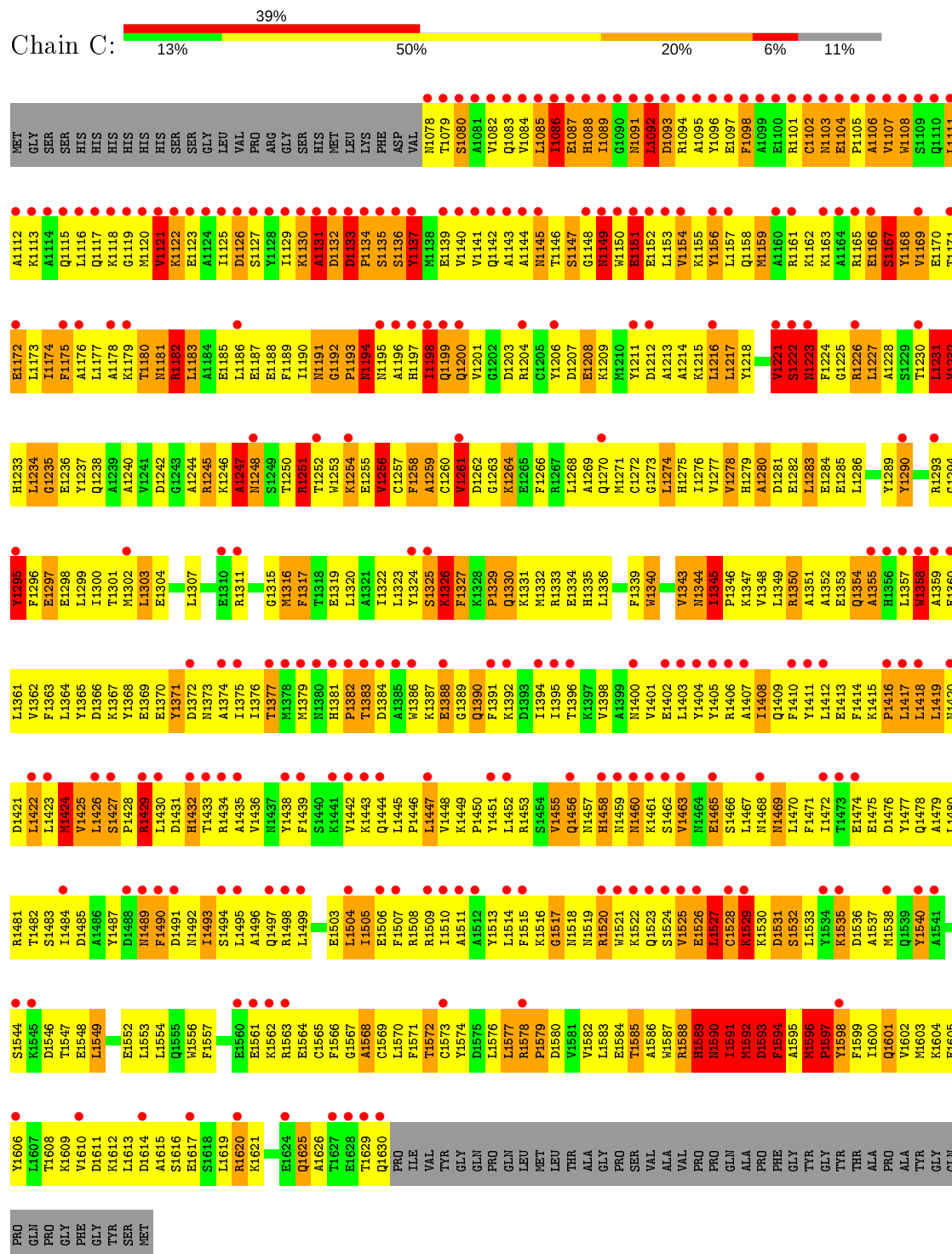
TYR	P1597
GLY	Y1888
TYR	F1599
THR	I1600
ALA	Q1601
PRO	V1602
ALA	M1603
TYR	K1604
GLY	E1605
GLN	Y1606
PRO	L1607
GLN	T1608
PRO	K1609
GLY	V1610
PHE	D1611
GLY	K1612
TYR	L1613
GLY	L1614
SER	A1615
MET	S1616
	S1617
	S1618
	L1619
	K1620
	E1622
	E1623
	E1624
	Q1625
	A1626
	T1627
	E1628
	T1629
	Q1630
	PRO
	I16
	VAL
	THR
	GLY
	GLN
	PRO
	GLN
	LEU
	MET
	LEU
	THR
	ALA
	GLY
	PRO
	SER
	VAL
	ALA
	VAL
	PRO
	PRO
	GLN
	ALA
	PRO
	PHE
	Q1110
	GLY

• Molecule 1: Clathrin heavy chain 1

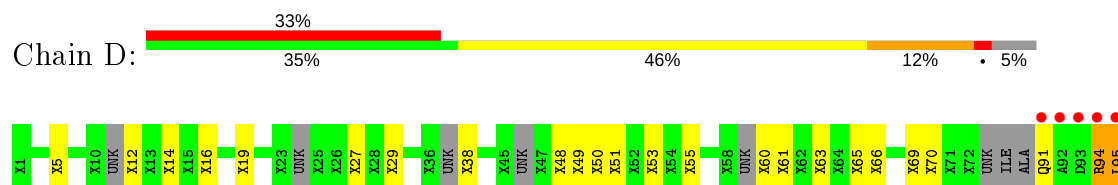


MET	A1172
GLY	K1113
SER	Q1114
SER	Q1115
HIS	L1116
HIS	Q1117
HIS	K1118
HIS	G1119
HIS	M1120
HIS	Y1121
SER	K1122
SER	E1123
GLY	A1124
LEU	I1125
VAL	D1126
PRO	S1127
ARG	Y1128
GLY	I1129
LYS	P1134
MET	A1131
HIS	K1130
SER	A1132
MET	D1133
LEU	P1134
ASP	S1136
VAL	Y1137
M1078	M1138
T1079	E1139
E1624	Q1140
A1081	V1141
Q1082	Q1142
Q1083	A1143
V1084	A1144
L1085	M1145
I1086	T1146
E1087	S1147
H1088	G1148
I1089	N1149
G1090	W1150
GLN	E1151
D1092	L1152
D1093	L1153
R1094	V1154
A1095	K1155
Y1096	Y1156
E1097	L1157
F1098	Q1158
GLY	M1159
PRO	A1160
SER	R1161
VAL	C1102
ALA	M1103
VAL	E1104
PRO	P1105
PRO	E1106
GLN	V1107
ALA	W1108
PRO	S1109
PHE	E1170
GLY	Q1110
GLY	L1111
	A1112
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	F1175
	L1176
	A1177
	K1178
	G1179
	T1180
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	R1182
	L1183
	A1184
	E1185
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	D1202
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	K1209
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	A1213
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	L1216
	L1217
	Y1218
	N1219
	A1220
	V1221
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	G1315
	M1316
	F1317
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	H1320
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	L1323
	Y1324
	S1325
	K1326
	F1327
	K1328
	P1329
	Q1330
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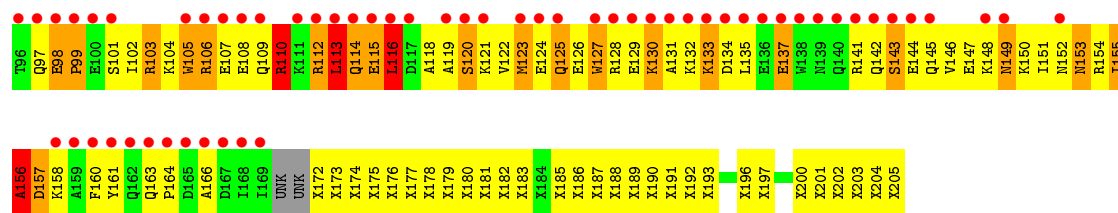
• Molecule 1: Clathrin heavy chain 1



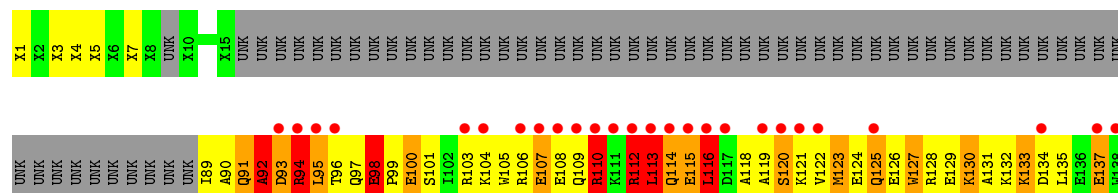
• Molecule 2: Clathrin light chain B







• Molecule 2: Clathrin light chain B



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	228.56 Å   228.56 Å   710.32 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	100.00 – 7.94 82.22 – 4.99	Depositor EDS
% Data completeness (in resolution range)	99.6 (100.00-7.94) 63.0 (82.22-4.99)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.97 (at 5.12 Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.419   ,   0.425 0.431   ,   0.441	Depositor DCC
$R_{free}$ test set	1304 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	310.7	Xtriage
Anisotropy	0.082	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41   ,   472.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.30$ , $\langle L^2 \rangle = 0.15$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.83	EDS
Total number of atoms	16504	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	295.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.39% 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 ⓘ

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	20/4638 (0.4%)	1.27	83/6266 (1.3%)
1	B	0.80	17/4638 (0.4%)	1.26	83/6266 (1.3%)
1	C	0.77	13/4638 (0.3%)	1.20	73/6266 (1.2%)
2	D	0.75	0/647	1.15	8/866 (0.9%)
2	E	0.69	0/589	1.24	5/785 (0.6%)
2	F	0.77	0/642	1.20	8/859 (0.9%)
All	All	0.79	50/15792 (0.3%)	1.24	260/21308 (1.2%)

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	1	8
1	B	0	3
1	C	2	3
2	F	0	1
All	All	3	15

The worst 5 of 50 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1162	LYS	C-O	-19.68	0.85	1.23
1	A	1222	SER	C-O	18.12	1.57	1.23
1	C	1182	ARG	C-O	17.19	1.56	1.23
1	C	1136	SER	C-O	-17.10	0.90	1.23
1	C	1248	ASN	N-CA	17.04	1.80	1.46

The worst 5 of 260 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1162	LYS	CA-C-O	22.12	166.55	120.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1279	HIS	O-C-N	-22.04	87.43	122.70
1	C	1223	ASN	N-CA-C	18.52	161.00	111.00
1	A	1103	ASN	C-N-CA	-17.51	77.93	121.70
1	A	1162	LYS	O-C-N	-16.77	95.87	122.70

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	1104	GLU	CA
1	C	1137	TYR	CA
1	C	1223	ASN	CA

5 of 15 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1103	ASN	Mainchain
1	A	1104	GLU	Mainchain
1	A	1133	ASP	Mainchain
1	A	1147	SER	Mainchain
1	A	1162	LYS	Mainchain

## 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	4543	0	4454	1296	1
1	B	4543	0	4456	1248	3
1	C	4543	0	4455	1291	4
2	D	1146	0	735	252	0
2	E	823	0	633	246	0
2	F	906	0	669	239	0
All	All	16504	0	15402	4313	5

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 135.

The worst 5 of 4313 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:1258:PHE:HB2	1:A:1289:TYR:CD2	1.19	1.69
1:A:1253:TRP:CZ3	1:A:1276:ILE:HG22	1.25	1.64
1:C:1253:TRP:CZ3	1:C:1276:ILE:HG22	1.25	1.64
1:B:1253:TRP:CZ3	1:B:1276:ILE:HG22	1.25	1.63
1:A:1258:PHE:CB	1:A:1289:TYR:CE2	1.75	1.63

All (5) 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:B:1340:TRP:CZ2	1:C:1222:SER:OG[12_655]	1.80	0.40
1:C:1304:GLU:OE2	1:C:1334:GLU:OE2[15_645]	1.98	0.22
1:A:1199:GLN:NE2	1:A:1431:ASP:OD2[10_555]	2.13	0.07
1:B:1340:TRP:CZ2	1:C:1222:SER:CB[12_655]	2.15	0.05
1:B:1341:SER:OG	1:C:1203:ASP:OD2[12_655]	2.18	0.02

## 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	551/624 (88%)	322 (58%)	152 (28%)	77 (14%)	0	4
1	B	551/624 (88%)	319 (58%)	161 (29%)	71 (13%)	0	5
1	C	551/624 (88%)	309 (56%)	164 (30%)	78 (14%)	0	4
2	D	77/190 (40%)	50 (65%)	16 (21%)	11 (14%)	0	4
2	E	66/190 (35%)	35 (53%)	21 (32%)	10 (15%)	0	4
2	F	76/190 (40%)	42 (55%)	20 (26%)	14 (18%)	0	2
All	All	1872/2442 (77%)	1077 (58%)	534 (28%)	261 (14%)	0	4

5 of 261 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1087	GLU
1	A	1091	ASN
1	A	1105	PRO
1	A	1122	LYS
1	A	1130	LYS

### 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	485/541 (90%)	409 (84%)	76 (16%)	2	14
1	B	485/541 (90%)	404 (83%)	81 (17%)	2	12
1	C	485/541 (90%)	395 (81%)	90 (19%)	1	9
2	D	62/73 (85%)	45 (73%)	17 (27%)	0	3
2	E	61/73 (84%)	42 (69%)	19 (31%)	0	2
2	F	62/73 (85%)	42 (68%)	20 (32%)	0	2
All	All	1640/1842 (89%)	1337 (82%)	303 (18%)	1	9

5 of 303 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1527	LEU
1	C	1108	TRP
2	E	140	GLN
1	B	1549	LEU
1	B	1601	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1390	GLN
1	B	1523	GLN
2	D	153	ASN
1	B	1456	GLN

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Mol	Chain	Res	Type
1	B	1468	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](#)

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, 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	553/624 (88%)	4.14	356 (64%) 0 0	306, 348, 348, 348	0
1	B	553/624 (88%)	4.69	361 (65%) 0 0	257, 257, 318, 319	0
1	C	553/624 (88%)	2.70	241 (43%) 0 1	232, 232, 308, 309	0
2	D	79/190 (41%)	4.35	63 (79%) 0 0	298, 298, 298, 298	0
2	E	68/190 (35%)	2.31	31 (45%) 0 1	314, 314, 314, 314	0
2	F	78/190 (41%)	3.34	37 (47%) 0 1	339, 339, 339, 339	0
All	All	1884/2442 (77%)	3.79	1089 (57%) 0 1	232, 307, 348, 348	0

The worst 5 of 1089 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1091	ASN	35.2
1	C	1078	ASN	33.8
1	C	1079	THR	31.8
1	C	1090	GLY	29.1
1	B	1105	PRO	27.6

### 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 carbohydrates 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.