



wwPDB X-ray Structure Validation Summary Report ⓘ

May 16, 2020 – 01:13 am BST

PDB ID : 3LVH
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 : 9.00 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 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

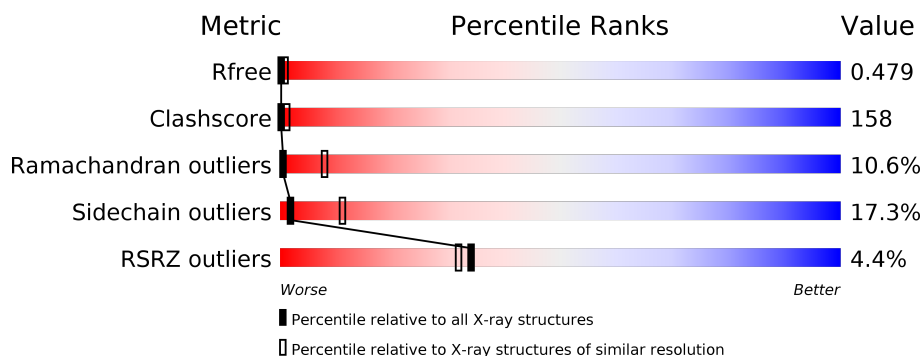
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 9.00 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 ≥ 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>7%</div> <div>13% 51% 20% 5% 11%</div> </div>
1	B	624	<div> <div>12% 52% 20% 5% 11%</div> </div>
1	C	624	<div> <div>2%</div> <div>13% 52% 20% 5% 11%</div> </div>
2	D	205	<div> <div>2%</div> <div>9% 33% 11% 45%</div> </div>
2	E	205	<div> <div>11%</div> <div>9% 28% 9% 50%</div> </div>
2	F	205	<div> <div>8% 32% 12% 45%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 16020 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	554	Total	C	N	O	S	0	0	0
			4550	2901	768	856	25			
1	B	554	Total	C	N	O	S	0	0	0
			4550	2901	768	856	25			
1	C	554	Total	C	N	O	S	0	0	0
			4550	2901	768	856	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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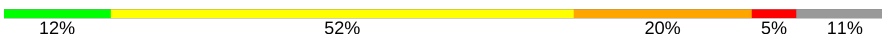
Chain	Residue	Modelled	Actual	Comment	Reference
C	1073	LEU	-	EXPRESSION TAG	UNP P49951

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

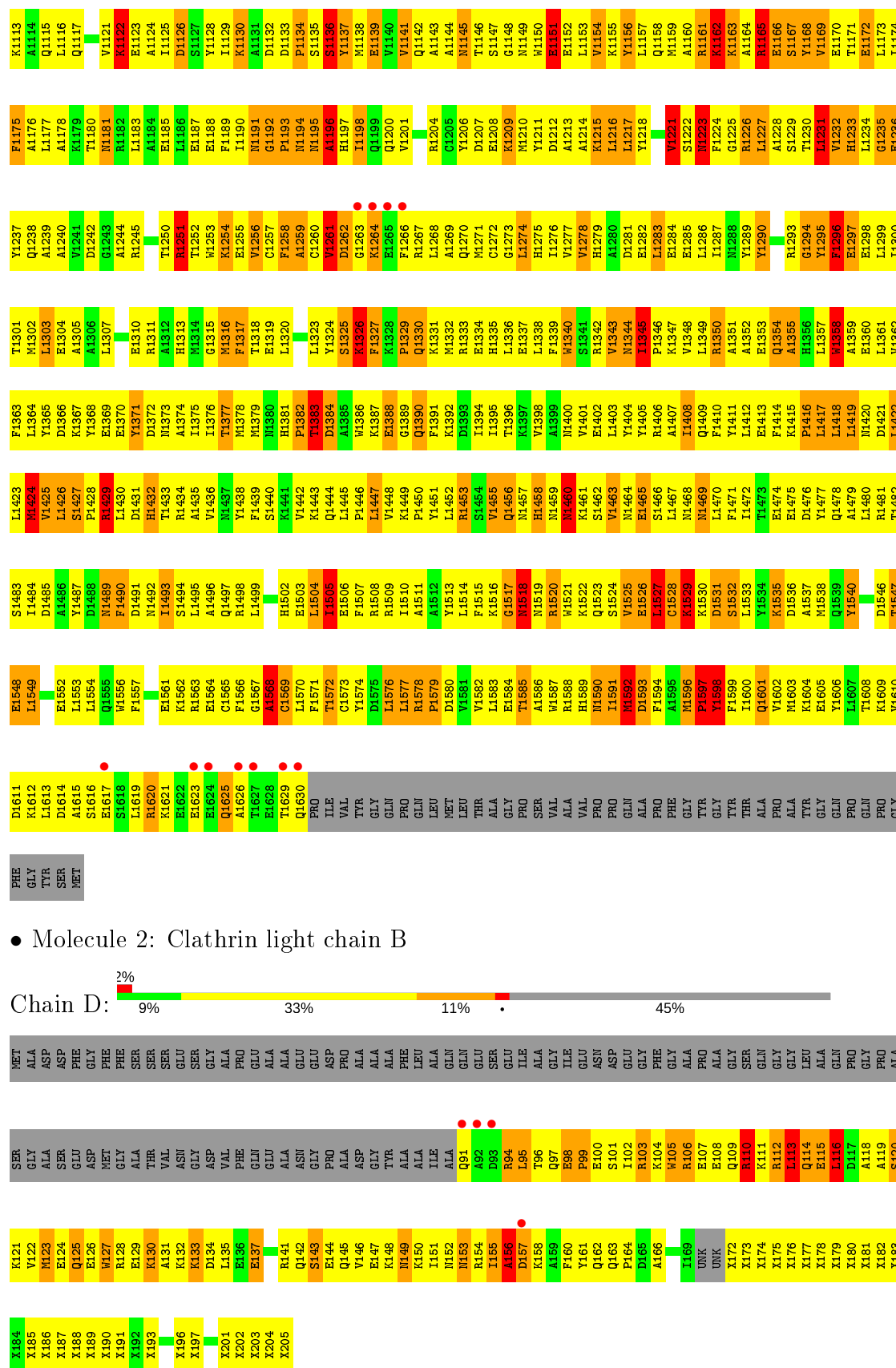
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	113	Total	C	N	O	S	0	0	0
			811	489	160	161	1			
2	E	102	Total	C	N	O	S	0	0	0
			753	455	149	148	1			
2	F	112	Total	C	N	O	S	0	0	0
			806	486	159	160	1			

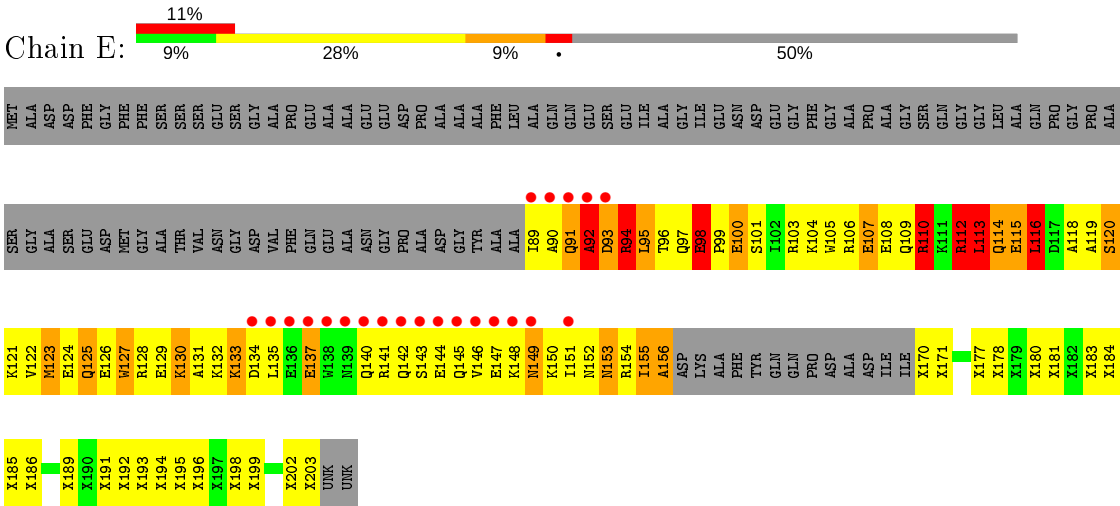
PRO
GLN
PRO
GLY
PHE
GLY
TYR
SER
MET

• Molecule 1: Clathrin heavy chain 1

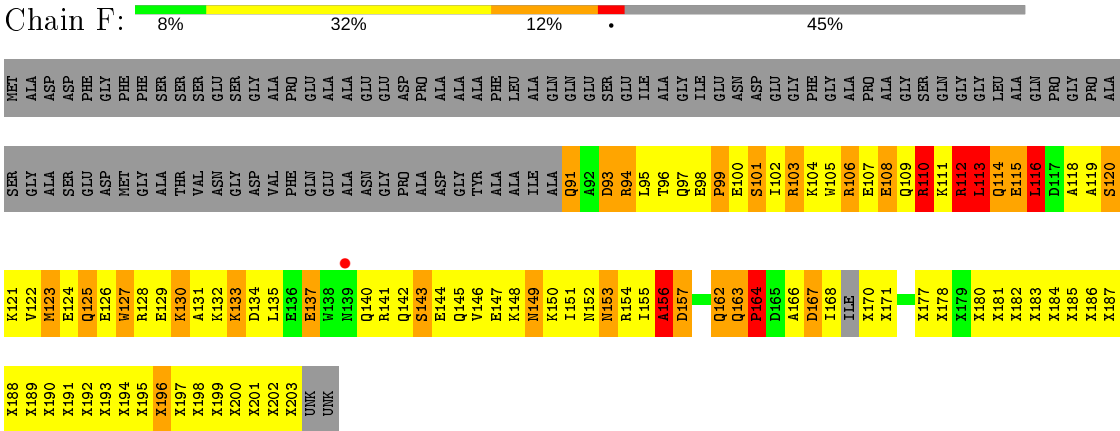
Chain B: 

PHE	V1610	T1547	T1482	L1422	V1362	L1299	E1236	F1175	K1113	MET
GLY	D1611	L1548	S1483	L1423	F1363	L1300	A1176	A1177	A1114	GLY
TYR	K1612	L1549	L1484	M1424	L1364	T1301	Q1238	L1177	Q1115	SER
SER	L1613		D1485	V1425	Y1365	M1302	A1239	A1178	L1116	SER
	D1614	E1552	D1486	L1426	L1366	L1303	E1241	K1179	Q1117	HIS
A1615		L1553	Y1487	S1427	K1367	E1304		T1180		HIS
S1616		L1554	D1488	P1428	Y1368		D1242	M1181	V1121	HIS
E1617		Q1555	M1489	R1429	E1369	L1307	G1243	L1182	K1122	HIS
S1618		F1556	F1490	L1430	E1370		A1244	L1183	E1123	HIS
L1619		F1557	D1491	D1431	Y1371	E1310		A1184	A1124	HIS
K1620		L1558	M1492	H1432	L1372	R1311		E1185	L1125	SER
R1621		E1561	L1493	T1433	M1373	M1312	T1250	L1186	D1126	SER
E1622		K1562	S1494	R1434	A1374	H1313	R1251	L1187	S1127	GLY
E1623		L1563	L1495	A1435	I1375	M1314	T1252	E1188	Y1128	LEU
E1624		E1564	A1496	V1436	L1376	G1315	W1253	F1189	I1129	VAL
Q1625		C1565	Q1497	N1437	T1377	M1316	K1254	T1190	K1130	PRO
A1626		F1566	L1498	Y1438	M1378	F1317	E1255	M1191	A1131	ARG
		G1567	L1499	F1439	M1379	T1318	V1256	G1192	D1132	GLY
				S1440	M1380	E1319	C1257	F1193	D1133	SER
				K1441	H1381	L1320	F1258	M1194	P1134	HIS
Q1630		C1569	H1502	V1442	L1382		A1259	M1195	S1135	MET
ILE	L1503	F1571	L1504	K1443	T1383		C1260	H1197	S1136	LEU
VAL	L1505	T1572	L1506	Q1444	D1384	Y1324	E1261	Y1137	Y1137	LYS
TYR	E1506	C1573	E1507	L1445	A1385	S1325	D1262	T1198	M1138	PHE
GLY	F1507	Y1574	F1508	P1446	K1386	K1326	G1263	Q1199	E1139	ASP
GLN	D1575	L1576	R1509	L1447	K1387	F1327	K1264	Q1200	V1140	
PRO	L1577		L1510	V1448	E1388	K1328	E1265	V1201		
GLN	L1578		L1511	K1449	G1389	P1329	F1266	R1204	A1143	
LEU	R1579		A1512	P1450	Q1390	Q1330	R1267	C1205	A1144	
MET		P1579		Y1451	F1391	K1331	L1268			
LEU										
LEU										
THR										
ALA										
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● Molecule 2: Clathrin light chain B



4 Data and refinement statistics

Property	Value	Source
Space group	P 4 ₂ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	229.71 Å 229.71 Å 512.27 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	500.00 – 9.00 86.66 – 9.00	Depositor EDS
% Data completeness (in resolution range)	78.7 (500.00-9.00) 78.9 (86.66-9.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.18	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.66 (at 8.41 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.473 , 0.487 0.483 , 0.479	Depositor DCC
R_{free} test set	430 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	604.9	Xtriage
Anisotropy	0.404	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.09 , -10.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.69	EDS
Total number of atoms	16020	wwPDB-VP
Average B, all atoms (Å ²)	103.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.04% 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

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	0.48	3/4645 (0.1%)	1.41	104/6276 (1.7%)
1	B	0.36	2/4645 (0.0%)	1.38	101/6276 (1.6%)
1	C	0.36	2/4645 (0.0%)	1.38	101/6276 (1.6%)
2	D	0.74	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	0.46	7/15813 (0.0%)	1.37	327/21338 (1.5%)

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	0	7
1	B	0	6
1	C	0	6
2	F	0	1
All	All	0	20

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1196	ALA	C-N	-21.36	0.84	1.34
1	C	1136	SER	C-N	-13.41	1.03	1.34
1	B	1136	SER	C-N	-13.39	1.03	1.34
1	A	1136	SER	C-N	-13.36	1.03	1.34
1	B	1592	MET	C-N	-10.33	1.10	1.34

The worst 5 of 327 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1136	SER	C-N-CA	22.64	178.31	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	1136	SER	C-N-CA	22.63	178.27	121.70
1	A	1136	SER	C-N-CA	22.58	178.15	121.70
1	A	1196	ALA	CB-CA-C	21.84	142.86	110.10
1	C	1196	ALA	CB-CA-C	21.79	142.78	110.10

There are no chirality outliers.

5 of 20 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1136	SER	Mainchain
1	A	1196	ALA	Mainchain,Peptide
1	A	1223	ASN	Peptide
1	A	1326	LYS	Peptide
1	A	1429	ARG	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	4550	0	4457	1578	23
1	B	4550	0	4456	1511	40
1	C	4550	0	4461	1420	30
2	D	811	0	641	286	0
2	E	753	0	615	220	0
2	F	806	0	640	345	35
All	All	16020	0	15270	4959	70

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 158.

The worst 5 of 4959 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:1253:TRP:CZ3	1:C:1276:ILE:HG22	1.19	1.67
1:A:1253:TRP:CZ3	1:A:1276:ILE:HG22	1.19	1.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1253:TRP:CZ3	1:B:1276:ILE:HG22	1.19	1.67
2:E:203:UNK:C	2:E:203:UNK:CA	1.76	1.62
1:B:1108:TRP:CH2	1:B:1129:ILE:HB	1.34	1.61

The worst 5 of 70 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:1198:ILE:N	2:F:103:ARG:NH1[5_545]	0.57	1.63
1:B:1199:GLN:N	2:F:103:ARG:NH2[5_545]	0.64	1.56
1:A:1097:GLU:OE1	1:C:1094:ARG:CG[8_465]	0.90	1.30
1:A:1097:GLU:CD	1:C:1094:ARG:CG[8_465]	0.92	1.28
1:B:1198:ILE:CD1	2:F:103:ARG:CB[5_545]	0.98	1.22

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	552/624 (88%)	332 (60%)	164 (30%)	56 (10%)	0	9
1	B	552/624 (88%)	332 (60%)	166 (30%)	54 (10%)	0	10
1	C	552/624 (88%)	332 (60%)	166 (30%)	54 (10%)	0	10
2	D	77/205 (38%)	50 (65%)	16 (21%)	11 (14%)	0	4
2	E	66/205 (32%)	35 (53%)	21 (32%)	10 (15%)	0	4
2	F	76/205 (37%)	42 (55%)	20 (26%)	14 (18%)	0	2
All	All	1875/2487 (75%)	1123 (60%)	553 (30%)	199 (11%)	0	8

5 of 199 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1086	ILE

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Mol	Chain	Res	Type
1	A	1122	LYS
1	A	1193	PRO
1	A	1231	LEU
1	A	1251	ARG

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	486/541 (90%)	410 (84%)	76 (16%)	2	14
1	B	486/541 (90%)	409 (84%)	77 (16%)	2	13
1	C	486/541 (90%)	410 (84%)	76 (16%)	2	14
2	D	62/128 (48%)	45 (73%)	17 (27%)	0	3
2	E	61/128 (48%)	42 (69%)	19 (31%)	0	2
2	F	62/128 (48%)	42 (68%)	20 (32%)	0	2
All	All	1643/2007 (82%)	1358 (83%)	285 (17%)	2	11

5 of 285 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1422	LEU
1	C	1111	LEU
2	E	153	ASN
1	B	1460	ASN
1	B	1574	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1381	HIS
1	B	1489	ASN
2	D	149	ASN
1	B	1390	GLN

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Mol	Chain	Res	Type
1	B	1457	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	3
1	B	2
1	C	2

The worst 5 of 7 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1592:MET	C	1593:ASP	N	1.10
1	B	1592:MET	C	1593:ASP	N	1.10
1	C	1592:MET	C	1593:ASP	N	1.10
1	A	1136:SER	C	1137:TYR	N	1.03

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	1136:SER	C	1137:TYR	N	1.03

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	554/624 (88%)	0.03	43 (7%) 13 15	50, 50, 132, 133	0
1	B	554/624 (88%)	-0.28	2 (0%) 92 87	50, 50, 132, 133	0
1	C	554/624 (88%)	-0.39	11 (1%) 65 58	50, 50, 132, 133	0
2	D	79/205 (38%)	0.13	4 (5%) 28 27	298, 298, 298, 298	0
2	E	68/205 (33%)	1.32	22 (32%) 0 2	314, 314, 314, 314	0
2	F	78/205 (38%)	-0.19	1 (1%) 77 68	339, 339, 339, 339	0
All	All	1887/2487 (75%)	-0.14	83 (4%) 34 32	50, 50, 314, 339	0

The worst 5 of 83 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1313	HIS	6.8
1	A	1306	ALA	6.2
1	A	1341	SER	6.2
1	A	1312	ALA	6.1
1	A	1279	HIS	5.8

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.