



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 07:04 AM UTC

PDB ID : 3LVG / pdb_00003lvg
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

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:

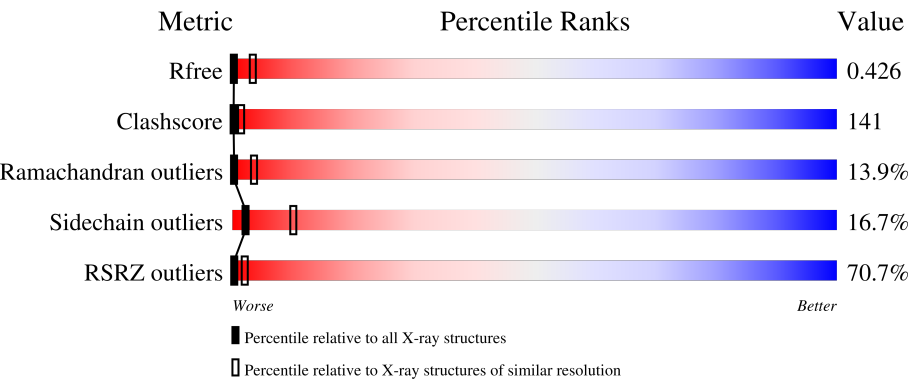
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

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}	180053	1168 (11.50-4.00)
Clashscore	190562	1001 (11.50-4.06)
Ramachandran outliers	187476	1055 (11.50-4.00)
Sidechain outliers	187428	1018 (11.50-4.00)
RSRZ outliers	180081	1162 (11.50-4.00)

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	624	66% 11% 48% 23% 7% 11%
1	B	624	65% 10% 49% 24% 6% 11%
1	C	624	57% 11% 48% 23% 7% 11%
2	D	190	26% 34% 44% 15% • 5%
2	E	190	26% 15% 29% 12% 5% 39%

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Mol	Chain	Length	Quality of chain
2	F	190	33% 15% 35% 15% 31%

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

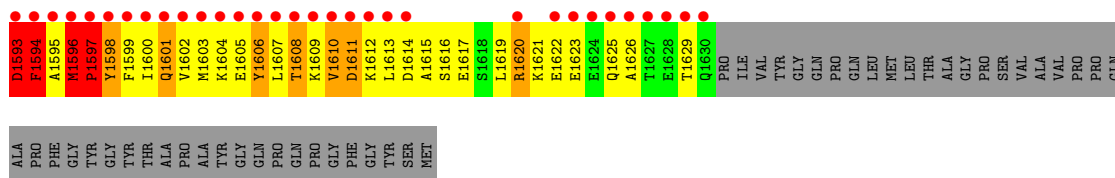
- Molecule 2 is a protein called Clathrin light chain B.

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			

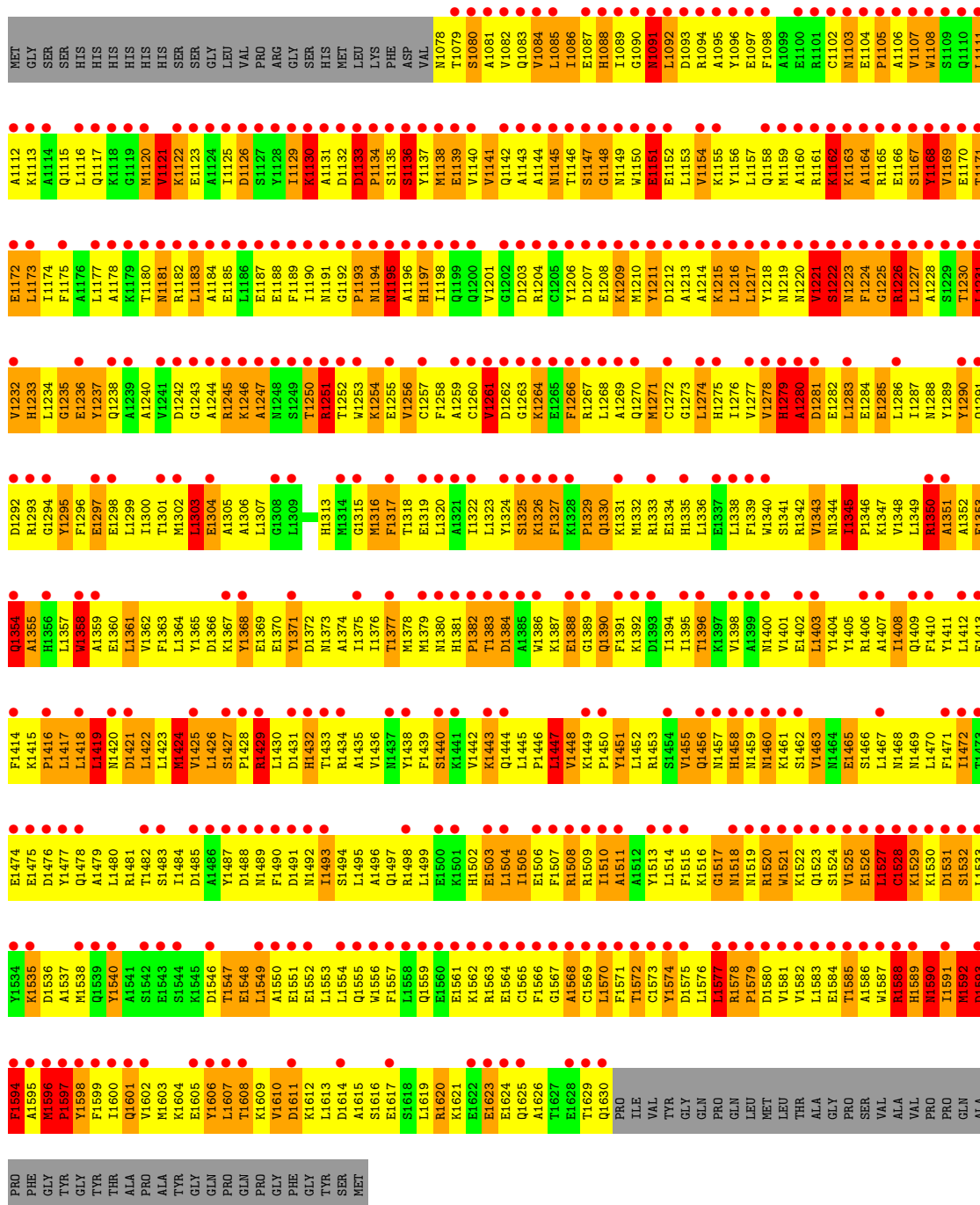
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

Chain A:

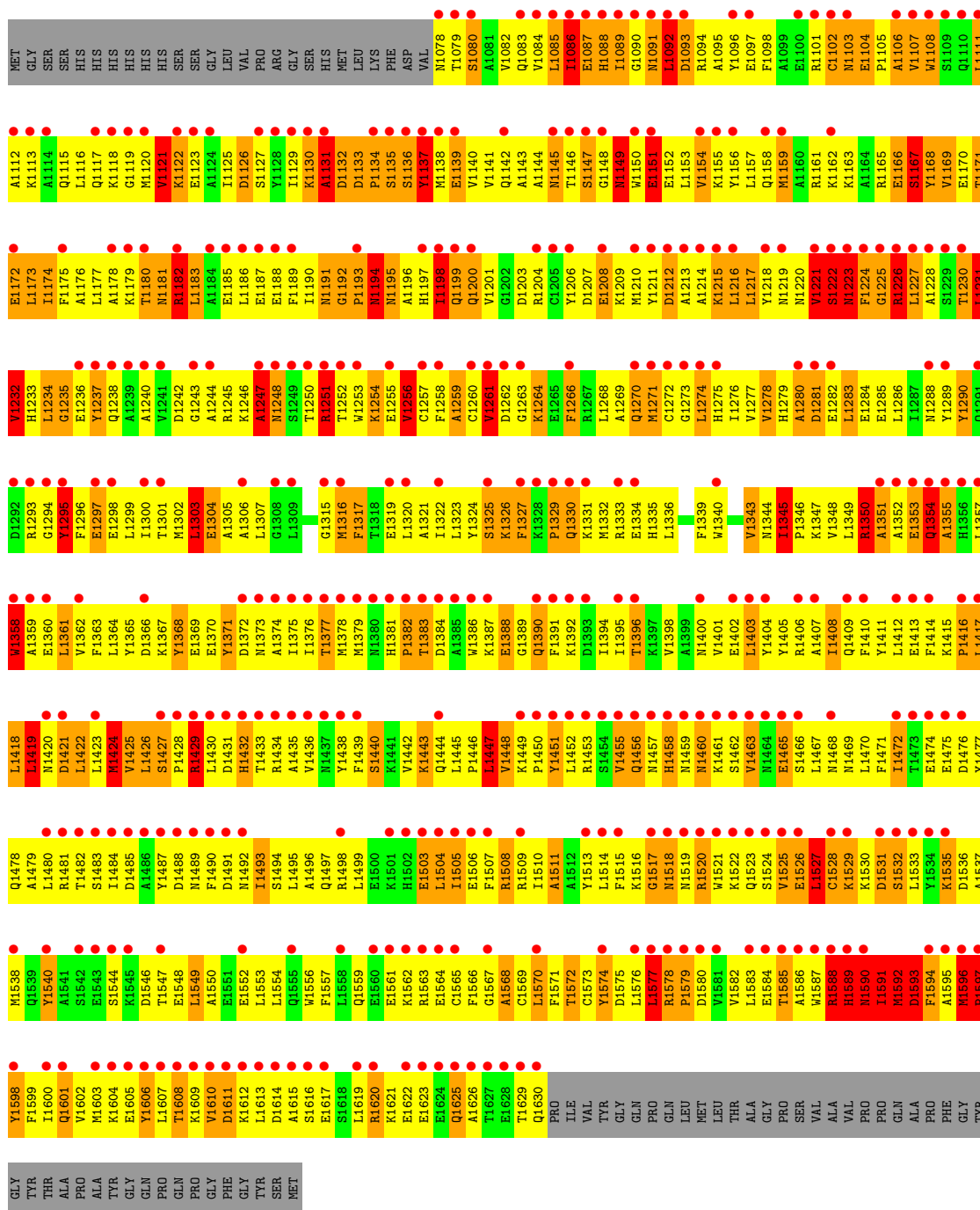
Node	Parent	Weight	Depth	Color
E1413	E1474	0.1	1	Blue
E1414	E1474	0.1	1	Blue
E1415	E1474	0.1	1	Blue
E1416	E1474	0.1	1	Blue
E1417	E1474	0.1	1	Blue
E1418	E1474	0.1	1	Blue
E1419	E1474	0.1	1	Blue
E1420	E1474	0.1	1	Blue
E1421	E1474	0.1	1	Blue
E1422	E1474	0.1	1	Blue
E1423	E1474	0.1	1	Blue
E1424	E1474	0.1	1	Blue
E1425	E1474	0.1	1	Blue
E1426	E1474	0.1	1	Blue
E1427	E1474	0.1	1	Blue
E1428	E1474	0.1	1	Blue
E1429	E1474	0.1	1	Blue
E1430	E1474	0.1	1	Blue
E1431	E1474	0.1	1	Blue
E1432	E1474	0.1	1	Blue
E1433	E1474	0.1	1	Blue
E1434	E1474	0.1	1	Blue
E1435	E1474	0.1	1	Blue
E1436	E1474	0.1	1	Blue
E1437	E1474	0.1	1	Blue
E1438	E1474	0.1	1	Blue
E1439	E1474	0.1	1	Blue
E1440	E1474	0.1	1	Blue
E1441	E1474	0.1	1	Blue
E1442	E1474	0.1	1	Blue
E1443	E1474	0.1	1	Blue
E1444	E1474	0.1	1	Blue
E1445	E1474	0.1	1	Blue
E1446	E1474	0.1	1	Blue
E1447	E1474	0.1	1	Blue
E1448	E1474	0.1	1	Blue
E1449	E1474	0.1	1	Blue
E1450	E1474	0.1	1	Blue
E1451	E1474	0.1	1	Blue
E1452	E1474	0.1	1	Blue
E1453	E1474	0.1	1	Blue
E1454	E1474	0.1	1	Blue
E1455	E1474	0.1	1	Blue
E1456	E1474	0.1	1	Blue
E1457	E1474	0.1	1	Blue
E1458	E1474	0.1	1	Blue
E1459	E1474	0.1	1	Blue
E1460	E1474	0.1	1	Blue
E1461	E1474	0.1	1	Blue
E1462	E1474	0.1	1	Blue
E1463	E1474	0.1	1	Blue
E1464	E1474	0.1	1	Blue
E1465	E1474	0.1	1	Blue
E1466	E1474	0.1	1	Blue
E1467	E1474	0.1	1	Blue
E1468	E1474	0.1	1	Blue
E1469	E1474	0.1	1	Blue
E1470	E1474	0.1	1	Blue
E1471	E1474	0.1	1	Blue
E1472	E1474	0.1	1	Blue
E1473	E1474	0.1	1	Blue
E1474	E1474	0.1	1	Blue
E1475	E1474	0.1	1	Blue
E1476	E1474	0.1	1	Blue
E1477	E1474	0.1	1	Blue
E1478	E1474	0.1	1	Blue
E1479	E1474	0.1	1	Blue
E1480	E1474	0.1	1	Blue
E1481	E1474	0.1	1	Blue
E1482	E1474	0.1	1	Blue
E1483	E1474	0.1	1	Blue
E1484	E1474	0.1	1	Blue
E1485	E1474	0.1	1	Blue
E1486	E1474	0.1	1	Blue
E1487	E1474	0.1	1	Blue
E1488	E1474	0.1	1	Blue
E1489	E1474	0.1	1	Blue
E1490	E1474	0.1	1	Blue
E1491	E1474	0.1	1	Blue
E1492	E1474	0.1	1	Blue
E1493	E1474	0.1	1	Blue
E1494	E1474	0.1	1	Blue
E1495	E1474	0.1	1	Blue
E1496	E1474	0.1	1	Blue
E1497	E1474	0.1	1	Blue
E1498	E1474	0.1	1	Blue
E1499	E1474	0.1	1	Blue
E1500	E1474	0.1	1	Blue
E1501	E1474	0.1	1	Blue
E1502	E1474	0.		



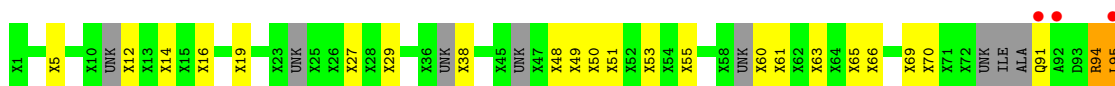
• Molecule 1: Clathrin heavy chain 1

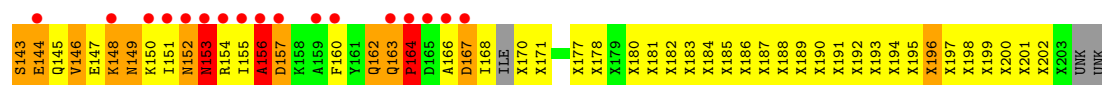


- Molecule 1: Clathrin heavy chain 1



- 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, α , β , γ	228.56Å 228.56Å 710.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 7.94 100.00 – 7.94	Depositor EDS
% Data completeness (in resolution range)	99.6 (100.00-7.94) 99.6 (100.00-7.94)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.97 (at 5.12Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.419 , 0.425 0.423 , 0.426	Depositor DCC
R_{free} test set	1304 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	310.7	Xtriage
Anisotropy	0.082	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 486.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.30$, $\langle L^2 \rangle = 0.15$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.77	EDS
Total number of atoms	16504	wwPDB-VP
Average B, all atoms (Å ²)	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.*

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	1.25	41/4638 (0.9%)	1.91	171/6266 (2.7%)
1	B	1.22	28/4638 (0.6%)	1.84	156/6266 (2.5%)
1	C	1.23	26/4638 (0.6%)	1.70	130/6266 (2.1%)
2	D	1.00	2/647 (0.3%)	1.65	17/866 (2.0%)
2	E	0.87	2/589 (0.3%)	1.69	19/785 (2.4%)
2	F	0.99	2/642 (0.3%)	1.74	21/859 (2.4%)
All	All	1.20	101/15792 (0.6%)	1.81	514/21308 (2.4%)

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 101 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1162	LYS	C-O	-33.40	0.85	1.24
1	C	1182	ARG	C-O	32.59	1.56	1.24
1	C	1247	ALA	CA-C	30.70	1.94	1.52
1	C	1248	ASN	N-CA	28.62	1.80	1.46
1	A	1222	SER	C-O	26.82	1.57	1.24

The worst 5 of 514 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1162	LYS	CA-C-O	43.22	166.55	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1104	GLU	CA-C-N	-39.66	70.27	119.84
1	A	1104	GLU	C-N-CA	-39.66	70.27	119.84
1	B	1279	HIS	O-C-N	-26.43	87.43	122.59
1	B	1223	ASN	N-CA-C	26.37	145.99	112.24

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	4455	1345	1
1	B	4543	0	4457	1295	3
1	C	4543	0	4456	1358	4
2	D	1146	0	735	252	0
2	E	823	0	633	248	0
2	F	906	0	669	248	0
All	All	16504	0	15405	4488	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 141.

The worst 5 of 4488 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:A:1258:PHE:CB	1:A:1289:TYR:CE2	1.75	1.63
1:B:1253:TRP:CZ3	1:B:1276:ILE:HG22	1.25	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	3
1	B	551/624 (88%)	319 (58%)	161 (29%)	71 (13%)	0	4
1	C	551/624 (88%)	309 (56%)	164 (30%)	78 (14%)	0	3
2	D	77/190 (40%)	50 (65%)	16 (21%)	11 (14%)	0	3
2	E	66/190 (35%)	35 (53%)	21 (32%)	10 (15%)	0	3
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	3

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%)	420 (87%)	65 (13%)	4	14
1	B	485/541 (90%)	414 (85%)	71 (15%)	3	13
1	C	485/541 (90%)	405 (84%)	80 (16%)	2	10
2	D	62/73 (85%)	44 (71%)	18 (29%)	0	2
2	E	61/73 (84%)	42 (69%)	19 (31%)	0	2
2	F	62/73 (85%)	41 (66%)	21 (34%)	0	1
All	All	1640/1842 (89%)	1366 (83%)	274 (17%)	2	10

5 of 274 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	146	VAL
2	E	100	GLU
2	F	112	ARG
1	B	1345	ILE
1	B	1303	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	1523	GLN
1	C	1590	ASN
2	F	149	ASN
1	B	1145	ASN

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Mol	Chain	Res	Type
1	B	1091	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 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	553/624 (88%)	3.37	410 (74%) 0 2	306, 348, 348, 348	0
1	B	553/624 (88%)	3.72	403 (72%) 0 2	257, 257, 318, 319	0
1	C	553/624 (88%)	2.96	356 (64%) 0 2	232, 232, 308, 309	0
2	D	79/190 (41%)	2.85	50 (63%) 0 2	298, 298, 298, 298	0
2	E	68/190 (35%)	3.52	50 (73%) 0 2	314, 314, 314, 314	0
2	F	78/190 (41%)	3.67	63 (80%) 0 1	339, 339, 339, 339	0
All	All	1884/2442 (77%)	3.35	1332 (70%) 0 2	232, 307, 348, 348	0

The worst 5 of 1332 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1222	SER	30.2
1	C	1489	ASN	19.2
1	A	1093	ASP	16.4
1	B	1165	ARG	15.1
1	C	1380	ASN	13.9

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.