



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 11, 2024 – 09:15 PM EDT

PDB ID : 1C9L
Title : PEPTIDE-IN-GROOVE INTERACTIONS LINK TARGET PROTEINS TO
THE B-PROPELLER OF CLATHRIN
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Deposited on : 1999-08-02
Resolution : 2.90 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	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
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)	:	2.36.2

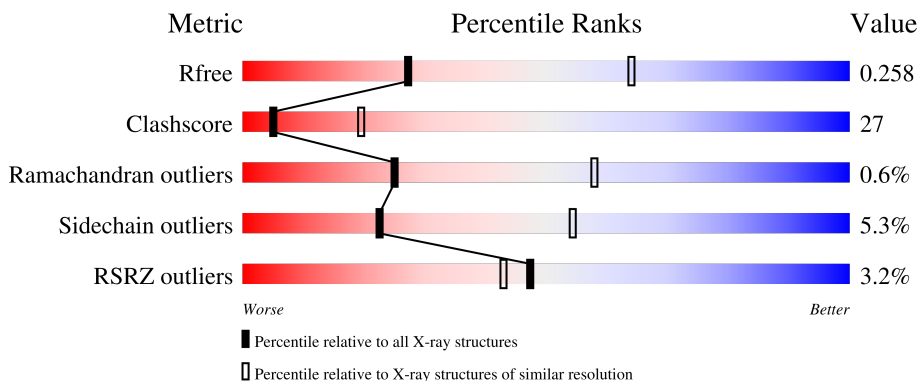
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



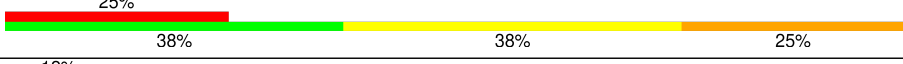

The reported resolution of this entry is 2.90 Å.

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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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	357	
1	B	357	
2	C	8	
2	D	8	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5716 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	357	Total	C	N	O	S	0	0	0
			2789	1773	480	518	18			
1	B	357	Total	C	N	O	S	0	0	0
			2789	1773	480	518	18			

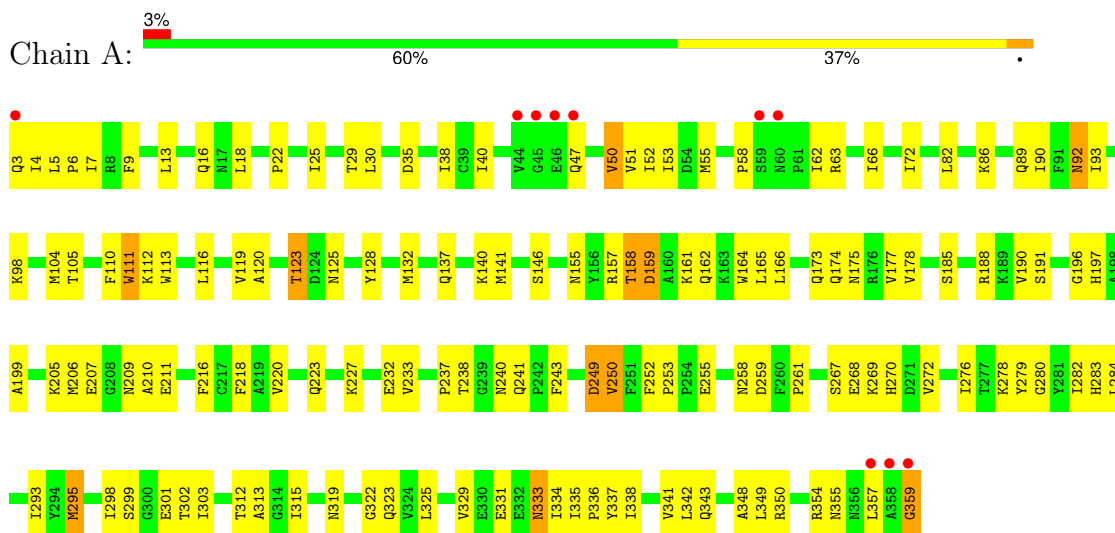
- Molecule 2 is a protein called B-ADAPTIN 3.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	8	Total	C	N	O	0	0	0
			69	43	9	17			
2	D	8	Total	C	N	O	0	0	0
			69	43	9	17			

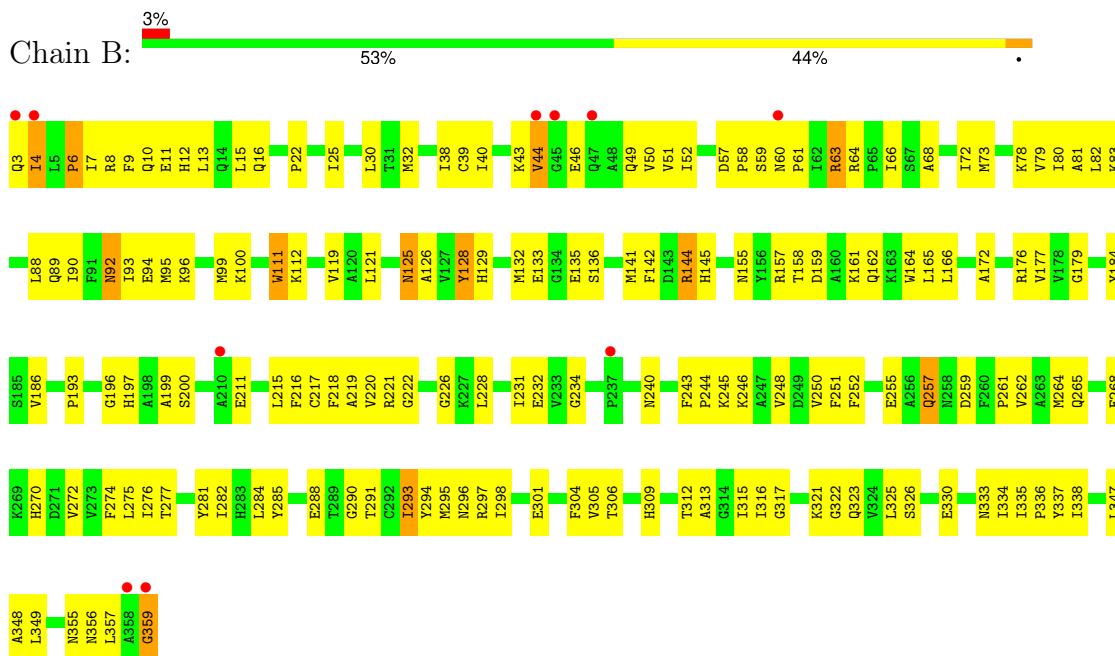
3 Residue-property plots

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: CLATHRIN



• Molecule 1: CLATHRIN



• Molecule 2: B-ADAPTIN 3



● Molecule 2: B-ADAPTIN 3



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	137.62Å 130.79Å 78.47Å 90.00° 115.47° 90.00°	Depositor
Resolution (Å)	30.00 – 2.90 29.94 – 2.90	Depositor EDS
% Data completeness (in resolution range)	92.4 (30.00-2.90) 92.5 (29.94-2.90)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.74 (at 2.90Å)	Xtriage
Refinement program	CNS 0.5	Depositor
R, R_{free}	0.221 , 0.263 0.217 , 0.258	Depositor DCC
R_{free} test set	1282 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	32.2	Xtriage
Anisotropy	0.323	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 56.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	5716	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.73% 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 [i](#)

5.1 Standard geometry [i](#)

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	1.12	2/2847 (0.1%)	0.78	1/3859 (0.0%)
1	B	1.12	2/2847 (0.1%)	0.79	5/3859 (0.1%)
2	C	1.88	3/69 (4.3%)	1.57	1/91 (1.1%)
2	D	1.53	1/69 (1.4%)	1.50	1/91 (1.1%)
All	All	1.14	8/5832 (0.1%)	0.81	8/7900 (0.1%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	359	GLY	C-OXT	53.00	2.24	1.23
1	B	359	GLY	C-OXT	53.00	2.24	1.23
2	C	377	GLU	C-OXT	9.93	1.42	1.23
2	D	377	GLU	C-OXT	9.75	1.41	1.23
2	C	377	GLU	N-CA	-6.50	1.33	1.46

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	6	PRO	CA-C-N	-8.35	98.83	117.20
1	A	3	GLN	C-N-CA	-8.33	100.88	121.70
1	B	3	GLN	C-N-CA	-6.61	105.17	121.70
1	B	63	ARG	C-N-CA	6.47	137.86	121.70
2	C	377	GLU	N-CA-C	6.41	128.32	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	2789	0	2799	136	0
1	B	2789	0	2799	171	0
2	C	69	0	58	4	0
2	D	69	0	59	10	0
All	All	5716	0	5715	310	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 27.

The worst 5 of 310 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:323:GLN:HE21	1:A:325:LEU:HD21	1.09	1.11
1:B:50:VAL:HG23	1:B:66:ILE:HG12	1.35	1.09
1:B:301:GLU:HG3	1:B:321:LYS:HG3	1.39	0.99
1:B:92:ASN:ND2	1:B:95:MET:H	1.61	0.97
1:B:51:VAL:HG22	1:B:63:ARG:HG2	1.46	0.95

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	355/357 (99%)	327 (92%)	28 (8%)	0	100	100
1	B	355/357 (99%)	328 (92%)	23 (6%)	4 (1%)	14	42
2	C	6/8 (75%)	6 (100%)	0	0	100	100
2	D	6/8 (75%)	5 (83%)	1 (17%)	0	100	100
All	All	722/730 (99%)	666 (92%)	52 (7%)	4 (1%)	25	58

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	44	VAL
1	B	136	SER
1	B	15	LEU
1	B	135	GLU

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	306/306 (100%)	287 (94%)	19 (6%)	18	47
1	B	306/306 (100%)	294 (96%)	12 (4%)	32	66
2	C	8/8 (100%)	6 (75%)	2 (25%)	0	2
2	D	8/8 (100%)	8 (100%)	0	100	100
All	All	628/628 (100%)	595 (95%)	33 (5%)	22	54

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	257	GLN
1	B	268	GLU
2	C	377	GLU
1	A	250	VAL
1	A	249	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	16	GLN
1	B	102	HIS
1	B	309	HIS
1	B	92	ASN
1	B	125	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 monosaccharides 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
2	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	376:PHE	C	377:GLU	N	1.19

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	357/357 (100%)	-0.34	10 (2%) 53 49	6, 24, 52, 82	0
1	B	357/357 (100%)	-0.29	10 (2%) 53 49	7, 25, 51, 73	0
2	C	8/8 (100%)	0.85	2 (25%) 0 0	25, 44, 63, 79	0
2	D	8/8 (100%)	1.31	1 (12%) 3 3	39, 58, 70, 88	0
All	All	730/730 (100%)	-0.29	23 (3%) 47 43	6, 25, 55, 88	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	359	GLY	6.8
2	D	370	ASP	5.0
1	A	359	GLY	4.9
1	B	3	GLN	3.7
1	A	358	ALA	3.6

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 monosaccharides 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.