



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:25 PM UTC

PDB ID : 5UF7 / pdb_00005uf7
Title : CRYSTAL STRUCTURE OF MUNC13-1 MUN DOMAIN
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Deposited on : 2017-01-03
Resolution : 2.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

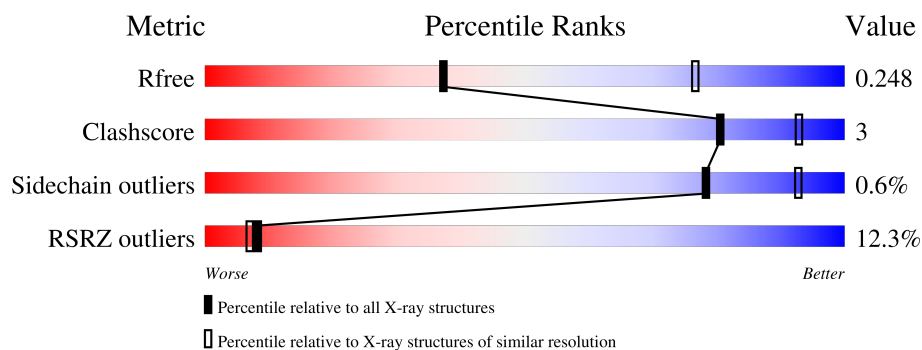
1 Overall quality at a glance

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}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (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	547	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 8563 atoms, of which 4282 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 Protein unc-13 homolog A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	530	Total	C	H	N	O	S	0	0	0
			8563	2731	4282	714	808	28			

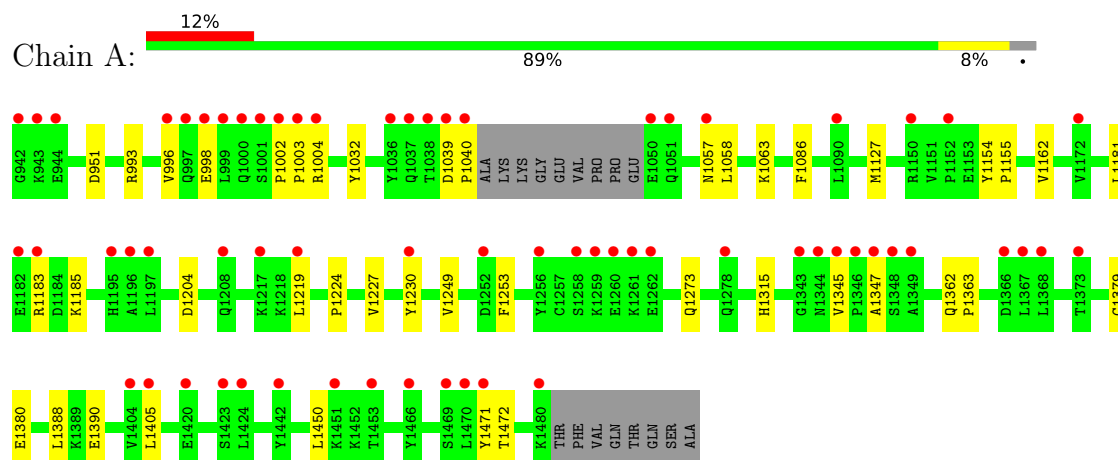
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1408	GLU	-	linker	UNP Q62768
A	1409	PHE	-	linker	UNP Q62768

3 Residue-property plots [i](#)

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: Protein unc-13 homolog A



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	114.06Å 270.92Å 47.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.02 – 2.90 39.02 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.2 (39.02-2.90) 99.1 (39.02-2.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.63 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.11.1 _2575	Depositor
R, R_{free}	0.228 , 0.253 (Not available) , 0.248	Depositor DCC
R_{free} test set	1712 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	85.4	Xtriage
Anisotropy	0.322	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 53.4	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	0.94	EDS
Total number of atoms	8563	wwPDB-VP
Average B, all atoms (Å ²)	112.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.77% 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	0.11	0/4368	0.26	0/5900

There are no bond length outliers.

There are no bond angle outliers.

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	4281	4282	4282	22	0
All	All	4281	4282	4282	22	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 3.

All (22) 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:1345:VAL:O	1:A:1347:ALA:N	2.25	0.70
1:A:1405:LEU:O	1:A:1471:TYR:OH	2.20	0.57
1:A:1249:VAL:O	1:A:1253:PHE:N	2.42	0.52
1:A:1181:LEU:O	1:A:1185:LYS:N	2.39	0.51
1:A:951:ASP:OD1	1:A:993:ARG:NH2	2.38	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1002:PRO:N	1:A:1003:PRO:CD	2.74	0.50
1:A:1162:VAL:HG21	1:A:1230:TYR:CZ	2.49	0.47
1:A:1183:ARG:NH2	1:A:1204:ASP:OD2	2.49	0.46
1:A:996:VAL:O	1:A:998:GLU:N	2.47	0.46
1:A:1154:TYR:N	1:A:1155:PRO:CD	2.79	0.46
1:A:1057:ASN:OD1	1:A:1058:LEU:N	2.48	0.46
1:A:1127:MET:HE3	1:A:1219:LEU:HD11	1.97	0.46
1:A:1472:THR:HG22	1:A:1472:THR:O	2.17	0.45
1:A:1002:PRO:O	1:A:1004:ARG:N	2.48	0.45
1:A:1388:LEU:CB	1:A:1450:LEU:HD11	2.48	0.45
1:A:1450:LEU:HD12	1:A:1450:LEU:N	2.34	0.43
1:A:1039:ASP:HB3	1:A:1040:PRO:CD	2.50	0.42
1:A:1362:GLN:N	1:A:1363:PRO:HD2	2.35	0.41
1:A:1032:TYR:CD1	1:A:1063:LYS:HD3	2.55	0.41
1:A:1315:HIS:HA	1:A:1390:GLU:HG2	2.03	0.40
1:A:1224:PRO:HA	1:A:1227:VAL:HG12	2.02	0.40
1:A:1273:GLN:HG2	1:A:1380:GLU:HG2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

There are no protein backbone outliers to report in this entry.

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	332/499 (66%)	330 (99%)	2 (1%)	78 93

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1086	PHE
1	A	1379	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

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, 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	530/547 (96%)	0.74	65 (12%) 8 7	60, 107, 174, 241	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1346	PRO	8.8
1	A	1347	ALA	8.0
1	A	1345	VAL	7.6
1	A	1040	PRO	6.9
1	A	1405	LEU	6.5
1	A	1368	LEU	6.1
1	A	998	GLU	5.9
1	A	1002	PRO	5.6
1	A	1208	GLN	5.1
1	A	1051	GLN	4.9
1	A	1404	VAL	4.9
1	A	1003	PRO	4.7
1	A	999	LEU	4.7
1	A	1348	SER	4.7
1	A	1259	LYS	4.6
1	A	1261	LYS	4.6
1	A	943	LYS	4.5
1	A	1039	ASP	4.3
1	A	997	GLN	4.2
1	A	1150	ARG	4.1
1	A	1258	SER	4.0
1	A	1367	LEU	4.0
1	A	1442	TYR	3.9
1	A	1260	GLU	3.5
1	A	942	GLY	3.4
1	A	1451	LYS	3.3
1	A	1152	PRO	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	1349	ALA	3.3
1	A	1050	GLU	3.2
1	A	1001	SER	3.1
1	A	1057	ASN	3.0
1	A	1373	THR	3.0
1	A	1036	TYR	3.0
1	A	1038	THR	2.9
1	A	996	VAL	2.8
1	A	1343	GLY	2.8
1	A	1195	HIS	2.6
1	A	1037	GLN	2.6
1	A	1278	GLN	2.6
1	A	1004	ARG	2.6
1	A	1471	TYR	2.5
1	A	1000	GLN	2.5
1	A	1424	LEU	2.5
1	A	1256	TYR	2.5
1	A	1183	ARG	2.4
1	A	944	GLU	2.4
1	A	1470	LEU	2.4
1	A	1344	ASN	2.4
1	A	1252	ASP	2.3
1	A	1480	LYS	2.3
1	A	1423	SER	2.3
1	A	1453	THR	2.2
1	A	1469	SER	2.2
1	A	1230	TYR	2.2
1	A	1197	LEU	2.2
1	A	1217	LYS	2.1
1	A	1262	GLU	2.1
1	A	1366	ASP	2.1
1	A	1182	GLU	2.1
1	A	1219	LEU	2.1
1	A	1196	ALA	2.1
1	A	1172	VAL	2.0
1	A	1420	GLU	2.0
1	A	1090	LEU	2.0
1	A	1466	TYR	2.0

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 [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.