



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:05 PM UTC

PDB ID : 5NS9 / pdb_00005ns9
Title : Crystal structure of the GluA2 LBD (L483Y-N754S-L758V) in complex with glutamate
Authors : Eibl, C.; Plested, A.J.R.
Deposited on : 2017-04-25
Resolution : 1.44 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
Mogul : 2022.3.0, CSD as543be (2022)
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

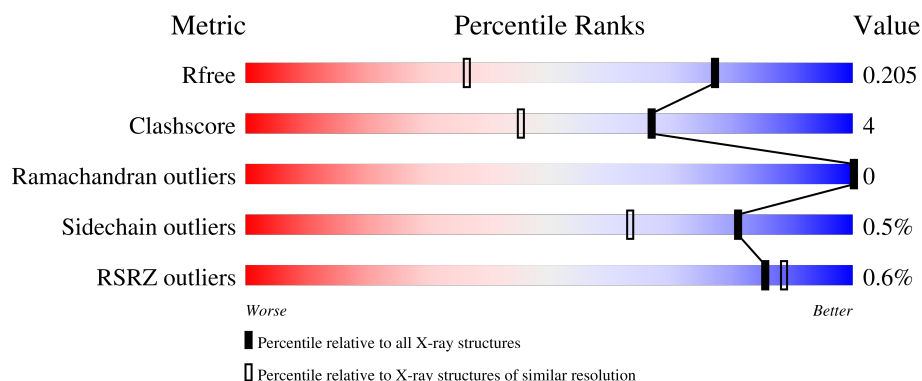
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.44 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	3234 (1.46-1.42)
Clashscore	190562	3289 (1.46-1.42)
Ramachandran outliers	187476	3248 (1.46-1.42)
Sidechain outliers	187428	3248 (1.46-1.42)
RSRZ outliers	180081	3234 (1.46-1.42)

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	292	81% 9% 10%
1	B	292	80% 9% 11%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 9845 atoms, of which 4504 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 Glutamate receptor 2, Glutamate receptor 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	263	Total	C	H	N	O	S	90	24	0
			4494	1423	2273	361	422	15			
1	B	261	Total	C	H	N	O	S	85	13	0
			4299	1361	2171	349	403	15			

There are 70 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-27	MET	-	initiating methionine	UNP P19491
A	-26	HIS	-	expression tag	UNP P19491
A	-25	HIS	-	expression tag	UNP P19491
A	-24	HIS	-	expression tag	UNP P19491
A	-23	HIS	-	expression tag	UNP P19491
A	-22	HIS	-	expression tag	UNP P19491
A	-21	HIS	-	expression tag	UNP P19491
A	-20	HIS	-	expression tag	UNP P19491
A	-19	HIS	-	expression tag	UNP P19491
A	-18	SER	-	expression tag	UNP P19491
A	-17	SER	-	expression tag	UNP P19491
A	-16	GLY	-	expression tag	UNP P19491
A	-15	LEU	-	expression tag	UNP P19491
A	-14	VAL	-	expression tag	UNP P19491
A	-13	PRO	-	expression tag	UNP P19491
A	-12	ARG	-	expression tag	UNP P19491
A	-11	GLY	-	expression tag	UNP P19491
A	-10	SER	-	expression tag	UNP P19491
A	-9	ALA	-	expression tag	UNP P19491
A	-8	MET	-	expression tag	UNP P19491
A	-7	GLY	-	expression tag	UNP P19491
A	-6	SER	-	expression tag	UNP P19491
A	-5	GLY	-	expression tag	UNP P19491
A	-4	ASN	-	expression tag	UNP P19491
A	-3	ASP	-	expression tag	UNP P19491

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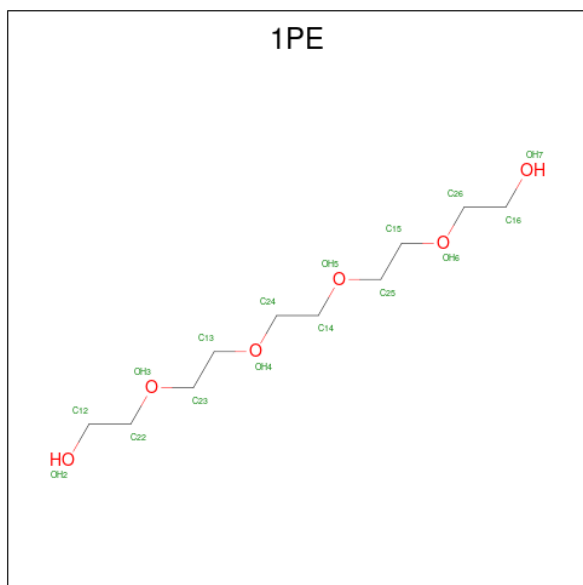
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	THR	-	expression tag	UNP P19491
A	-1	SER	-	expression tag	UNP P19491
A	0	ARG	-	expression tag	UNP P19491
A	1	GLY	-	expression tag	UNP P19491
A	2	ALA	-	expression tag	UNP P19491
A	94	TYR	LEU	engineered mutation	UNP P19491
A	118	GLY	-	linker	UNP P19491
A	119	THR	-	linker	UNP P19491
A	242	SER	ASN	engineered mutation	UNP P19491
A	246	VAL	LEU	engineered mutation	UNP P19491
B	-27	MET	-	initiating methionine	UNP P19491
B	-26	HIS	-	expression tag	UNP P19491
B	-25	HIS	-	expression tag	UNP P19491
B	-24	HIS	-	expression tag	UNP P19491
B	-23	HIS	-	expression tag	UNP P19491
B	-22	HIS	-	expression tag	UNP P19491
B	-21	HIS	-	expression tag	UNP P19491
B	-20	HIS	-	expression tag	UNP P19491
B	-19	HIS	-	expression tag	UNP P19491
B	-18	SER	-	expression tag	UNP P19491
B	-17	SER	-	expression tag	UNP P19491
B	-16	GLY	-	expression tag	UNP P19491
B	-15	LEU	-	expression tag	UNP P19491
B	-14	VAL	-	expression tag	UNP P19491
B	-13	PRO	-	expression tag	UNP P19491
B	-12	ARG	-	expression tag	UNP P19491
B	-11	GLY	-	expression tag	UNP P19491
B	-10	SER	-	expression tag	UNP P19491
B	-9	ALA	-	expression tag	UNP P19491
B	-8	MET	-	expression tag	UNP P19491
B	-7	GLY	-	expression tag	UNP P19491
B	-6	SER	-	expression tag	UNP P19491
B	-5	GLY	-	expression tag	UNP P19491
B	-4	ASN	-	expression tag	UNP P19491
B	-3	ASP	-	expression tag	UNP P19491
B	-2	THR	-	expression tag	UNP P19491
B	-1	SER	-	expression tag	UNP P19491
B	0	ARG	-	expression tag	UNP P19491
B	1	GLY	-	expression tag	UNP P19491
B	2	ALA	-	expression tag	UNP P19491
B	94	TYR	LEU	engineered mutation	UNP P19491
B	118	GLY	-	linker	UNP P19491

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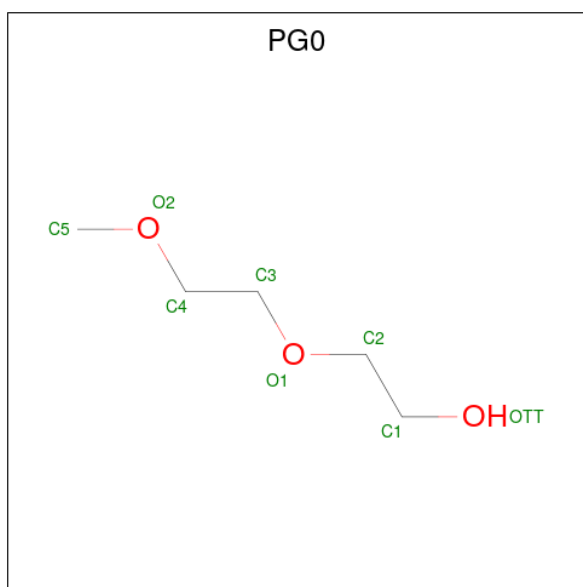
Chain	Residue	Modelled	Actual	Comment	Reference
B	119	THR	-	linker	UNP P19491
B	242	SER	ASN	engineered mutation	UNP P19491
B	246	VAL	LEU	engineered mutation	UNP P19491

- Molecule 2 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	1	0
			33	9	19	5		
2	A	1	Total	C	H	O	1	0
			23	6	13	4		

- Molecule 3 is 2-(2-METHOXYETHOXY)ETHANOL (CCD ID: PG0) (formula: $C_5H_{12}O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			20	5	12	3		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		

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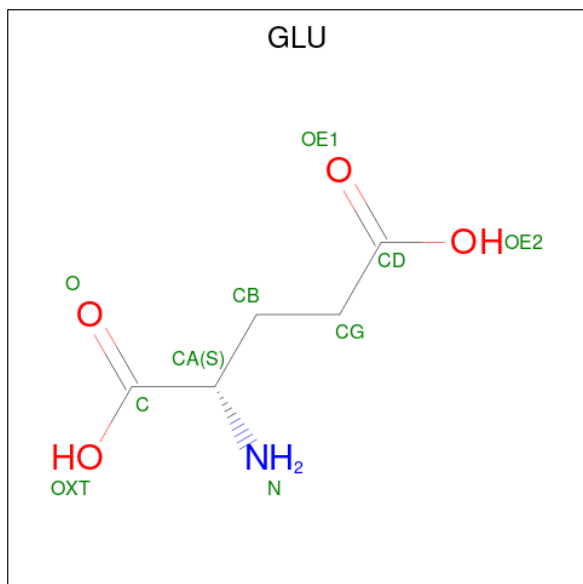
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total	Na	0	0
			3	3		
5	B	2	Total	Na	0	0
			2	2		

- Molecule 6 is GLUTAMIC ACID (CCD ID: GLU) (formula: C₅H₉NO₄).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	H	N	O	0	0
			18	5	8	1	4		
6	B	1	Total	C	H	N	O	0	0
			18	5	8	1	4		

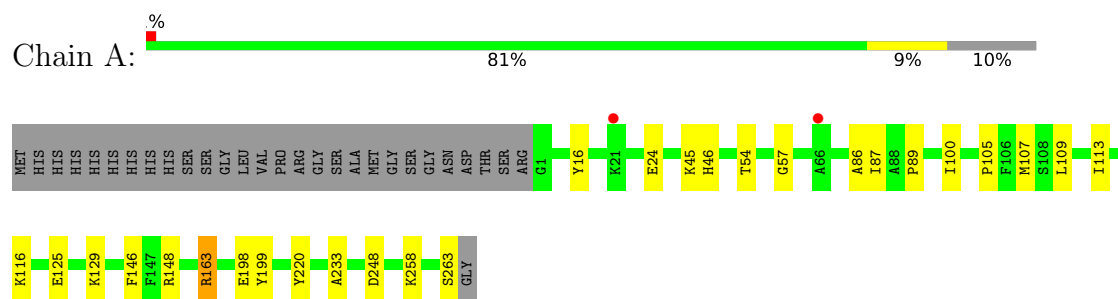
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	473	Total 473	O 473	0	0
7	B	432	Total 432	O 432	0	0

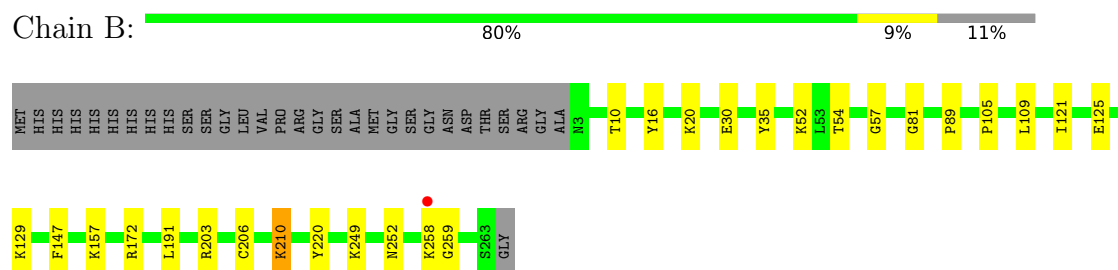
3 Residue-property plots [i](#)

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: Glutamate receptor 2, Glutamate receptor 2



- Molecule 1: Glutamate receptor 2, Glutamate receptor 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	95.99Å 121.30Å 47.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.99 – 1.44 47.99 – 1.44	Depositor EDS
% Data completeness (in resolution range)	99.2 (47.99-1.44) 99.3 (47.99-1.44)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 1.44Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.147 , 0.205 0.147 , 0.205	Depositor DCC
R_{free} test set	4968 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	11.9	Xtriage
Anisotropy	0.951	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 51.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	9845	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.51% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PG0, 1PE, SO4, NA

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	1.53	13/2293 (0.6%)	1.14	1/3079 (0.0%)
1	B	1.52	7/2184 (0.3%)	1.18	0/2939
All	All	1.52	20/4477 (0.4%)	1.16	1/6018 (0.0%)

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	87	ILE	C-O	7.09	1.32	1.24
1	A	45	LYS	C-O	-7.08	1.15	1.24
1	B	121	ILE	C-O	-6.83	1.17	1.24
1	A	163	ARG	CZ-NH1	6.73	1.42	1.32
1	B	10	THR	CA-C	-6.43	1.44	1.52
1	A	148	ARG	N-CA	-5.96	1.38	1.46
1	A	258	LYS	N-CA	5.81	1.52	1.46
1	B	210	LYS	C-O	5.80	1.30	1.24
1	B	57	GLY	C-O	-5.65	1.17	1.23
1	B	35	TYR	C-O	-5.50	1.17	1.24
1	A	107	MET	SD-CE	-5.39	1.66	1.79
1	A	45	LYS	CA-C	5.33	1.59	1.52
1	A	86	ALA	CA-C	-5.32	1.46	1.52
1	A	100	ILE	CA-C	-5.30	1.46	1.52
1	A	248	ASP	C-O	-5.29	1.18	1.24
1	B	157	LYS	CA-C	5.24	1.59	1.52
1	B	206	CYS	C-O	5.22	1.30	1.23
1	A	113	ILE	CA-CB	-5.21	1.48	1.54
1	A	233	ALA	CA-CB	-5.20	1.45	1.53
1	A	146	PHE	C-O	5.03	1.29	1.24

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	57	GLY	N-CA-C	5.81	119.91	112.83

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	2221	2273	2272	12	0
1	B	2128	2171	2167	19	0
2	A	24	32	30	1	0
3	A	8	12	12	2	0
4	A	20	0	0	0	0
4	B	10	0	0	0	0
5	A	3	0	0	0	0
5	B	2	0	0	0	0
6	A	10	8	5	0	0
6	B	10	8	5	0	0
7	A	473	0	0	9	2
7	B	432	0	0	10	3
All	All	5341	4504	4491	33	4

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 4.

All (33) 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:B:210:LYS:HE2	7:B:607:HOH:O	1.62	0.98
1:A:163:ARG:NH2	7:A:403:HOH:O	2.11	0.83
1:A:198:GLU:OE1	7:A:402:HOH:O	2.07	0.72
1:B:30[A]:GLU:OE1	7:B:401:HOH:O	2.10	0.69
1:A:199[B]:TYR:OH	7:A:401:HOH:O	1.85	0.67
1:A:116[B]:LYS:NZ	7:A:405:HOH:O	2.28	0.66
1:A:263[B]:SER:HB2	2:A:301:1PE:H232	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:ARG:CZ	7:A:403:HOH:O	2.45	0.63
1:B:147:PHE:CE2	1:B:191[B]:LEU:HD23	2.33	0.63
1:B:172:ARG:NH2	7:B:404:HOH:O	2.31	0.63
1:B:52:LYS:HE3	7:B:679:HOH:O	1.99	0.61
1:B:125:GLU:HG2	1:B:129:LYS:HE2	1.83	0.61
3:A:303:PG0:H51	7:A:645:HOH:O	2.01	0.60
1:B:203:ARG:NH1	1:B:258:LYS:HG3	2.18	0.58
1:B:81:GLY:HA2	7:B:453:HOH:O	2.03	0.57
1:B:203:ARG:HH12	1:B:258:LYS:HG3	1.70	0.55
1:B:249:LYS:HG3	7:B:592:HOH:O	2.08	0.54
1:A:54[B]:THR:HG21	7:A:606:HOH:O	2.08	0.52
1:B:105:PRO:HA	1:B:220:TYR:O	2.14	0.48
3:A:303:PG0:C5	7:A:645:HOH:O	2.61	0.46
1:A:46:HIS:HD2	7:A:787:HOH:O	1.98	0.46
1:B:20:LYS:NZ	1:B:30[B]:GLU:OE1	2.50	0.45
1:B:258:LYS:O	1:B:259:GLY:C	2.55	0.44
1:B:16[B]:TYR:CE1	1:B:89:PRO:HB3	2.52	0.44
1:B:258:LYS:NZ	7:B:417:HOH:O	2.49	0.43
1:B:172:ARG:NH1	7:B:407:HOH:O	2.36	0.43
1:B:54[B]:THR:HG21	7:B:628:HOH:O	2.18	0.43
1:B:203:ARG:HH12	1:B:258:LYS:CG	2.31	0.43
1:A:24[B]:GLU:H	1:A:24[B]:GLU:CD	2.26	0.42
1:A:16[A]:TYR:CE1	1:A:89:PRO:HB3	2.55	0.42
1:B:252:ASN:ND2	7:B:427:HOH:O	2.54	0.41
1:A:125:GLU:HG2	1:A:129:LYS:HE2	2.03	0.41
1:A:105:PRO:HA	1:A:220:TYR:O	2.22	0.40

All (4) 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)
7:A:868:HOH:O	7:B:792:HOH:O[4_439]	1.90	0.30
7:B:453:HOH:O	7:B:782:HOH:O[1_556]	1.90	0.30
7:B:789:HOH:O	7:B:794:HOH:O[1_556]	2.00	0.20
7:A:455:HOH:O	7:A:668:HOH:O[1_556]	2.06	0.14

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	285/292 (98%)	283 (99%)	2 (1%)	0	100	100
1	B	272/292 (93%)	269 (99%)	3 (1%)	0	100	100
All	All	557/584 (95%)	552 (99%)	5 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	244/242 (101%)	243 (100%)	1 (0%)	84	69
1	B	232/242 (96%)	231 (100%)	1 (0%)	84	69
All	All	476/484 (98%)	474 (100%)	2 (0%)	81	69

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

Mol	Chain	Res	Type
1	A	109	LEU
1	B	109	LEU

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 16 ligands modelled in this entry, 5 are monoatomic - leaving 11 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	GLU	B	305	-	8,9,9	1.10	0	8,11,11	1.61	2 (25%)
4	SO4	A	307	-	4,4,4	0.44	0	6,6,6	0.28	0
3	PG0	A	303	-	7,7,7	0.83	0	6,6,6	0.33	0
4	SO4	A	304	-	4,4,4	0.54	0	6,6,6	0.35	0
4	SO4	A	306	-	4,4,4	1.02	0	6,6,6	0.42	0
4	SO4	B	302	-	4,4,4	1.33	1 (25%)	6,6,6	0.38	0
2	1PE	A	301	-	13,13,15	0.85	0	12,12,14	0.67	0
2	1PE	A	302	-	9,9,15	0.65	0	8,8,14	0.61	0
6	GLU	A	311	-	8,9,9	1.54	2 (25%)	8,11,11	1.29	1 (12%)
4	SO4	A	305	-	4,4,4	0.99	0	6,6,6	0.57	0
4	SO4	B	301	-	4,4,4	0.77	0	6,6,6	0.58	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GLU	B	305	-	-	0/9/9/9	-
3	PG0	A	303	-	-	0/5/5/5	-
2	1PE	A	301	-	-	3/11/11/13	-
2	1PE	A	302	-	-	1/7/7/13	-
6	GLU	A	311	-	-	1/9/9/9	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	311	GLU	OXT-C	-2.79	1.21	1.30
6	A	311	GLU	OE1-CD	2.56	1.30	1.22
4	B	302	SO4	O1-S	2.52	1.59	1.44

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	305	GLU	OE1-CD-CG	-3.25	112.78	123.09
6	A	311	GLU	OE2-CD-CG	2.73	122.63	114.00
6	B	305	GLU	OE2-CD-CG	2.69	122.51	114.00

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	1PE	C23-C13-OH4-C24
2	A	302	1PE	OH2-C12-C22-OH3
6	A	311	GLU	O-C-CA-N
2	A	301	1PE	C13-C23-OH3-C22
2	A	301	1PE	OH4-C13-C23-OH3

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	303	PG0	2	0
2	A	301	1PE	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	263/292 (90%)	-0.85	2 (0%) 82 86	5, 14, 32, 63	24 (9%)
1	B	261/292 (89%)	-0.76	1 (0%) 88 91	6, 15, 35, 67	13 (4%)
All	All	524/584 (89%)	-0.80	3 (0%) 85 89	5, 15, 34, 67	37 (7%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	21[A]	LYS	3.8
1	B	258	LYS	3.1
1	A	66	ALA	2.0

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	SO4	A	304	5/5	0.86	0.08	79,80,81,85	0
4	SO4	A	305	5/5	0.90	0.12	47,47,55,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	SO4	A	306	5/5	0.93	0.08	39,41,50,55	0
5	NA	A	310	1/1	0.93	0.09	48,48,48,48	0
5	NA	A	308	1/1	0.94	0.10	33,33,33,33	0
2	1PE	A	301	14/16	0.94	0.08	24,28,34,36	1
5	NA	B	304	1/1	0.94	0.10	48,48,48,48	0
2	1PE	A	302	10/16	0.95	0.08	4,36,38,40	1
3	PG0	A	303	8/8	0.96	0.06	25,29,33,33	0
5	NA	A	309	1/1	0.97	0.12	34,34,34,34	0
5	NA	B	303	1/1	0.98	0.06	29,29,29,29	0
4	SO4	B	302	5/5	0.98	0.05	25,27,29,31	0
4	SO4	B	301	5/5	0.99	0.04	28,29,37,40	0
6	GLU	A	311	10/10	0.99	0.02	9,11,13,14	0
6	GLU	B	305	10/10	0.99	0.03	10,11,12,13	0
4	SO4	A	307	5/5	1.00	0.03	18,18,20,21	0

6.5 Other polymers [i](#)

There are no such residues in this entry.