



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 12:17 PM UTC

PDB ID : 5TQ0 / pdb_00005tq0
Title : Crystal structure of amino terminal domains of the NMDA receptor subunit GluN1 and GluN2A in the presence of EDTA
Authors : Romero-Hernandez, A.; Simorowski, N.; Karakas, E.; Furukawa, H.
Deposited on : 2016-10-21
Resolution : 2.70 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
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

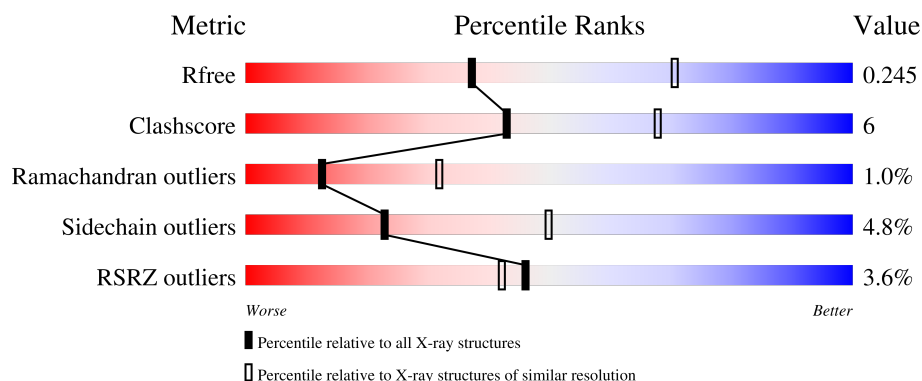
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	391	3% 79% 13% • 7%
2	B	360	4% 76% 16% •• 6%
3	H	221	3% 81% 14% ••
4	L	214	2% 78% 15% • 5%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 8351 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 NMDA glutamate receptor subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	364	Total	C	N	O	S	0	0	0
			2729	1743	467	508	11			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	61	GLN	ASN	engineered mutation	UNP Q91977
A	371	GLN	ASN	engineered mutation	UNP Q91977
A	409	GLY	-	expression tag	UNP Q91977
A	410	THR	-	expression tag	UNP Q91977
A	411	LEU	-	expression tag	UNP Q91977
A	412	VAL	-	expression tag	UNP Q91977
A	413	PRO	-	expression tag	UNP Q91977
A	414	ARG	-	expression tag	UNP Q91977

- Molecule 2 is a protein called Glutamate receptor ionotropic, NMDA 2A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	338	Total	C	N	O	S	0	0	0
			2449	1570	407	460	12			

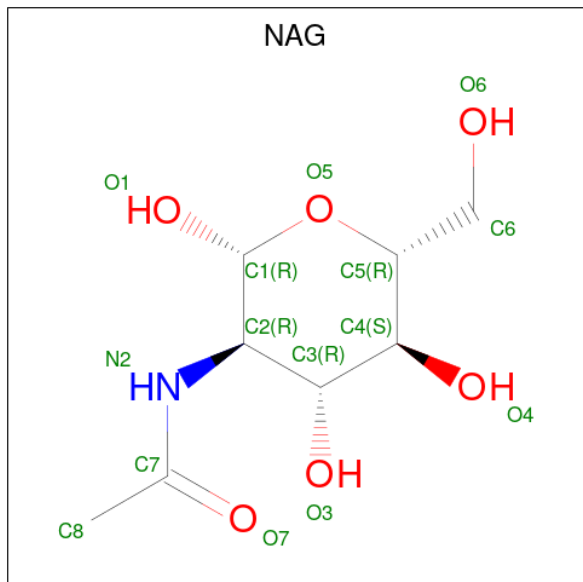
- Molecule 3 is a protein called FAB, HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	212	Total	C	N	O	S	0	0	0
			1534	989	243	295	7			

- Molecule 4 is a protein called FAB, LIGHT CHAIN.

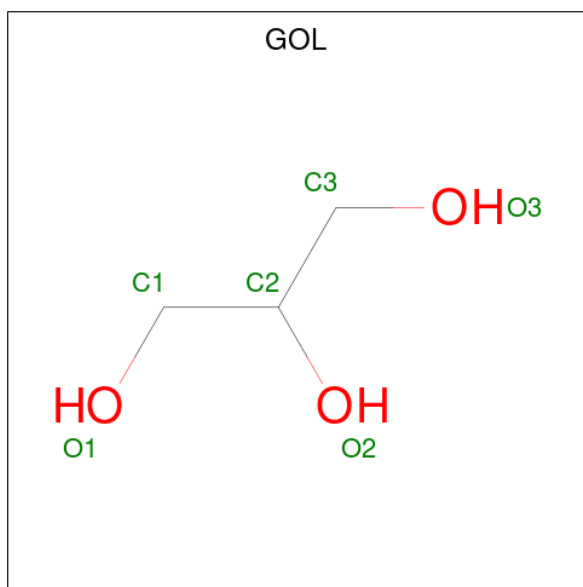
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	L	204	Total	C	N	O	S	0	0	0
			1485	933	252	293	7			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



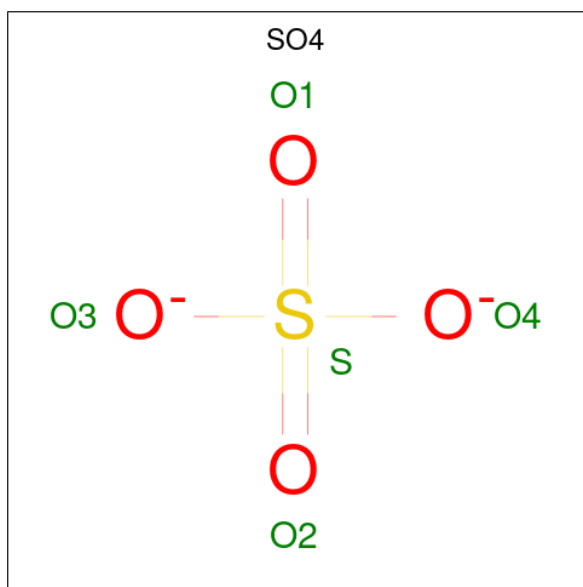
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		
6	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



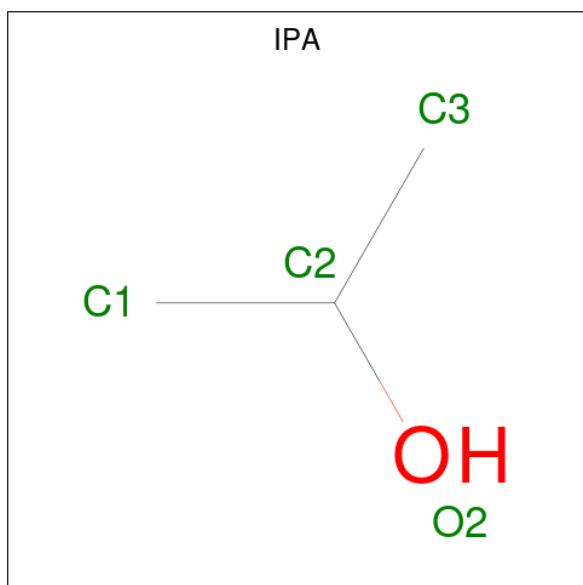
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	O	S	0	0
			5	4	1		
7	A	1	Total	O	S	0	0
			5	4	1		
7	A	1	Total	O	S	0	0
			5	4	1		
7	A	1	Total	O	S	0	0
			5	4	1		
7	A	1	Total	O	S	0	0
			5	4	1		
7	B	1	Total	O	S	0	0
			5	4	1		
7	B	1	Total	O	S	0	0
			5	4	1		
7	B	1	Total	O	S	0	0
			5	4	1		
7	B	1	Total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

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

- Molecule 8 is ISOPROPYL ALCOHOL (CCD ID: IPA) (formula: C_3H_8O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	H	1	Total	C	O	0	0
			4	3	1		

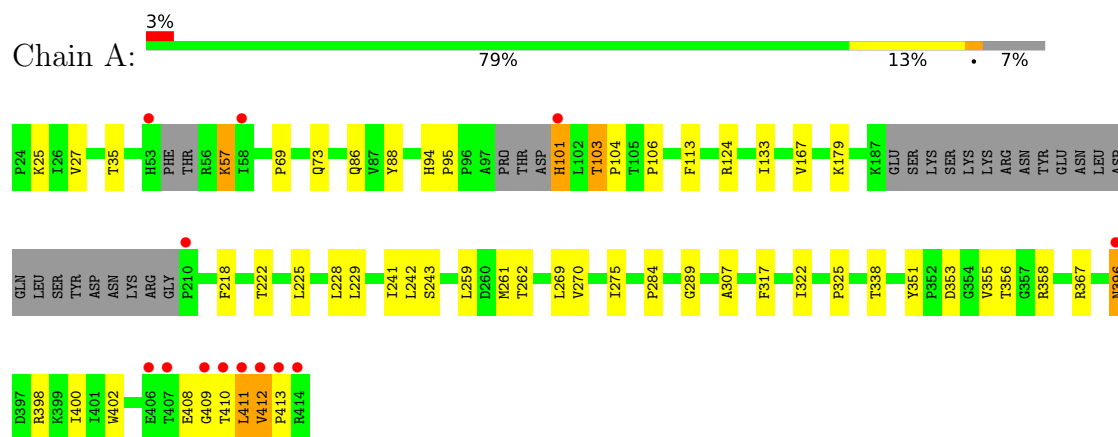
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	27	Total	O	0	0
			27	27		
9	B	12	Total	O	0	0
			12	12		
9	H	8	Total	O	0	0
			8	8		
9	L	3	Total	O	0	0
			3	3		

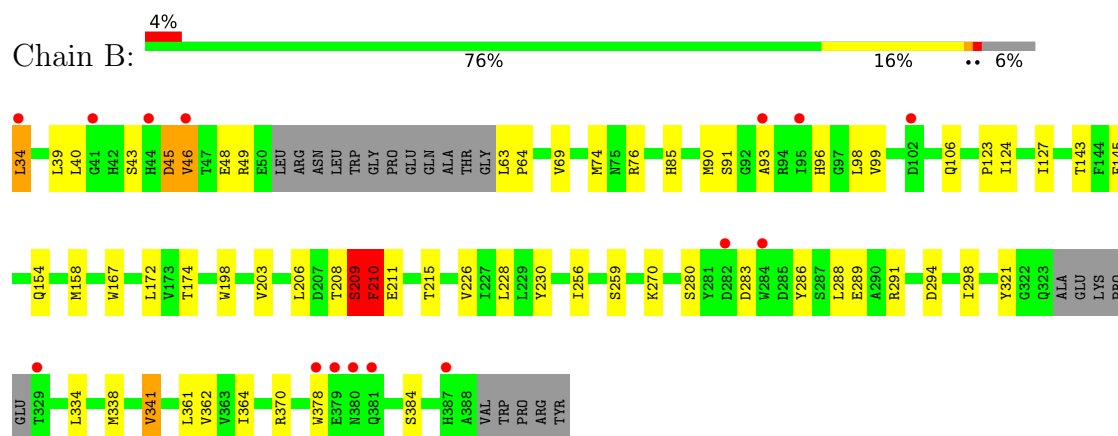
3 Residue-property plots [i](#)

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.

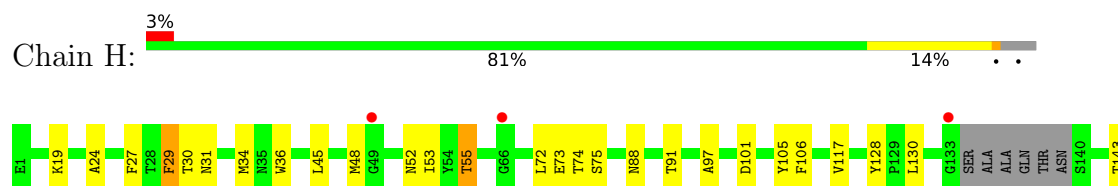
- Molecule 1: NMDA glutamate receptor subunit

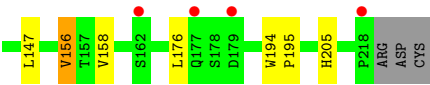


- Molecule 2: Glutamate receptor ionotropic, NMDA 2A

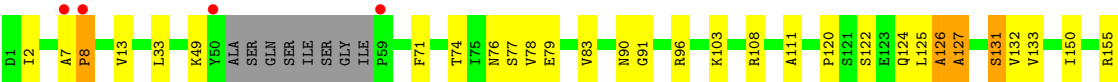
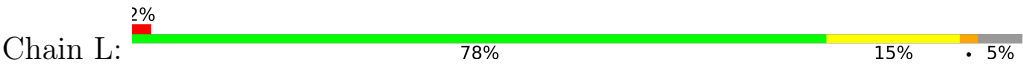


- Molecule 3: FAB, HEAVY CHAIN





● Molecule 4: FAB, LIGHT CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.98Å 118.35Å 156.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.57 – 2.70 47.57 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.1 (47.57-2.70) 93.7 (47.57-2.70)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.18 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.10_2155	Depositor
R, R_{free}	0.208 , 0.246 0.208 , 0.245	Depositor DCC
R_{free} test set	4124 reflections (9.91%)	wwPDB-VP
Wilson B-factor (Å ²)	62.6	Xtriage
Anisotropy	0.116	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 60.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8351	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.84% 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: GOL, IPA, SO4, NAG

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	0.17	0/2783	0.40	2/3790 (0.1%)
2	B	0.19	0/2500	0.40	0/3415
3	H	0.18	0/1582	0.38	0/2179
4	L	0.18	0/1521	0.41	3/2077 (0.1%)
All	All	0.18	0/8386	0.40	5/11461 (0.0%)

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
2	B	0	2
3	H	0	1
All	All	0	3

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L	127	ALA	N-CA-C	-6.12	100.24	108.86
1	A	353	ASP	CA-C-N	-6.09	117.98	122.18
1	A	353	ASP	C-N-CA	-6.09	117.98	122.18
4	L	126	ALA	CA-C-N	5.69	131.69	122.53
4	L	126	ALA	C-N-CA	5.69	131.69	122.53

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	45	ASP	Peptide
2	B	48	GLU	Peptide
3	H	101	ASP	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	2729	0	2652	30	0
2	B	2449	0	2250	40	0
3	H	1534	0	1366	15	0
4	L	1485	0	1310	18	0
5	A	28	0	26	0	0
6	A	12	0	16	2	0
7	A	25	0	0	1	0
7	B	25	0	0	0	0
7	L	10	0	0	0	0
8	H	4	0	8	0	0
9	A	27	0	0	0	0
9	B	12	0	0	0	0
9	H	8	0	0	0	0
9	L	3	0	0	0	0
All	All	8351	0	7628	99	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 6.

The worst 5 of 99 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)
3:H:72:LEU:HD13	3:H:74:THR:HG23	1.60	0.83
3:H:91:THR:HG22	3:H:117:VAL:H	1.44	0.80
1:A:229:LEU:HB3	1:A:261:MET:HE1	1.66	0.78
2:B:206:LEU:HD23	2:B:215:THR:HG22	1.65	0.78
4:L:125:LEU:C	4:L:127:ALA:H	1.91	0.75

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	356/391 (91%)	335 (94%)	17 (5%)	4 (1%)	11	29
2	B	332/360 (92%)	316 (95%)	11 (3%)	5 (2%)	8	22
3	H	208/221 (94%)	196 (94%)	12 (6%)	0	100	100
4	L	200/214 (94%)	191 (96%)	7 (4%)	2 (1%)	12	32
All	All	1096/1186 (92%)	1038 (95%)	47 (4%)	11 (1%)	12	32

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	412	VAL
1	A	413	PRO
2	B	46	VAL
2	B	209	SER
2	B	210	PHE

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	280/336 (83%)	269 (96%)	11 (4%)	28	57
2	B	239/318 (75%)	231 (97%)	8 (3%)	33	63
3	H	149/188 (79%)	139 (93%)	10 (7%)	15	36
4	L	146/188 (78%)	136 (93%)	10 (7%)	14	35
All	All	814/1030 (79%)	775 (95%)	39 (5%)	23	50

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	H	176	LEU
4	L	131	SER
4	L	2	ILE
4	L	90	ASN
4	L	181	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	163	GLN
2	B	218	GLN
4	L	190	ASN
2	B	358	HIS
1	A	161	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](#)

17 ligands are modelled in this entry.

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
8	IPA	H	301	-	3,3,3	0.55	0	3,3,3	0.28	0
7	SO4	A	507	-	4,4,4	0.24	0	6,6,6	0.08	0
7	SO4	A	505	-	4,4,4	0.23	0	6,6,6	0.10	0
7	SO4	B	402	-	4,4,4	0.24	0	6,6,6	0.12	0
7	SO4	B	404	-	4,4,4	0.24	0	6,6,6	0.09	0
7	SO4	L	301	-	4,4,4	0.24	0	6,6,6	0.06	0
7	SO4	L	302	-	4,4,4	0.24	0	6,6,6	0.15	0
7	SO4	A	509	-	4,4,4	0.21	0	6,6,6	0.21	0
5	NAG	A	501	1	14,14,15	0.25	0	17,19,21	0.44	0
6	GOL	A	504	-	5,5,5	0.37	0	5,5,5	0.30	0
7	SO4	B	401	-	4,4,4	0.23	0	6,6,6	0.13	0
6	GOL	A	503	-	5,5,5	0.37	0	5,5,5	0.36	0
5	NAG	A	502	1	14,14,15	0.22	0	17,19,21	0.44	0
7	SO4	B	403	-	4,4,4	0.23	0	6,6,6	0.08	0
7	SO4	B	405	-	4,4,4	0.24	0	6,6,6	0.11	0
7	SO4	A	506	-	4,4,4	0.25	0	6,6,6	0.14	0
7	SO4	A	508	-	4,4,4	0.26	0	6,6,6	0.06	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	GOL	A	503	-	-	2/4/4/4	-
5	NAG	A	501	1	-	0/6/23/26	0/1/1/1
6	GOL	A	504	-	-	2/4/4/4	-
5	NAG	A	502	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	503	GOL	O1-C1-C2-C3
6	A	504	GOL	O1-C1-C2-O2
5	A	502	NAG	O5-C5-C6-O6
5	A	502	NAG	C4-C5-C6-O6
6	A	504	GOL	O1-C1-C2-C3

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	504	GOL	1	0
6	A	503	GOL	1	0
7	A	508	SO4	1	0

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	364/391 (93%)	0.05	13 (3%) 46 42	34, 54, 88, 114	0
2	B	338/360 (93%)	0.48	15 (4%) 39 35	47, 72, 109, 123	0
3	H	212/221 (95%)	0.27	7 (3%) 49 45	47, 65, 87, 99	0
4	L	204/214 (95%)	0.47	5 (2%) 58 55	47, 70, 97, 109	0
All	All	1118/1186 (94%)	0.30	40 (3%) 46 42	34, 64, 98, 123	0

The worst 5 of 40 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	L	7	ALA	4.1
1	A	413	PRO	4.0
1	A	53	HIS	3.7
2	B	46	VAL	3.7
3	H	133	GLY	3.3

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($\text{\AA}^2$)	Q<0.9
7	SO4	B	405	5/5	0.50	0.11	135,139,143,147	0
7	SO4	L	301	5/5	0.66	0.10	100,118,132,135	0
7	SO4	B	404	5/5	0.68	0.10	96,113,135,140	0
6	GOL	A	503	6/6	0.75	0.17	62,77,89,90	0
5	NAG	A	502	14/15	0.75	0.12	84,94,97,103	0
7	SO4	A	509	5/5	0.78	0.29	76,85,96,121	0
7	SO4	A	508	5/5	0.82	0.07	88,99,113,143	0
7	SO4	A	506	5/5	0.85	0.16	81,85,95,96	0
7	SO4	B	403	5/5	0.86	0.14	92,103,105,110	0
7	SO4	L	302	5/5	0.86	0.14	91,96,106,122	0
7	SO4	A	507	5/5	0.89	0.17	84,93,104,115	0
5	NAG	A	501	14/15	0.91	0.09	56,73,79,84	0
8	IPA	H	301	4/4	0.91	0.20	64,65,69,79	0
6	GOL	A	504	6/6	0.92	0.10	66,73,74,75	0
7	SO4	B	401	5/5	0.92	0.08	68,78,82,83	0
7	SO4	A	505	5/5	0.95	0.07	65,66,68,68	0
7	SO4	B	402	5/5	0.96	0.08	66,68,79,86	0

6.5 Other polymers [i](#)

There are no such residues in this entry.