



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 21, 2019 – 12:14 PM EST

PDB ID : 6E7U  
Title : Heterodimer of the GluN1b-GluN2B NMDA receptor amino-terminal domains bound to allosteric inhibitor 93-31  
Authors : Regan, M.C.; Furukawa, H.  
Deposited on : 2018-07-27  
Resolution : 2.27 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : rb-20031633  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20031633

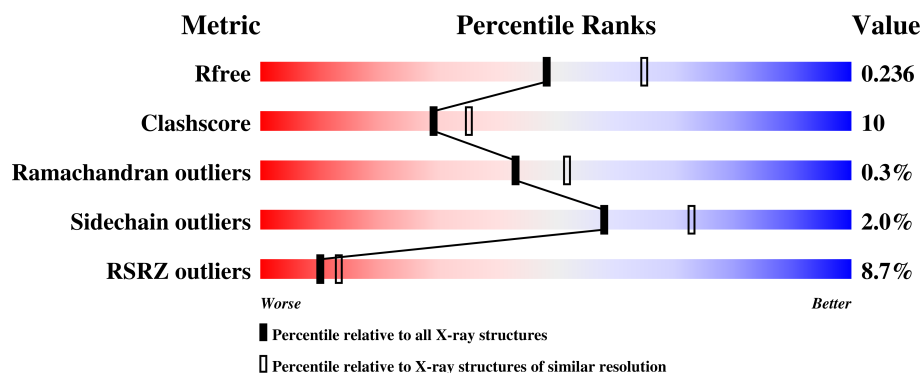
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.27 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))
$R_{free}$	111664	6121 (2.30-2.26)
Clashscore	122126	6842 (2.30-2.26)
Ramachandran outliers	120053	6755 (2.30-2.26)
Sidechain outliers	120020	6755 (2.30-2.26)
RSRZ outliers	108989	5992 (2.30-2.26)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	385	<div> <div>2%</div> <div>78%</div> <div>15%</div> <div>7%</div> </div>
1	C	385	<div> <div>9%</div> <div>73%</div> <div>18%</div> <div>7%</div> </div>
2	B	363	<div> <div>10%</div> <div>84%</div> <div>14%</div> <div>..</div> </div>
2	D	363	<div> <div>12%</div> <div>82%</div> <div>16%</div> <div>..</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	B	501	-	-	-	X
3	NAG	B	502	-	-	-	X
3	NAG	C	501	-	-	-	X
3	NAG	D	401	-	-	-	X
5	MAN	A	506	-	-	-	X
7	CL	A	509	-	-	X	-
7	CL	D	406	-	-	X	-

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 11538 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 Glutamate receptor ionotropic, NMDA 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	359	Total	C	N	O	S	0	0	0
			2765	1763	482	509	11			
1	C	357	Total	C	N	O	S	0	0	0
			2728	1738	473	506	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	61	GLN	ASN	engineered mutation	UNP A0A1L8F5J9
A	371	GLN	ASN	engineered mutation	UNP A0A1L8F5J9
C	61	GLN	ASN	engineered mutation	UNP A0A1L8F5J9
C	371	GLN	ASN	engineered mutation	UNP A0A1L8F5J9

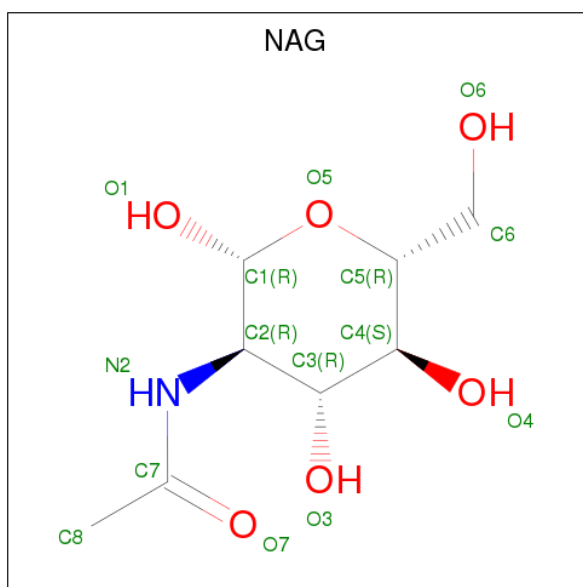
- Molecule 2 is a protein called Glutamate receptor ionotropic, NMDA 2B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	359	Total	C	N	O	S	0	1	0
			2771	1785	443	527	16			
2	D	360	Total	C	N	O	S	0	0	0
			2720	1751	436	517	16			

There are 2 discrepancies between the modelled and reference sequences:

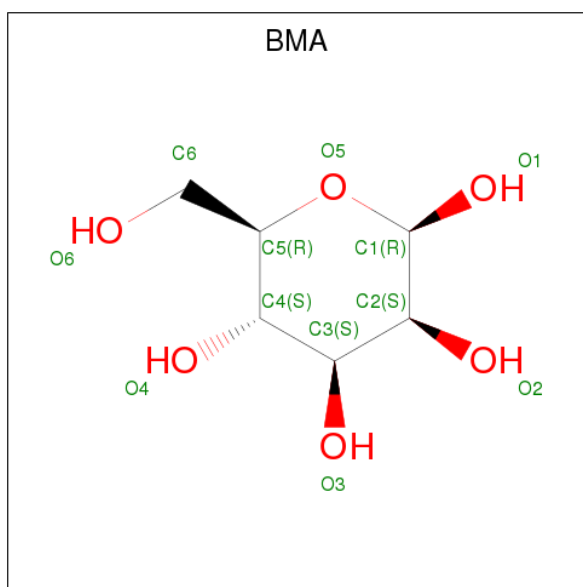
Chain	Residue	Modelled	Actual	Comment	Reference
B	348	ASP	ASN	engineered mutation	UNP Q00960
D	348	ASP	ASN	engineered mutation	UNP Q00960

- Molecule 3 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



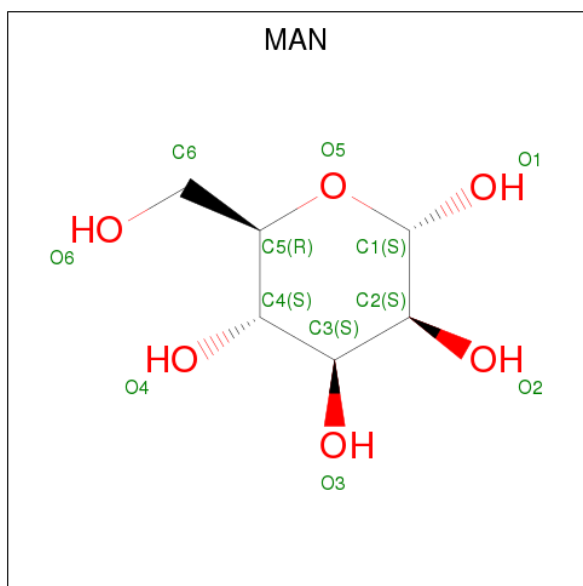
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1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

- Molecule 4 is BETA-D-MANNOSE (three-letter code: BMA) (formula:  $C_6H_{12}O_6$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			11	6	5		

- Molecule 5 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula:  $C_6H_{12}O_6$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			11	6	5		
5	A	1	Total	C	O	0	0
			11	6	5		

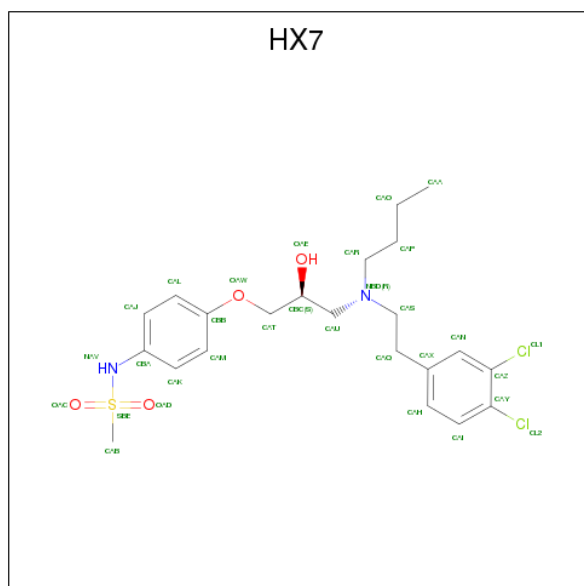
- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	4	Total	Cl	0	0
			4	4		
7	A	2	Total	Cl	0	0
			2	2		
7	D	4	Total	Cl	0	0
			4	4		
7	C	2	Total	Cl	0	0
			2	2		

- Molecule 8 is N-{4-[(2S)-3-{butyl[2-(3,4-dichlorophenyl)ethyl]amino}-2-hydroxypropoxy]phenyl}methanesulfonamide (three-letter code: HX7) (formula: C<sub>22</sub>H<sub>30</sub>Cl<sub>2</sub>N<sub>2</sub>O<sub>4</sub>S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
8	B	1	Total	C	Cl	N	O	S	0	0
			31	22	2	2	4	1		
8	D	1	Total	C	Cl	N	O	S	0	0
			31	22	2	2	4	1		

- Molecule 9 is water.

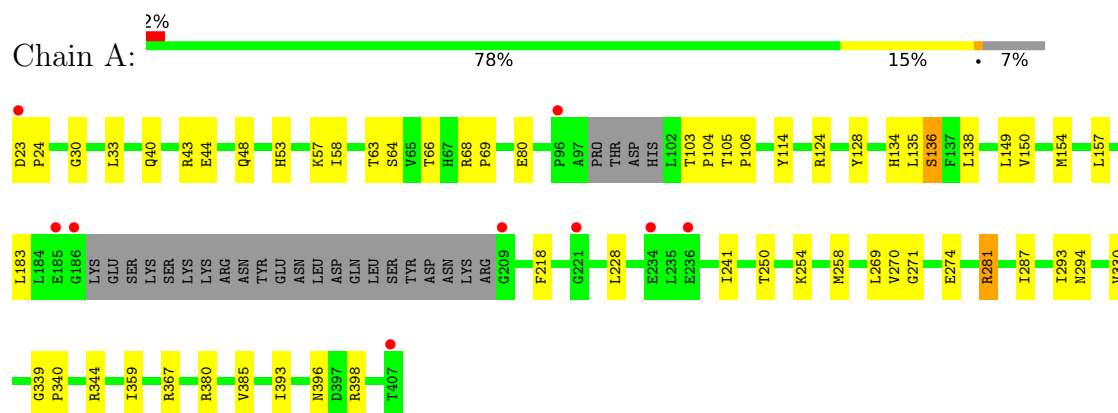
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	135	Total 135	O 135	0	0
9	B	76	Total 76	O 76	0	0
9	C	75	Total 75	O 75	0	0
9	D	47	Total 47	O 47	0	0



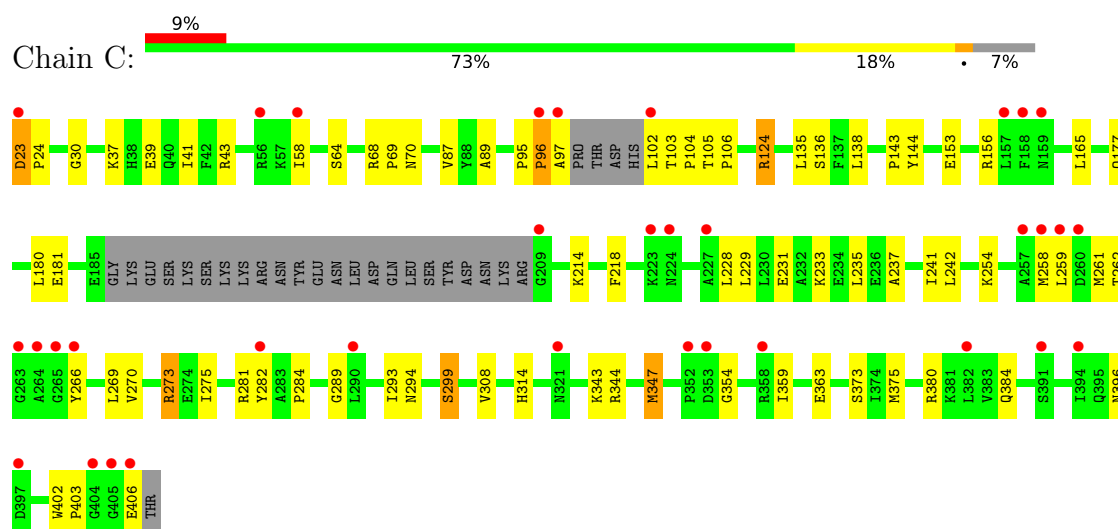
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

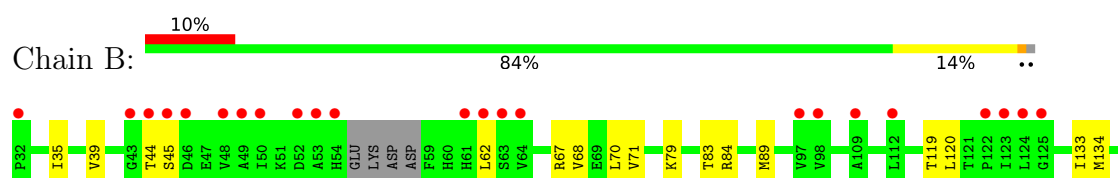
- Molecule 1: Glutamate receptor ionotropic, NMDA 1

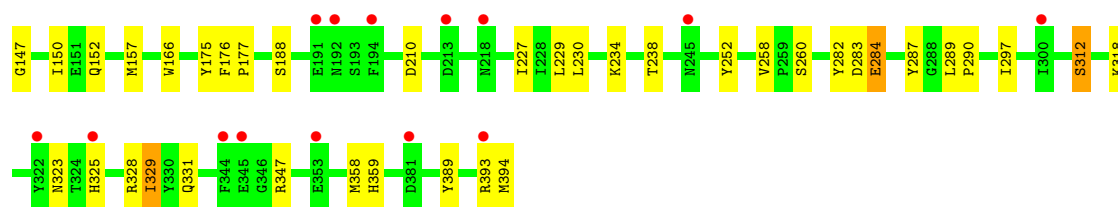


- Molecule 1: Glutamate receptor ionotropic, NMDA 1

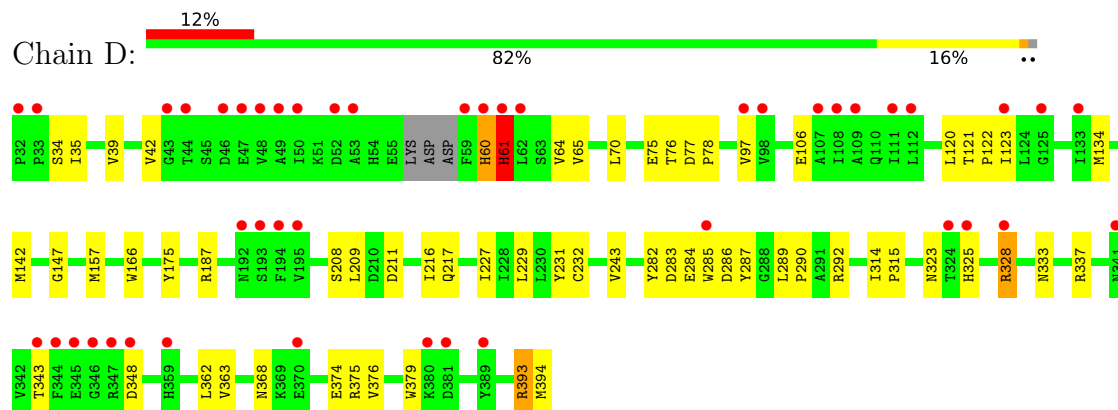


- Molecule 2: Glutamate receptor ionotropic, NMDA 2B





● Molecule 2: Glutamate receptor ionotropic, NMDA 2B



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	268.62Å 59.59Å 145.91Å 90.00° 117.10° 90.00°	Depositor
Resolution (Å)	25.00 – 2.27 34.26 – 2.27	Depositor EDS
% Data completeness (in resolution range)	82.0 (25.00-2.27) 82.1 (34.26-2.27)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.54 (at 2.27Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.202 , 0.237 0.207 , 0.236	Depositor DCC
$R_{free}$ test set	3929 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.9	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 54.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	11538	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, NAG, CL, NA, HX7, MAN

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	0.32	0/2822	0.36	0/3834
1	C	0.30	0/2783	0.35	0/3783
2	B	0.31	0/2838	0.36	0/3871
2	D	0.30	0/2781	0.36	0/3797
All	All	0.31	0/11224	0.36	0/15285

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	0	2
1	C	0	3
2	B	0	2
2	D	0	4
All	All	0	11

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	114	TYR	Sidechain
1	A	124	ARG	Sidechain
2	B	347	ARG	Sidechain
2	B	45	SER	Peptide
1	C	43	ARG	Sidechain

## 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	2765	0	2731	47	0
1	C	2728	0	2694	63	2
2	B	2771	0	2637	50	2
2	D	2720	0	2563	60	0
3	A	42	0	37	0	0
3	B	28	0	26	3	0
3	C	28	0	26	0	0
3	D	14	0	13	0	0
4	A	11	0	8	0	0
5	A	22	0	20	0	0
6	A	1	0	0	0	0
6	C	1	0	0	0	0
7	A	2	0	0	3	0
7	B	4	0	0	2	0
7	C	2	0	0	0	0
7	D	4	0	0	3	0
8	B	31	0	0	4	0
8	D	31	0	0	5	0
9	A	135	0	0	5	0
9	B	76	0	0	8	0
9	C	75	0	0	4	0
9	D	47	0	0	3	0
All	All	11538	0	10755	225	2

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 10.

The worst 5 of 225 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)
2:D:283:ASP:O	2:D:285:TRP:HD1	1.12	1.30
2:D:283:ASP:O	2:D:285:TRP:CD1	1.93	1.21
1:C:237:ALA:O	9:C:601:HOH:O	1.70	1.07
1:A:270:VAL:CG1	1:A:274:GLU:HB2	1.89	1.02
1:C:41:ILE:HD13	1:C:299:SER:OG	1.73	0.88

All (2) 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)
2:B:393:ARG:NH2	1:C:384:GLN:OE1[4_7510]	1.92	0.28
2:B:389:TYR:O	1:C:380:ARG:NH1[4_7510]	2.18	0.02

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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	353/385 (92%)	338 (96%)	15 (4%)	0	100	100
1	C	351/385 (91%)	339 (97%)	11 (3%)	1 (0%)	43	52
2	B	356/363 (98%)	337 (95%)	18 (5%)	1 (0%)	43	52
2	D	356/363 (98%)	341 (96%)	13 (4%)	2 (1%)	27	31
All	All	1416/1496 (95%)	1355 (96%)	57 (4%)	4 (0%)	43	52

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	284	GLU
2	D	61	HIS
2	D	60	HIS
1	C	96	PRO

### 5.3.2 Protein sidechains [i](#)

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	289/331 (87%)	285 (99%)	4 (1%)	69	82
1	C	287/331 (87%)	281 (98%)	6 (2%)	56	71
2	B	293/326 (90%)	283 (97%)	10 (3%)	40	53
2	D	281/326 (86%)	277 (99%)	4 (1%)	69	82
All	All	1150/1314 (88%)	1126 (98%)	24 (2%)	58	71

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	329	ILE
2	B	359[B]	HIS
2	D	337	ARG
2	B	358	MET
2	B	359[A]	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	ASN
1	A	61	GLN
1	A	321	ASN
1	C	73	GLN
2	D	331	GLN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry

Of 27 ligands modelled in this entry, 14 are monoatomic - leaving 13 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	$\# Z  > 2$
3	NAG	A	501	1	14,14,15	0.26	0	17,19,21	0.77	0
3	NAG	A	502	1,3	14,14,15	0.36	0	17,19,21	0.67	0
3	NAG	A	503	3,4	14,14,15	0.37	0	17,19,21	0.82	1 (5%)
4	BMA	A	504	3,5	11,11,12	0.38	0	15,15,17	0.60	0
5	MAN	A	505	4	11,11,12	0.29	0	15,15,17	0.62	0
5	MAN	A	506	4	11,11,12	0.39	0	15,15,17	0.82	0
3	NAG	B	501	2	14,14,15	0.41	0	17,19,21	0.65	0
3	NAG	B	502	2	14,14,15	0.44	0	17,19,21	0.77	1 (5%)
8	HX7	B	503	-	32,32,32	1.70	5 (15%)	43,43,43	2.04	4 (9%)
3	NAG	C	501	1	14,14,15	0.66	1 (7%)	17,19,21	0.63	0
3	NAG	C	502	1	14,14,15	0.33	0	17,19,21	0.70	0
3	NAG	D	401	2	14,14,15	0.85	1 (7%)	17,19,21	1.52	3 (17%)
8	HX7	D	402	-	32,32,32	1.63	7 (21%)	43,43,43	2.02	3 (6%)

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
3	NAG	A	501	1	-	0/6/23/26	0/1/1/1
3	NAG	A	502	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	503	3,4	-	0/6/23/26	0/1/1/1
4	BMA	A	504	3,5	-	0/2/19/22	0/1/1/1
5	MAN	A	505	4	-	0/2/19/22	0/1/1/1
5	MAN	A	506	4	-	0/2/19/22	0/1/1/1
3	NAG	B	501	2	-	0/6/23/26	0/1/1/1
3	NAG	B	502	2	-	0/6/23/26	0/1/1/1
8	HX7	B	503	-	-	0/23/23/23	0/2/2/2
3	NAG	C	501	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	C	502	1	-	0/6/23/26	0/1/1/1
3	NAG	D	401	2	-	0/6/23/26	0/1/1/1
8	HX7	D	402	-	-	0/23/23/23	0/2/2/2

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	501	NAG	C1-C2	2.10	1.55	1.52
3	D	401	NAG	O5-C1	2.13	1.47	1.43
8	D	402	HX7	OAC-SBE	2.13	1.47	1.43
8	D	402	HX7	CAZ-CL1	2.14	1.78	1.73
8	D	402	HX7	CAY-CL2	2.28	1.79	1.73

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	503	HX7	OAD-SBE-OAC	-11.69	101.29	118.79
8	D	402	HX7	OAD-SBE-OAC	-11.45	101.66	118.79
3	A	503	NAG	O5-C1-C2	-2.24	108.43	111.52
8	B	503	HX7	OAC-SBE-NAV	2.00	111.24	107.12
8	B	503	HX7	OAD-SBE-NAV	2.00	111.24	107.12

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	502	NAG	3	0
8	B	503	HX7	4	0
8	D	402	HX7	5	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	359/385 (93%)	0.08	9 (2%) 57 64	17, 30, 60, 74	0
1	C	357/385 (92%)	0.41	34 (9%) 8 10	22, 42, 69, 83	0
2	B	359/363 (98%)	0.56	37 (10%) 6 8	17, 43, 70, 83	0
2	D	360/363 (99%)	0.59	45 (12%) 4 5	22, 43, 77, 93	0
All	All	1435/1496 (95%)	0.41	125 (8%) 10 13	17, 39, 69, 93	0

The worst 5 of 125 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	48	VAL	9.1
2	D	194	PHE	7.7
2	D	48	VAL	6.0
2	D	344	PHE	5.7
1	C	97	ALA	5.2

### 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 carbohydrates 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, 95<sup>th</sup> 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
3	NAG	B	502	14/15	0.58	0.58	72,76,81,84	0
5	MAN	A	506	11/12	0.66	0.45	82,85,91,94	0
3	NAG	D	401	14/15	0.70	0.51	74,77,82,84	0
3	NAG	B	501	14/15	0.72	0.40	61,66,70,71	0
3	NAG	C	501	14/15	0.78	0.46	65,74,81,81	0
5	MAN	A	505	11/12	0.81	0.15	63,68,71,71	0
7	CL	B	506	1/1	0.86	0.12	53,53,53,53	0
7	CL	D	403	1/1	0.87	0.27	57,57,57,57	0
7	CL	D	405	1/1	0.87	0.10	66,66,66,66	0
3	NAG	A	502	14/15	0.87	0.16	41,46,51,52	0
7	CL	B	504	1/1	0.88	0.21	53,53,53,53	0
4	BMA	A	504	11/12	0.88	0.25	69,73,79,81	0
8	HX7	B	503	31/31	0.88	0.20	34,38,42,43	0
3	NAG	C	502	14/15	0.89	0.16	44,47,51,52	0
7	CL	C	504	1/1	0.91	0.18	69,69,69,69	0
3	NAG	A	503	14/15	0.91	0.20	56,58,64,66	0
3	NAG	A	501	14/15	0.91	0.22	35,38,40,41	0
8	HX7	D	402	31/31	0.91	0.18	34,40,46,52	0
7	CL	A	509	1/1	0.92	0.07	48,48,48,48	0
7	CL	A	508	1/1	0.92	0.06	57,57,57,57	0
7	CL	D	404	1/1	0.93	0.21	77,77,77,77	0
7	CL	D	406	1/1	0.94	0.08	70,70,70,70	0
7	CL	B	505	1/1	0.95	0.18	72,72,72,72	0
7	CL	B	507	1/1	0.95	0.12	61,61,61,61	0
7	CL	C	505	1/1	0.95	0.08	43,43,43,43	0
6	NA	C	503	1/1	0.98	0.05	28,28,28,28	0
6	NA	A	507	1/1	0.99	0.10	19,19,19,19	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.