



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 03:59 PM UTC

PDB ID : 5UN1 / pdb_00005un1
Title : Crystal structure of GluN1/GluN2B delta-ATD NMDA receptor
Authors : Song, X.; Gouaux, E.
Deposited on : 2017-01-30
Resolution : 3.60 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

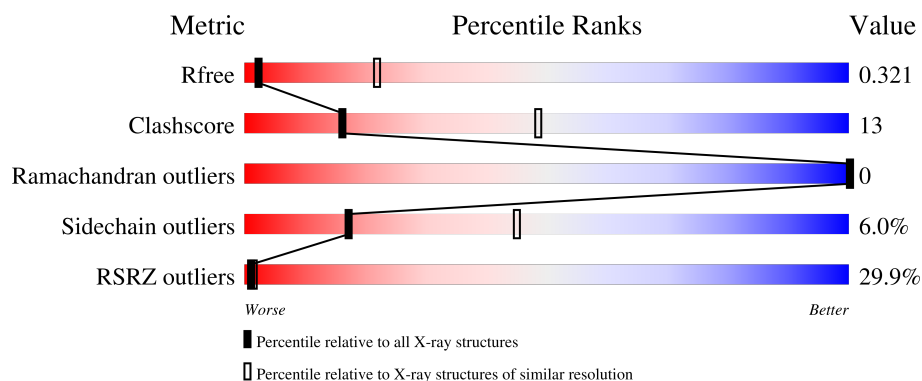
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 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	1747 (3.70-3.50)
Clashscore	190562	1827 (3.70-3.50)
Ramachandran outliers	187476	1773 (3.70-3.50)
Sidechain outliers	187428	1772 (3.70-3.50)
RSRZ outliers	180081	1745 (3.70-3.50)

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	451	26% 78% 14% 8%
1	C	451	28% 73% 17% 8%
1	E	451	31% 75% 16% 9%
1	G	451	19% 71% 20% 6%
2	B	448	28% 74% 13% 11%

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Mol	Chain	Length	Quality of chain
2	D	448	
2	F	448	
2	H	448	

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	GLY	G	1001	-	-	X	-
6	GLU	B	1001	-	-	X	-
6	GLU	D	1002	-	-	X	-
6	GLU	H	1001	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 20143 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 N-methyl-D-aspartate receptor subunit NR1-3a.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	G	424	Total	C	N	O	S	0	0	0
			2753	1727	499	512	15			
1	A	416	Total	C	N	O	S	0	0	0
			2643	1655	466	508	14			
1	E	412	Total	C	N	O	S	0	0	0
			2486	1549	448	477	12			
1	C	415	Total	C	N	O	S	0	0	0
			2591	1629	461	487	14			

There are 132 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	440	ASP	ASN	conflict	UNP C0KD15
G	469	ASP	ASN	conflict	UNP C0KD15
G	493	ALA	LYS	conflict	UNP C0KD15
G	494	ALA	LYS	conflict	UNP C0KD15
G	495	ALA	GLU	conflict	UNP C0KD15
G	?	-	LYS	deletion	UNP C0KD15
G	?	-	VAL	deletion	UNP C0KD15
G	?	-	ASN	deletion	UNP C0KD15
G	?	-	SER	deletion	UNP C0KD15
G	?	-	GLU	deletion	UNP C0KD15
G	?	-	GLU	deletion	UNP C0KD15
G	?	-	GLU	deletion	UNP C0KD15
G	?	-	GLU	deletion	UNP C0KD15
G	602	ARG	GLY	conflict	UNP C0KD15
G	609	LEU	ILE	conflict	UNP C0KD15
G	648	ARG	ASP	conflict	UNP C0KD15
G	761	GLU	ASN	conflict	UNP C0KD15
G	829	SER	-	expression tag	UNP C0KD15
G	830	ARG	-	expression tag	UNP C0KD15
G	831	ALA	-	expression tag	UNP C0KD15
G	832	GLU	-	expression tag	UNP C0KD15

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Chain	Residue	Modelled	Actual	Comment	Reference
G	833	ALA	-	expression tag	UNP C0KD15
G	834	LYS	-	expression tag	UNP C0KD15
G	835	ARG	-	expression tag	UNP C0KD15
G	836	MET	-	expression tag	UNP C0KD15
G	837	LYS	-	expression tag	UNP C0KD15
G	838	GLY	-	expression tag	UNP C0KD15
G	839	LEU	-	expression tag	UNP C0KD15
G	840	GLU	-	expression tag	UNP C0KD15
G	841	VAL	-	expression tag	UNP C0KD15
G	842	LEU	-	expression tag	UNP C0KD15
G	843	PHE	-	expression tag	UNP C0KD15
G	844	GLN	-	expression tag	UNP C0KD15
A	440	ASP	ASN	conflict	UNP C0KD15
A	469	ASP	ASN	conflict	UNP C0KD15
A	493	ALA	LYS	conflict	UNP C0KD15
A	494	ALA	LYS	conflict	UNP C0KD15
A	495	ALA	GLU	conflict	UNP C0KD15
A	?	-	LYS	deletion	UNP C0KD15
A	?	-	VAL	deletion	UNP C0KD15
A	?	-	ASN	deletion	UNP C0KD15
A	?	-	SER	deletion	UNP C0KD15
A	?	-	GLU	deletion	UNP C0KD15
A	?	-	GLU	deletion	UNP C0KD15
A	?	-	GLU	deletion	UNP C0KD15
A	?	-	GLU	deletion	UNP C0KD15
A	?	-	GLU	deletion	UNP C0KD15
A	602	ARG	GLY	conflict	UNP C0KD15
A	609	LEU	ILE	conflict	UNP C0KD15
A	648	ARG	ASP	conflict	UNP C0KD15
A	761	GLU	ASN	conflict	UNP C0KD15
A	829	SER	-	expression tag	UNP C0KD15
A	830	ARG	-	expression tag	UNP C0KD15
A	831	ALA	-	expression tag	UNP C0KD15
A	832	GLU	-	expression tag	UNP C0KD15
A	833	ALA	-	expression tag	UNP C0KD15
A	834	LYS	-	expression tag	UNP C0KD15
A	835	ARG	-	expression tag	UNP C0KD15
A	836	MET	-	expression tag	UNP C0KD15
A	837	LYS	-	expression tag	UNP C0KD15
A	838	GLY	-	expression tag	UNP C0KD15
A	839	LEU	-	expression tag	UNP C0KD15
A	840	GLU	-	expression tag	UNP C0KD15
A	841	VAL	-	expression tag	UNP C0KD15

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Chain	Residue	Modelled	Actual	Comment	Reference
A	842	LEU	-	expression tag	UNP C0KD15
A	843	PHE	-	expression tag	UNP C0KD15
A	844	GLN	-	expression tag	UNP C0KD15
E	440	ASP	ASN	conflict	UNP C0KD15
E	469	ASP	ASN	conflict	UNP C0KD15
E	493	ALA	LYS	conflict	UNP C0KD15
E	494	ALA	LYS	conflict	UNP C0KD15
E	495	ALA	GLU	conflict	UNP C0KD15
E	?	-	LYS	deletion	UNP C0KD15
E	?	-	VAL	deletion	UNP C0KD15
E	?	-	ASN	deletion	UNP C0KD15
E	?	-	SER	deletion	UNP C0KD15
E	?	-	GLU	deletion	UNP C0KD15
E	?	-	GLU	deletion	UNP C0KD15
E	?	-	GLU	deletion	UNP C0KD15
E	?	-	GLU	deletion	UNP C0KD15
E	602	ARG	GLY	conflict	UNP C0KD15
E	609	LEU	ILE	conflict	UNP C0KD15
E	648	ARG	ASP	conflict	UNP C0KD15
E	761	GLU	ASN	conflict	UNP C0KD15
E	829	SER	-	expression tag	UNP C0KD15
E	830	ARG	-	expression tag	UNP C0KD15
E	831	ALA	-	expression tag	UNP C0KD15
E	832	GLU	-	expression tag	UNP C0KD15
E	833	ALA	-	expression tag	UNP C0KD15
E	834	LYS	-	expression tag	UNP C0KD15
E	835	ARG	-	expression tag	UNP C0KD15
E	836	MET	-	expression tag	UNP C0KD15
E	837	LYS	-	expression tag	UNP C0KD15
E	838	GLY	-	expression tag	UNP C0KD15
E	839	LEU	-	expression tag	UNP C0KD15
E	840	GLU	-	expression tag	UNP C0KD15
E	841	VAL	-	expression tag	UNP C0KD15
E	842	LEU	-	expression tag	UNP C0KD15
E	843	PHE	-	expression tag	UNP C0KD15
E	844	GLN	-	expression tag	UNP C0KD15
C	440	ASP	ASN	conflict	UNP C0KD15
C	469	ASP	ASN	conflict	UNP C0KD15
C	493	ALA	LYS	conflict	UNP C0KD15
C	494	ALA	LYS	conflict	UNP C0KD15
C	495	ALA	GLU	conflict	UNP C0KD15
C	?	-	LYS	deletion	UNP C0KD15

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	VAL	deletion	UNP C0KD15
C	?	-	ASN	deletion	UNP C0KD15
C	?	-	SER	deletion	UNP C0KD15
C	?	-	GLU	deletion	UNP C0KD15
C	?	-	GLU	deletion	UNP C0KD15
C	?	-	GLU	deletion	UNP C0KD15
C	?	-	GLU	deletion	UNP C0KD15
C	602	ARG	GLY	conflict	UNP C0KD15
C	609	LEU	ILE	conflict	UNP C0KD15
C	648	ARG	ASP	conflict	UNP C0KD15
C	761	GLU	ASN	conflict	UNP C0KD15
C	829	SER	-	expression tag	UNP C0KD15
C	830	ARG	-	expression tag	UNP C0KD15
C	831	ALA	-	expression tag	UNP C0KD15
C	832	GLU	-	expression tag	UNP C0KD15
C	833	ALA	-	expression tag	UNP C0KD15
C	834	LYS	-	expression tag	UNP C0KD15
C	835	ARG	-	expression tag	UNP C0KD15
C	836	MET	-	expression tag	UNP C0KD15
C	837	LYS	-	expression tag	UNP C0KD15
C	838	GLY	-	expression tag	UNP C0KD15
C	839	LEU	-	expression tag	UNP C0KD15
C	840	GLU	-	expression tag	UNP C0KD15
C	841	VAL	-	expression tag	UNP C0KD15
C	842	LEU	-	expression tag	UNP C0KD15
C	843	PHE	-	expression tag	UNP C0KD15
C	844	GLN	-	expression tag	UNP C0KD15

- Molecule 2 is a protein called Ionotropic glutamate receptor subunit NR2B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	397	Total	C	N	O	S	0	0	0
			2328	1452	427	440	9			
2	H	409	Total	C	N	O	S	0	0	0
			2382	1460	443	466	13			
2	F	416	Total	C	N	O	S	0	0	0
			2319	1436	430	445	8			
2	D	405	Total	C	N	O	S	0	0	0
			2413	1502	439	461	11			

There are 128 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	486	VAL	THR	conflict	UNP A7XY94
B	?	-	ARG	deletion	UNP A7XY94
B	?	-	CYS	deletion	UNP A7XY94
B	?	-	LEU	deletion	UNP A7XY94
B	?	-	ALA	deletion	UNP A7XY94
B	?	-	ASP	deletion	UNP A7XY94
B	?	-	GLY	deletion	UNP A7XY94
B	?	-	ARG	deletion	UNP A7XY94
B	?	-	GLU	deletion	UNP A7XY94
B	?	-	PRO	deletion	UNP A7XY94
B	?	-	GLY	deletion	UNP A7XY94
B	601	LEU	VAL	conflict	UNP A7XY94
B	640	ARG	GLU	conflict	UNP A7XY94
B	641	ARG	GLU	conflict	UNP A7XY94
B	826	TYR	-	expression tag	UNP A7XY94
B	827	LYS	-	expression tag	UNP A7XY94
B	828	SER	-	expression tag	UNP A7XY94
B	829	ARG	-	expression tag	UNP A7XY94
B	830	ALA	-	expression tag	UNP A7XY94
B	831	GLU	-	expression tag	UNP A7XY94
B	832	ALA	-	expression tag	UNP A7XY94
B	833	LYS	-	expression tag	UNP A7XY94
B	834	ARG	-	expression tag	UNP A7XY94
B	835	MET	-	expression tag	UNP A7XY94
B	836	LYS	-	expression tag	UNP A7XY94
B	837	GLY	-	expression tag	UNP A7XY94
B	838	LEU	-	expression tag	UNP A7XY94
B	839	GLU	-	expression tag	UNP A7XY94
B	840	VAL	-	expression tag	UNP A7XY94
B	841	LEU	-	expression tag	UNP A7XY94
B	842	PHE	-	expression tag	UNP A7XY94
B	843	GLN	-	expression tag	UNP A7XY94
H	486	VAL	THR	conflict	UNP A7XY94
H	?	-	ARG	deletion	UNP A7XY94
H	?	-	CYS	deletion	UNP A7XY94
H	?	-	LEU	deletion	UNP A7XY94
H	?	-	ALA	deletion	UNP A7XY94
H	?	-	ASP	deletion	UNP A7XY94
H	?	-	GLY	deletion	UNP A7XY94
H	?	-	ARG	deletion	UNP A7XY94
H	?	-	GLU	deletion	UNP A7XY94
H	?	-	PRO	deletion	UNP A7XY94
H	?	-	GLY	deletion	UNP A7XY94

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Chain	Residue	Modelled	Actual	Comment	Reference
H	601	LEU	VAL	conflict	UNP A7XY94
H	640	ARG	GLU	conflict	UNP A7XY94
H	641	ARG	GLU	conflict	UNP A7XY94
H	826	TYR	-	expression tag	UNP A7XY94
H	827	LYS	-	expression tag	UNP A7XY94
H	828	SER	-	expression tag	UNP A7XY94
H	829	ARG	-	expression tag	UNP A7XY94
H	830	ALA	-	expression tag	UNP A7XY94
H	831	GLU	-	expression tag	UNP A7XY94
H	832	ALA	-	expression tag	UNP A7XY94
H	833	LYS	-	expression tag	UNP A7XY94
H	834	ARG	-	expression tag	UNP A7XY94
H	835	MET	-	expression tag	UNP A7XY94
H	836	LYS	-	expression tag	UNP A7XY94
H	837	GLY	-	expression tag	UNP A7XY94
H	838	LEU	-	expression tag	UNP A7XY94
H	839	GLU	-	expression tag	UNP A7XY94
H	840	VAL	-	expression tag	UNP A7XY94
H	841	LEU	-	expression tag	UNP A7XY94
H	842	PHE	-	expression tag	UNP A7XY94
H	843	GLN	-	expression tag	UNP A7XY94
F	486	VAL	THR	conflict	UNP A7XY94
F	?	-	ARG	deletion	UNP A7XY94
F	?	-	CYS	deletion	UNP A7XY94
F	?	-	LEU	deletion	UNP A7XY94
F	?	-	ALA	deletion	UNP A7XY94
F	?	-	ASP	deletion	UNP A7XY94
F	?	-	GLY	deletion	UNP A7XY94
F	?	-	ARG	deletion	UNP A7XY94
F	?	-	GLU	deletion	UNP A7XY94
F	?	-	PRO	deletion	UNP A7XY94
F	?	-	GLY	deletion	UNP A7XY94
F	601	LEU	VAL	conflict	UNP A7XY94
F	640	ARG	GLU	conflict	UNP A7XY94
F	641	ARG	GLU	conflict	UNP A7XY94
F	826	TYR	-	expression tag	UNP A7XY94
F	827	LYS	-	expression tag	UNP A7XY94
F	828	SER	-	expression tag	UNP A7XY94
F	829	ARG	-	expression tag	UNP A7XY94
F	830	ALA	-	expression tag	UNP A7XY94
F	831	GLU	-	expression tag	UNP A7XY94
F	832	ALA	-	expression tag	UNP A7XY94

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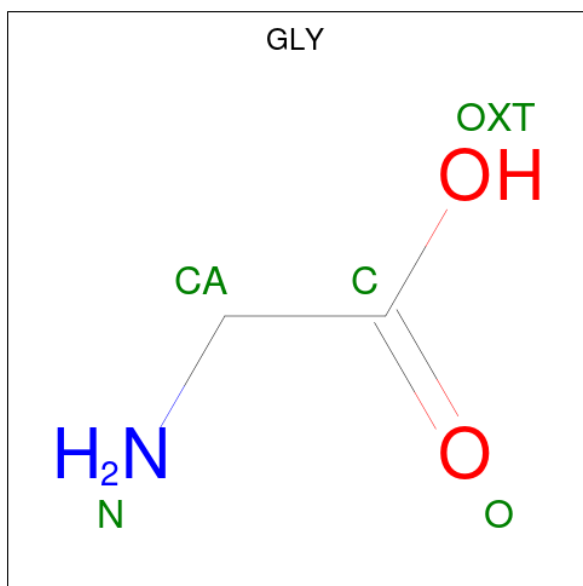
Chain	Residue	Modelled	Actual	Comment	Reference
F	833	LYS	-	expression tag	UNP A7XY94
F	834	ARG	-	expression tag	UNP A7XY94
F	835	MET	-	expression tag	UNP A7XY94
F	836	LYS	-	expression tag	UNP A7XY94
F	837	GLY	-	expression tag	UNP A7XY94
F	838	LEU	-	expression tag	UNP A7XY94
F	839	GLU	-	expression tag	UNP A7XY94
F	840	VAL	-	expression tag	UNP A7XY94
F	841	LEU	-	expression tag	UNP A7XY94
F	842	PHE	-	expression tag	UNP A7XY94
F	843	GLN	-	expression tag	UNP A7XY94
D	486	VAL	THR	conflict	UNP A7XY94
D	?	-	ARG	deletion	UNP A7XY94
D	?	-	CYS	deletion	UNP A7XY94
D	?	-	LEU	deletion	UNP A7XY94
D	?	-	ALA	deletion	UNP A7XY94
D	?	-	ASP	deletion	UNP A7XY94
D	?	-	GLY	deletion	UNP A7XY94
D	?	-	ARG	deletion	UNP A7XY94
D	?	-	GLU	deletion	UNP A7XY94
D	?	-	PRO	deletion	UNP A7XY94
D	?	-	GLY	deletion	UNP A7XY94
D	601	LEU	VAL	conflict	UNP A7XY94
D	640	ARG	GLU	conflict	UNP A7XY94
D	641	ARG	GLU	conflict	UNP A7XY94
D	826	TYR	-	expression tag	UNP A7XY94
D	827	LYS	-	expression tag	UNP A7XY94
D	828	SER	-	expression tag	UNP A7XY94
D	829	ARG	-	expression tag	UNP A7XY94
D	830	ALA	-	expression tag	UNP A7XY94
D	831	GLU	-	expression tag	UNP A7XY94
D	832	ALA	-	expression tag	UNP A7XY94
D	833	LYS	-	expression tag	UNP A7XY94
D	834	ARG	-	expression tag	UNP A7XY94
D	835	MET	-	expression tag	UNP A7XY94
D	836	LYS	-	expression tag	UNP A7XY94
D	837	GLY	-	expression tag	UNP A7XY94
D	838	LEU	-	expression tag	UNP A7XY94
D	839	GLU	-	expression tag	UNP A7XY94
D	840	VAL	-	expression tag	UNP A7XY94
D	841	LEU	-	expression tag	UNP A7XY94
D	842	PHE	-	expression tag	UNP A7XY94

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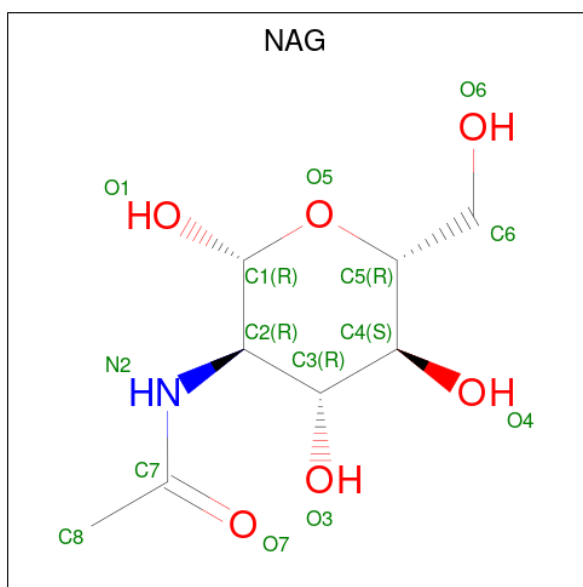
Chain	Residue	Modelled	Actual	Comment	Reference
D	843	GLN	-	expression tag	UNP A7XY94

- Molecule 3 is GLYCINE (CCD ID: GLY) (formula: $C_2H_5NO_2$).



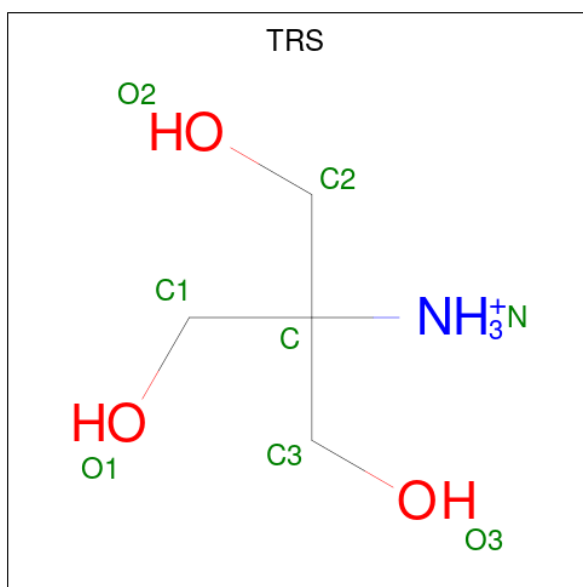
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	G	1	Total	C	N	O	0	0
			5	2	1	2		
3	A	1	Total	C	N	O	0	0
			5	2	1	2		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



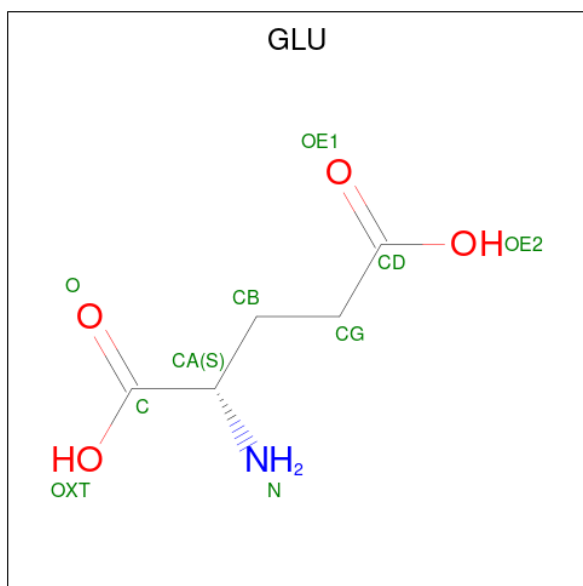
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	G	1	Total	C	N	O	0	0
			15	8	1	6		
4	B	1	Total	C	N	O	0	0
			15	8	1	6		
4	H	1	Total	C	N	O	0	0
			15	8	1	6		
4	F	1	Total	C	N	O	0	0
			15	8	1	6		
4	D	1	Total	C	N	O	0	0
			15	8	1	6		
4	D	1	Total	C	N	O	0	0
			15	8	1	6		

- Molecule 5 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	G	1	Total	C	N	O	0	0
			8	4	1	3		

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



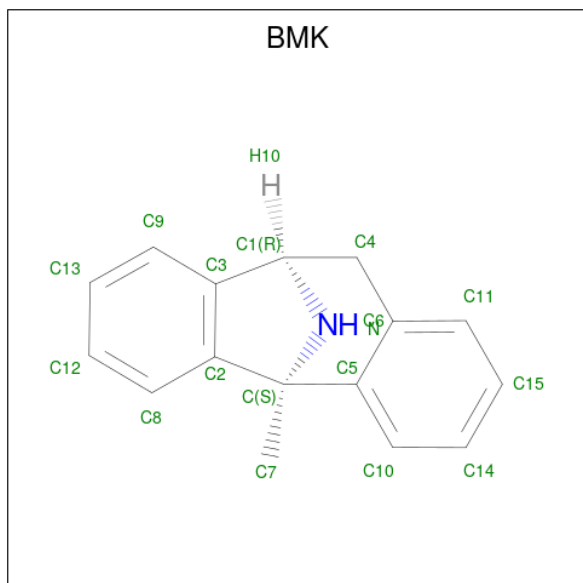
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	G	1	Total	C	N	O	0	0
			10	5	1	4		
6	G	1	Total	C	N	O	0	0
			10	5	1	4		
6	B	1	Total	C	N	O	0	0
			10	5	1	4		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	H	1	Total	C	N	O	0	0
			10	5	1	4		
6	D	1	Total	C	N	O	0	0
			10	5	1	4		

- Molecule 7 is (5S,10R)-5-methyl-10,11-dihydro-5H-5,10-epiminodibenzo[a,d][7]annulene (CCD ID: BMK) (formula: C₁₆H₁₅N).

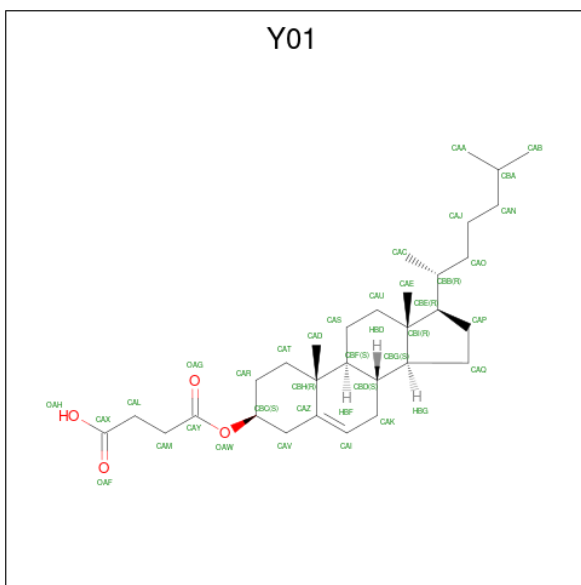


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	G	1	Total	C	N	0	0
			17	16	1		
7	B	1	Total	C	N	0	0
			17	16	1		

- Molecule 8 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	Mg	0	0
			1	1		

- Molecule 9 is CHOLESTEROL HEMISUCCINATE (CCD ID: Y01) (formula: C₃₁H₅₀O₄).

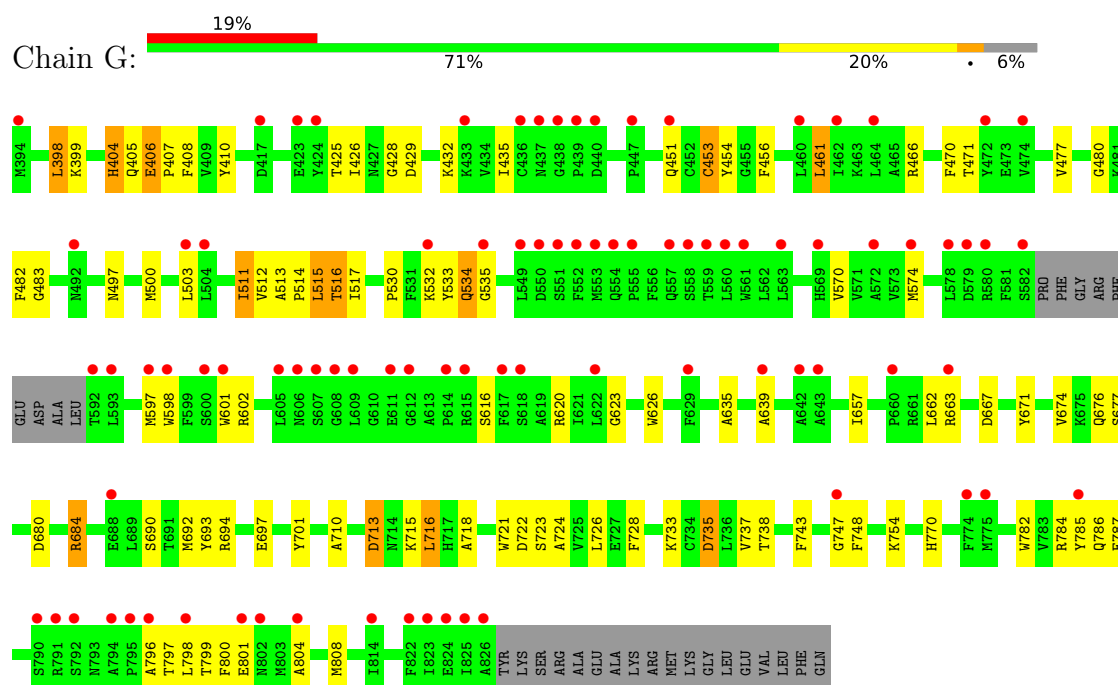


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	E	1	Total	C	O	0	0
			35	31	4		

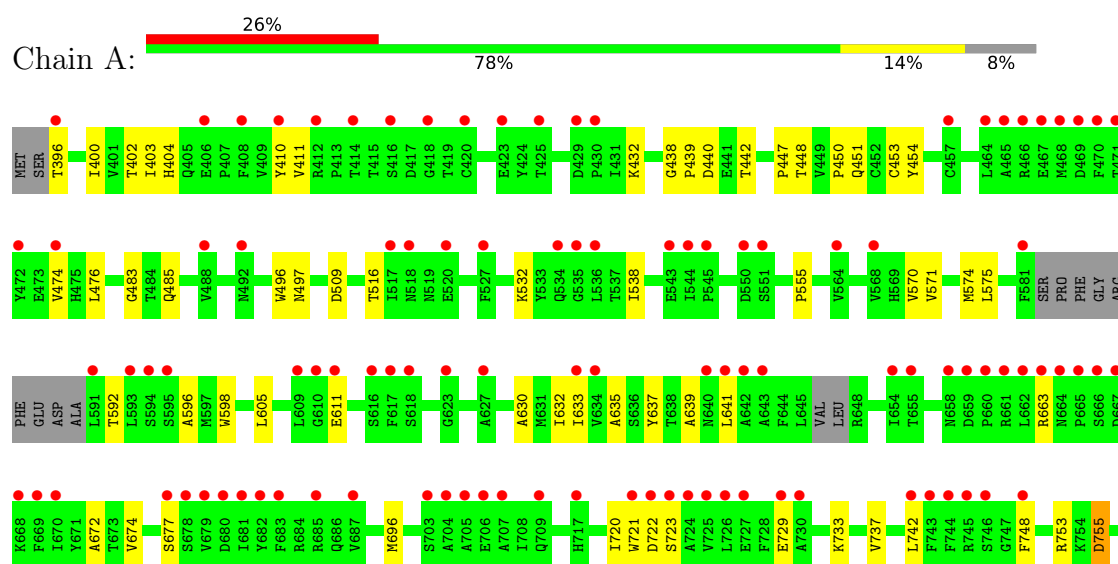
3 Residue-property plots

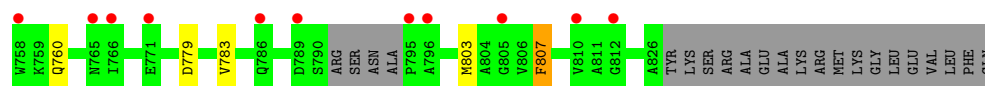
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: N-methyl-D-aspartate receptor subunit NR1-3a

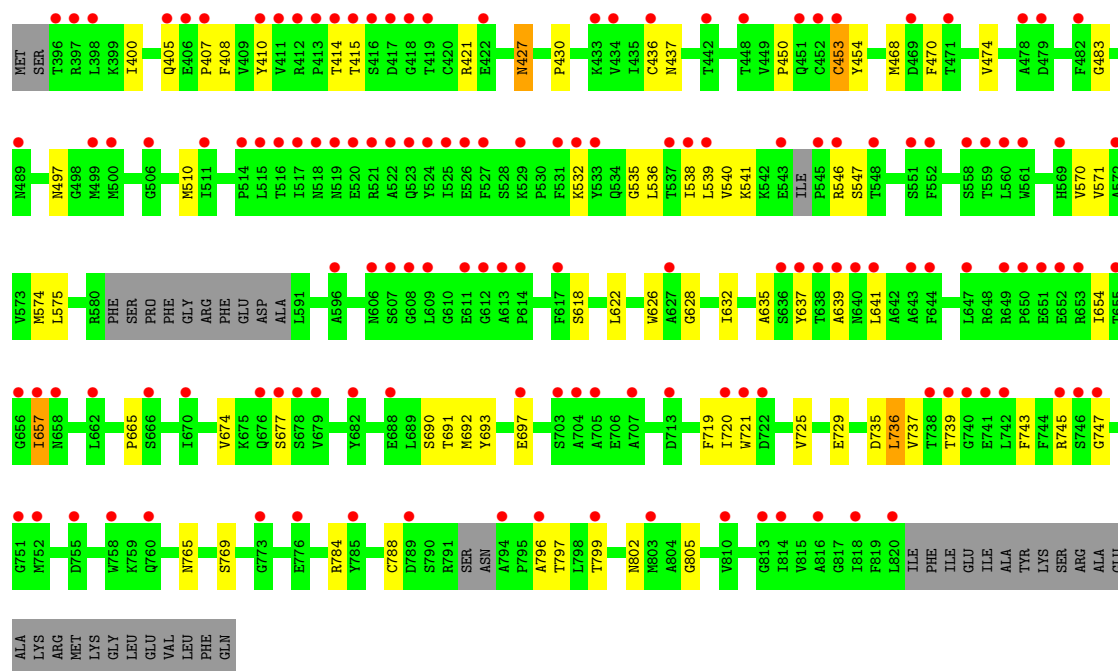
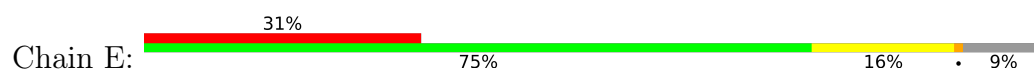


- Molecule 1: N-methyl-D-aspartate receptor subunit NR1-3a

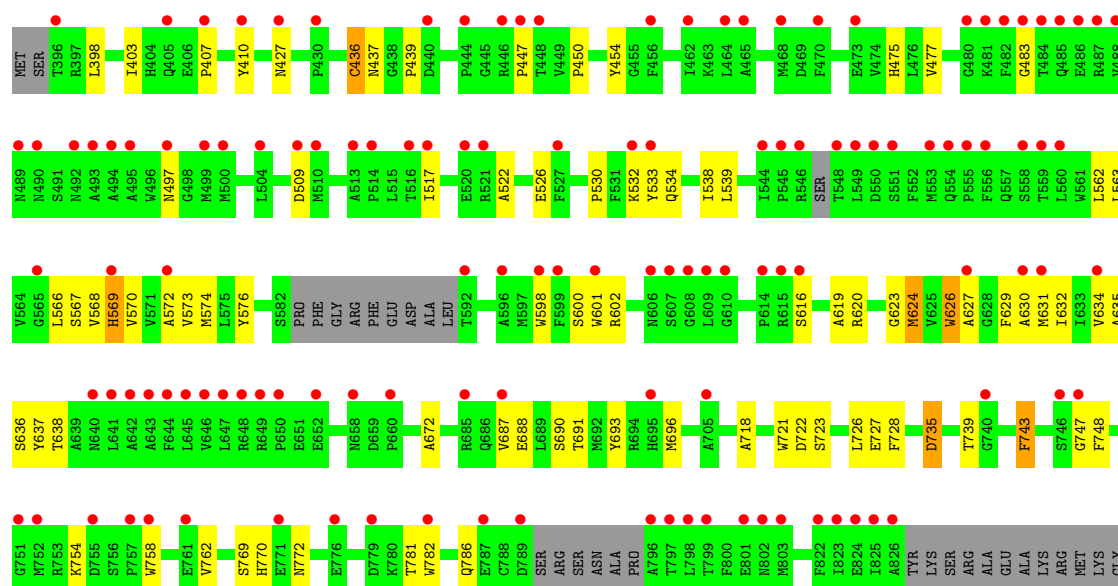
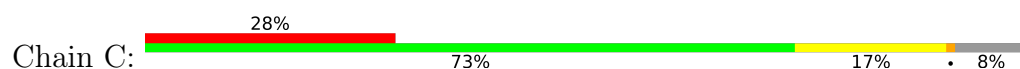




• Molecule 1: N-methyl-D-aspartate receptor subunit NR1-3a



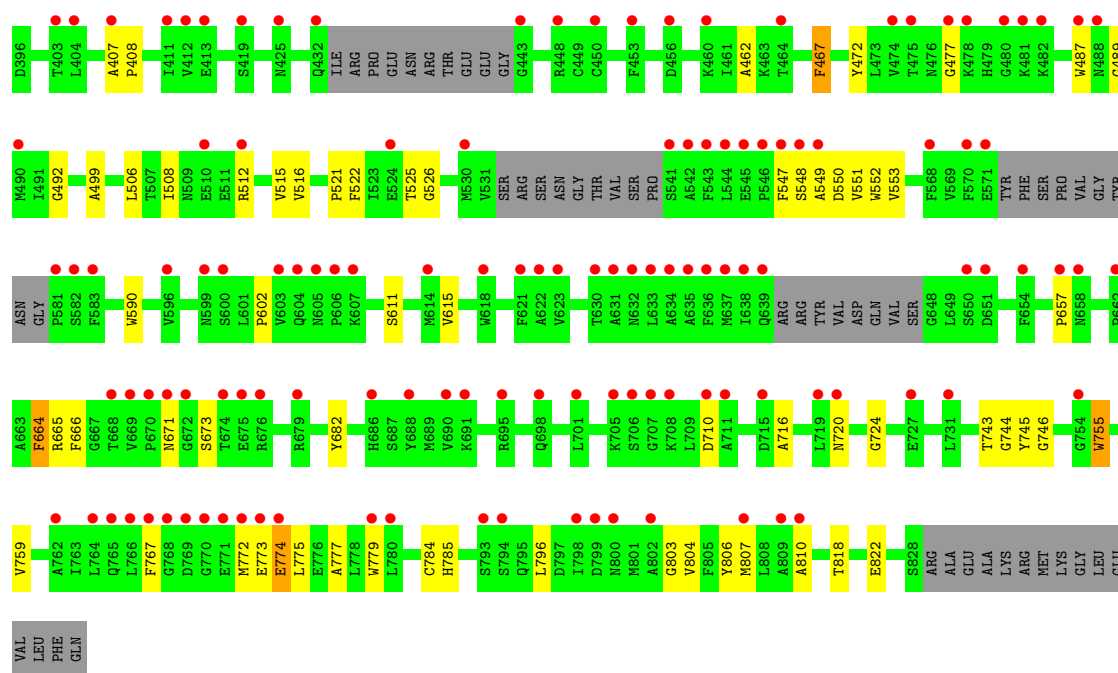
• Molecule 1: N-methyl-D-aspartate receptor subunit NR1-3a



LEU
GLU
VAL
LEU
PHE
GLN

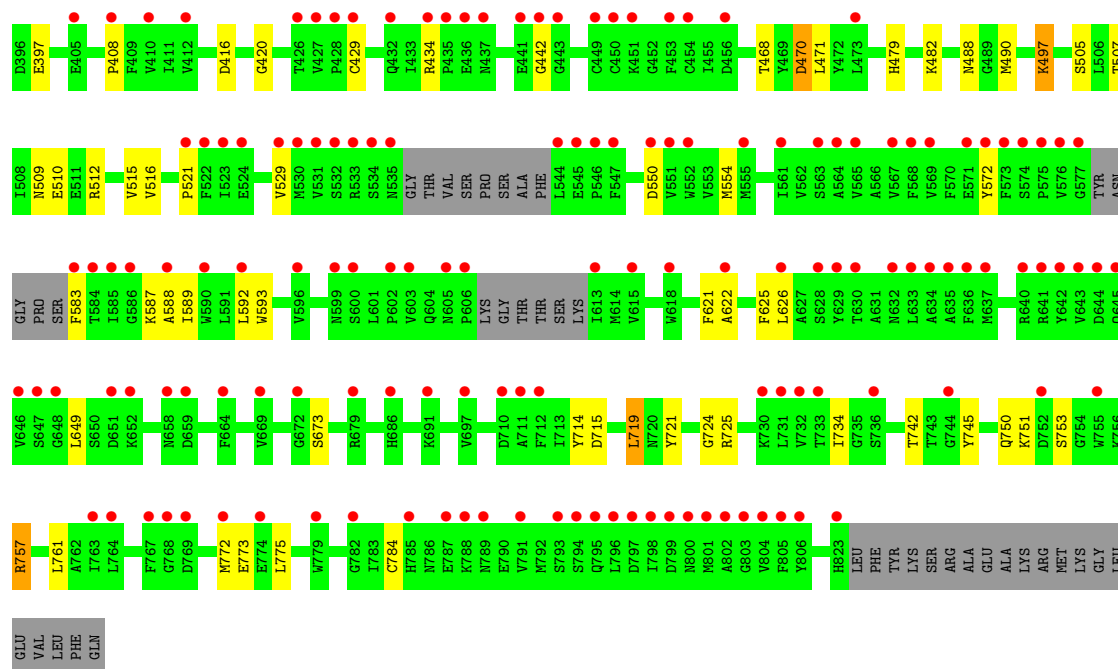
● Molecule 2: Ionotropic glutamate receptor subunit NR2B

Chain B: 28% 74% 13% 11%



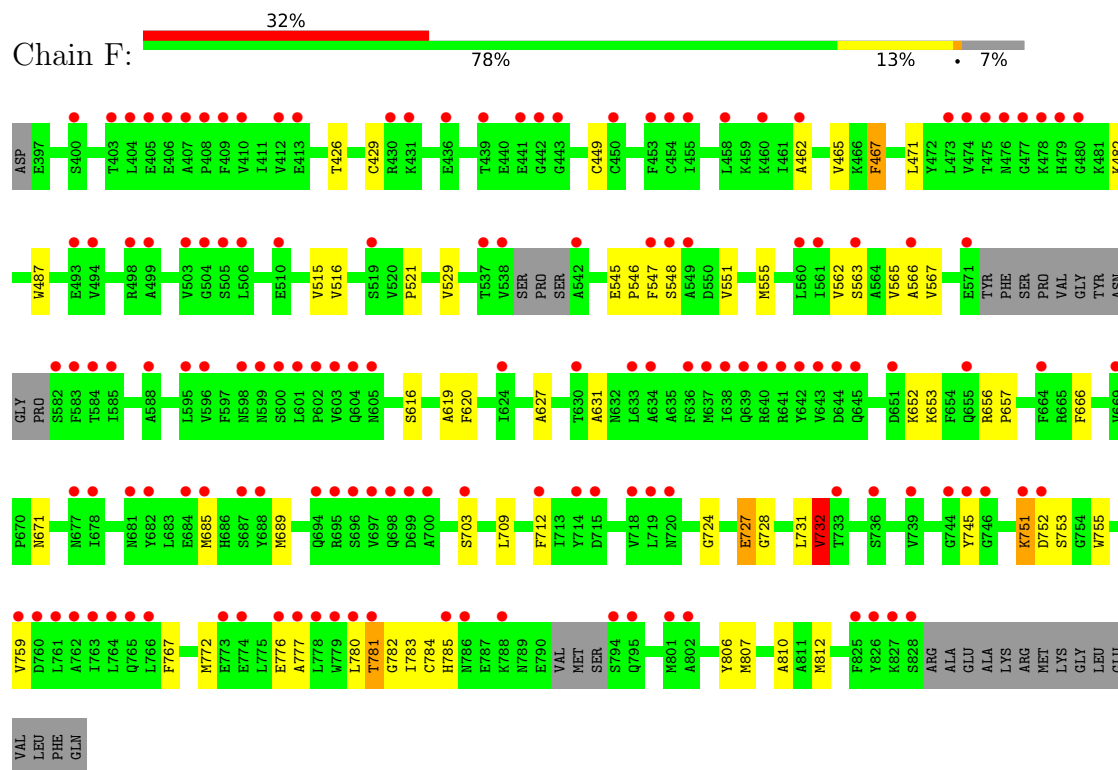
● Molecule 2: Ionotropic glutamate receptor subunit NR2B

Chain H: 32% 79% 12% 9%



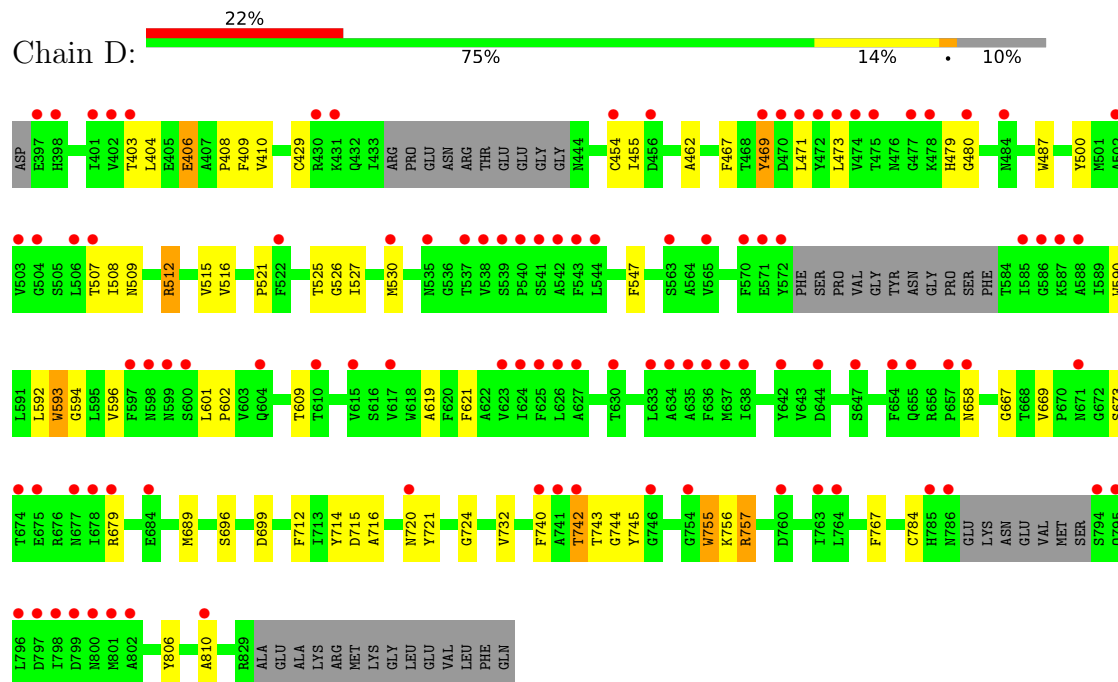
● Molecule 2: Ionotropic glutamate receptor subunit NR2B

Chain F:



● Molecule 2: Ionotropic glutamate receptor subunit NR2B

Chain D:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	181.57Å 108.47Å 182.46Å 90.00° 111.44° 90.00°	Depositor
Resolution (Å)	49.99 – 3.60 49.99 – 3.60	Depositor EDS
% Data completeness (in resolution range)	91.0 (49.99-3.60) 91.0 (49.99-3.60)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 3.41Å)	Xtriage
Refinement program	PHENIX (dev_2597: ???)	Depositor
R, R_{free}	0.288 , 0.316 0.291 , 0.321	Depositor DCC
R_{free} test set	3670 reflections (4.01%)	wwPDB-VP
Wilson B-factor (Å ²)	104.5	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.15 , 82.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.34$, $\langle L^2 \rangle = 0.17$	Xtriage
Estimated twinning fraction	0.117 for l,-k,h	Xtriage
F_o, F_c correlation	0.81	EDS
Total number of atoms	20143	wwPDB-VP
Average B, all atoms (Å ²)	133.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.85% 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: MG, TRS, BMK, NAG, Y01

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	0.22	0/2694	0.34	0/3703
1	C	0.26	0/2647	0.42	2/3648 (0.1%)
1	E	0.20	0/2529	0.41	2/3491 (0.1%)
1	G	0.35	0/2808	0.51	1/3848 (0.0%)
2	B	0.19	0/2363	0.42	1/3260 (0.0%)
2	D	0.24	0/2452	0.49	3/3384 (0.1%)
2	F	0.28	0/2344	0.58	6/3245 (0.2%)
2	H	0.24	0/2409	0.43	1/3317 (0.0%)
All	All	0.25	0/20246	0.45	16/27896 (0.1%)

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	728	GLY	N-CA-C	-7.50	105.39	115.36
2	H	572	TYR	CB-CA-C	-6.15	109.50	116.63
2	F	565	VAL	CA-C-N	6.08	128.74	120.54
2	F	565	VAL	C-N-CA	6.08	128.74	120.54
1	E	546	ARG	N-CA-C	6.07	117.90	111.28

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	2643	0	1928	44	0
1	C	2591	0	1819	73	0
1	E	2486	0	1710	46	0
1	G	2753	0	2092	91	0
2	B	2328	0	1521	60	0
2	D	2413	0	1600	64	0
2	F	2319	0	1436	59	0
2	H	2382	0	1585	37	0
3	A	5	0	2	1	0
3	G	5	0	2	5	0
4	B	15	0	15	3	0
4	D	30	0	30	0	0
4	F	15	0	15	0	0
4	G	15	0	15	0	0
4	H	15	0	15	0	0
5	G	8	0	12	2	0
6	B	10	0	5	4	0
6	D	10	0	5	8	0
6	G	20	0	10	2	0
6	H	10	0	5	4	0
7	B	17	0	0	0	0
7	G	17	0	0	0	0
8	A	1	0	0	0	0
9	E	35	0	42	5	0
All	All	20143	0	13864	447	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 13.

The worst 5 of 447 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)
9:E:1001:Y01:CAP	9:E:1001:Y01:CAQ	1.82	1.51
1:C:624:MET:CB	2:D:593:TRP:HE1	1.33	1.41
1:C:624:MET:CB	2:D:593:TRP:NE1	1.90	1.31
2:D:512:ARG:NH2	6:D:1002:GLU:OXT	1.73	1.20
1:C:624:MET:CB	2:D:593:TRP:CD1	2.31	1.13

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	408/451 (90%)	388 (95%)	20 (5%)	0	100	100
1	C	407/451 (90%)	385 (95%)	22 (5%)	0	100	100
1	E	404/451 (90%)	387 (96%)	17 (4%)	0	100	100
1	G	420/451 (93%)	400 (95%)	20 (5%)	0	100	100
2	B	387/448 (86%)	350 (90%)	37 (10%)	0	100	100
2	D	397/448 (89%)	376 (95%)	21 (5%)	0	100	100
2	F	408/448 (91%)	377 (92%)	31 (8%)	0	100	100
2	H	401/448 (90%)	369 (92%)	32 (8%)	0	100	100
All	All	3232/3596 (90%)	3032 (94%)	200 (6%)	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	163/387 (42%)	159 (98%)	4 (2%)	42	63
1	C	145/387 (38%)	141 (97%)	4 (3%)	38	60
1	E	130/387 (34%)	123 (95%)	7 (5%)	20	47
1	G	176/387 (46%)	161 (92%)	15 (8%)	10	35
2	B	99/383 (26%)	93 (94%)	6 (6%)	17	45
2	D	114/383 (30%)	105 (92%)	9 (8%)	11	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	F	78/383 (20%)	71 (91%)	7 (9%)	9	33
2	H	110/383 (29%)	102 (93%)	8 (7%)	13	40
All	All	1015/3080 (33%)	955 (94%)	60 (6%)	17	45

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	649	LEU
2	D	593	TRP
1	E	657	ILE
2	D	512	ARG
2	D	767	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	681	ASN
1	C	569	HIS
1	E	497	ASN
2	B	680	ASN
1	C	507	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 1 is monoatomic - leaving 17 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$
4	NAG	G	1002	-	15,15,15	0.22	0	21,21,21	0.21	0
7	BMK	B	1003	-	17,20,20	2.46	4 (23%)	18,31,31	1.58	3 (16%)
4	NAG	F	1001	-	15,15,15	0.14	0	21,21,21	0.13	0
5	TRS	G	1003	-	7,7,7	0.40	0	9,9,9	0.63	0
6	GLU	H	1001	-	8,9,9	1.10	1 (12%)	8,11,11	1.34	3 (37%)
4	NAG	B	1002	-	15,15,15	0.18	0	21,21,21	0.27	0
4	NAG	D	1003	-	15,15,15	0.08	0	21,21,21	0.13	0
6	GLU	D	1002	-	8,9,9	1.13	0	8,11,11	1.42	2 (25%)
7	BMK	G	1005	-	17,20,20	2.43	4 (23%)	18,31,31	1.55	4 (22%)
6	GLU	B	1001	-	8,9,9	1.11	1 (12%)	8,11,11	1.24	1 (12%)
3	GLY	A	902	-	4,4,4	1.17	1 (25%)	3,4,4	1.69	2 (66%)
4	NAG	D	1001	-	15,15,15	0.12	0	21,21,21	0.16	0
6	GLU	G	1004	-	8,9,9	1.06	1 (12%)	8,11,11	1.34	1 (12%)
9	Y01	E	1001	-	38,38,38	8.30	26 (68%)	57,57,57	2.84	26 (45%)
3	GLY	G	1001	-	4,4,4	1.18	1 (25%)	3,4,4	1.47	0
6	GLU	G	1006	-	8,9,9	1.10	1 (12%)	8,11,11	1.23	1 (12%)
4	NAG	H	1002	-	15,15,15	0.13	0	21,21,21	0.12	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
4	NAG	G	1002	-	-	2/6/26/26	0/1/1/1
7	BMK	B	1003	-	-	-	0/5/4/4
4	NAG	F	1001	-	-	2/6/26/26	0/1/1/1
5	TRS	G	1003	-	-	8/9/9/9	-
6	GLU	H	1001	-	-	3/9/9/9	-
4	NAG	B	1002	-	-	1/6/26/26	0/1/1/1
4	NAG	D	1003	-	-	2/6/26/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GLU	D	1002	-	-	3/9/9/9	-
7	BMK	G	1005	-	-	-	0/5/4/4
6	GLU	B	1001	-	-	1/9/9/9	-
3	GLY	A	902	-	-	0/2/2/2	-
4	NAG	D	1001	-	-	2/6/26/26	0/1/1/1
6	GLU	G	1004	-	-	2/9/9/9	-
9	Y01	E	1001	-	-	12/19/77/77	0/4/4/4
3	GLY	G	1001	-	-	0/2/2/2	-
6	GLU	G	1006	-	-	3/9/9/9	-
4	NAG	H	1002	-	-	2/6/26/26	0/1/1/1

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	E	1001	Y01	CBD-CBG	-28.13	1.00	1.53
9	E	1001	Y01	CAU-CAS	-18.25	1.17	1.53
9	E	1001	Y01	CAU-CBI	-16.77	1.24	1.54
9	E	1001	Y01	CAK-CBD	-16.03	1.27	1.53
9	E	1001	Y01	CBH-CAZ	-12.16	1.29	1.52

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	E	1001	Y01	CAC-CBB-CBE	7.05	123.47	112.88
9	E	1001	Y01	CAS-CBF-CBH	-6.21	105.43	113.08
9	E	1001	Y01	CBH-CAZ-CAI	-6.08	114.05	122.93
9	E	1001	Y01	CAT-CBH-CAZ	5.99	119.07	108.74
9	E	1001	Y01	CAK-CAI-CAZ	-5.49	115.75	125.02

There are no chirality outliers.

5 of 43 torsion outliers are listed below:

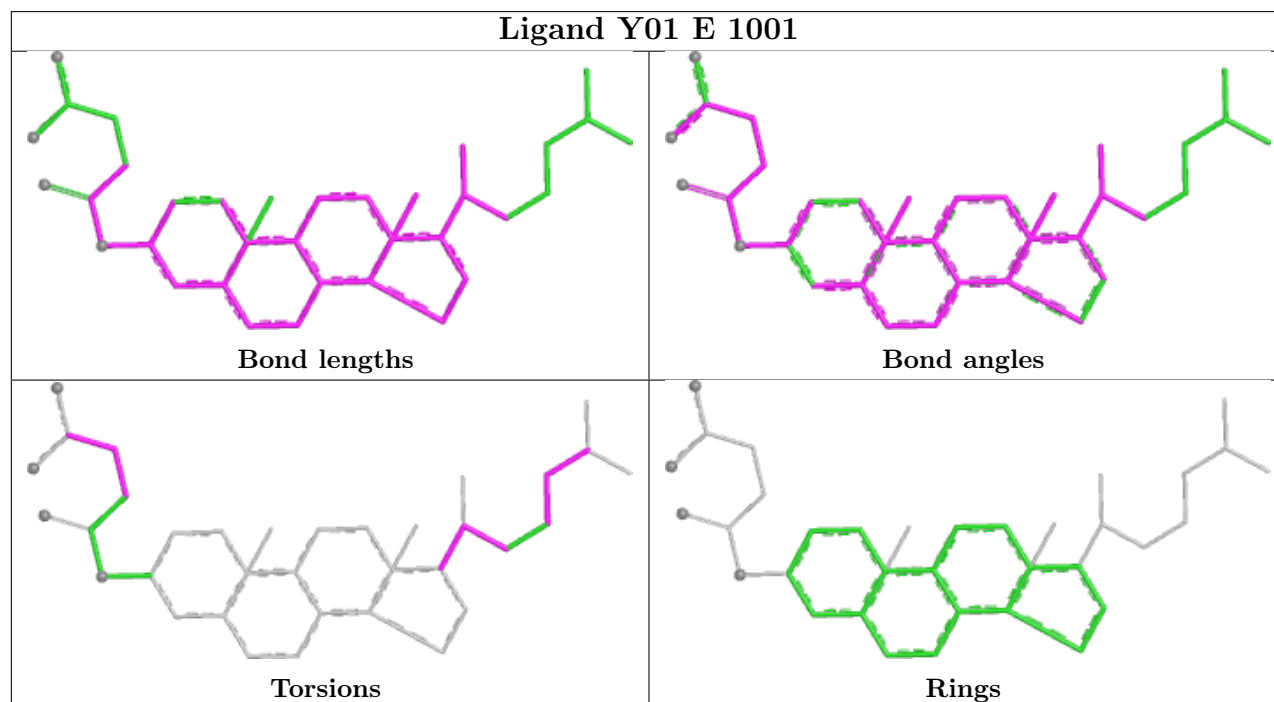
Mol	Chain	Res	Type	Atoms
5	G	1003	TRS	C3-C-C1-O1
5	G	1003	TRS	C2-C-C3-O3
6	H	1001	GLU	N-CA-CB-CG
9	E	1001	Y01	CAO-CBB-CBE-CAP
9	E	1001	Y01	CAO-CBB-CBE-CBI

There are no ring outliers.

9 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	G	1003	TRS	2	0
6	H	1001	GLU	4	0
4	B	1002	NAG	3	0
6	D	1002	GLU	8	0
6	B	1001	GLU	4	0
3	A	902	GLY	1	0
6	G	1004	GLU	2	0
9	E	1001	Y01	5	0
3	G	1001	GLY	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	416/451 (92%)	1.45	116 (27%) 1 1	39, 115, 206, 238	0
1	C	415/451 (92%)	1.83	127 (30%) 1 1	64, 138, 201, 264	0
1	E	412/451 (91%)	1.91	142 (34%) 1 1	74, 186, 251, 316	0
1	G	424/451 (94%)	0.99	87 (20%) 2 3	13, 73, 214, 287	0
2	B	397/448 (88%)	1.83	125 (31%) 1 1	43, 137, 209, 244	0
2	D	405/448 (90%)	1.60	100 (24%) 2 2	46, 123, 197, 225	0
2	F	416/448 (92%)	2.09	144 (34%) 1 1	92, 167, 216, 273	0
2	H	409/448 (91%)	1.96	144 (35%) 1 1	22, 119, 215, 251	0
All	All	3294/3596 (91%)	1.70	985 (29%) 1 1	13, 140, 220, 316	0

The worst 5 of 985 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	799	ASP	33.9
2	F	405	GLU	30.4
2	D	539	SER	30.2
2	D	540	PRO	28.7
1	C	796	ALA	28.6

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](#)

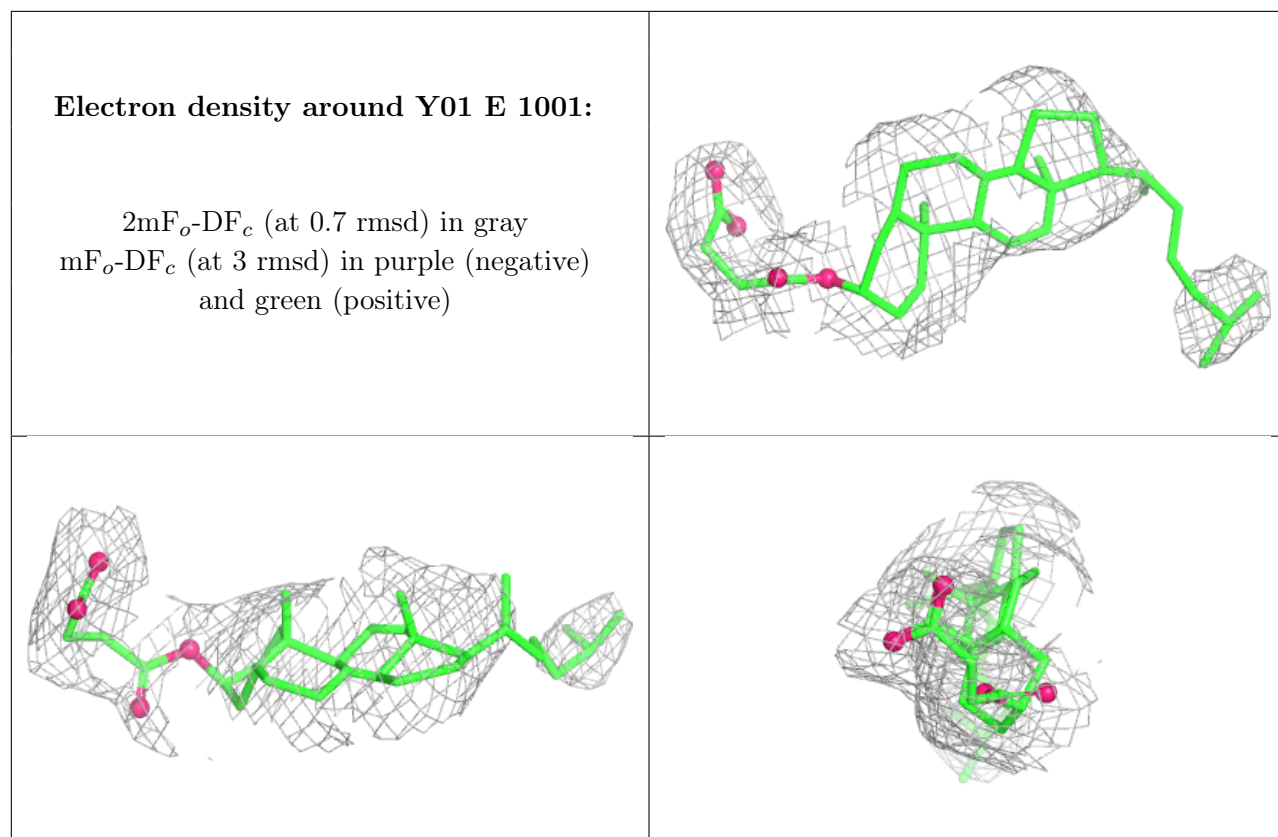
There are no oligosaccharides in this entry.

6.4 Ligands

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
6	GLU	D	1002	10/10	0.54	0.20	84,114,139,149	0
9	Y01	E	1001	35/35	0.70	0.18	66,152,172,179	0
7	BMK	G	1005	17/17	0.74	0.30	128,155,191,209	0
4	NAG	D	1001	15/15	0.77	0.15	101,150,172,201	0
4	NAG	F	1001	15/15	0.78	0.09	113,149,175,194	0
4	NAG	D	1003	15/15	0.78	0.14	128,160,180,195	0
6	GLU	G	1004	10/10	0.78	0.18	58,86,122,166	0
4	NAG	G	1002	15/15	0.85	0.12	90,111,144,148	0
4	NAG	B	1002	15/15	0.85	0.09	109,152,165,169	0
6	GLU	B	1001	10/10	0.85	0.15	57,87,105,131	0
7	BMK	B	1003	17/17	0.89	0.21	111,153,186,199	0
5	TRS	G	1003	8/8	0.89	0.23	6,17,56,81	0
3	GLY	A	902	5/5	0.90	0.16	67,67,79,81	0
6	GLU	G	1006	10/10	0.92	0.20	71,97,108,112	0
4	NAG	H	1002	15/15	0.94	0.08	96,119,134,145	0
6	GLU	H	1001	10/10	0.94	0.12	28,77,102,104	0
3	GLY	G	1001	5/5	0.97	0.07	28,30,42,59	0
8	MG	A	901	1/1	0.98	0.21	37,37,37,37	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.