



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 25, 2020 – 03:41 PM BST

PDB ID : 3PD9
Title : X-ray structure of the ligand-binding core of GluA2 in complex with (R)-5-HPCA at 2.1 Å resolution
Authors : Frydenvang, K.; Kastrup, J.S.
Deposited on : 2010-10-22
Resolution : 2.10 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13

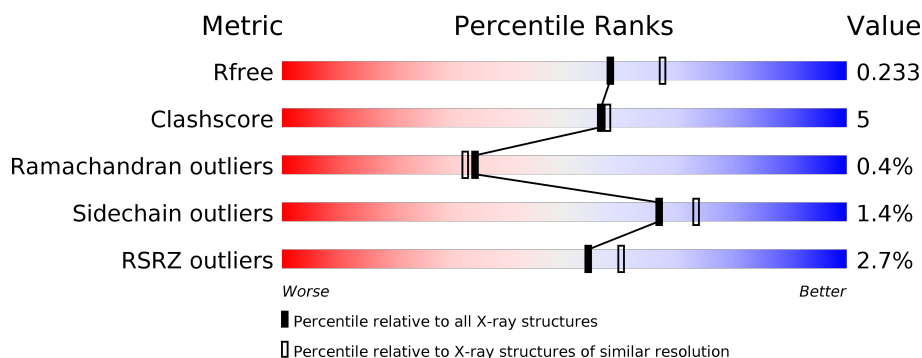
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 ≥ 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	260	<div> <div>3%</div> <div> <div></div> <div>87%</div> <div>12%</div> <div></div> </div> </div>
1	B	260	<div> <div>2%</div> <div> <div></div> <div>89%</div> <div>11%</div> <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
4	GOL	B	264	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4540 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.

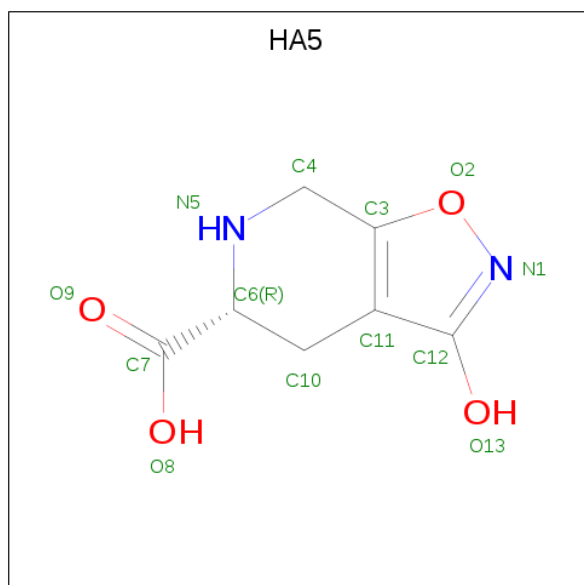
- Molecule 1 is a protein called Glutamate receptor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	0	5	0
			2054	1311	341	387	15			
1	B	260	Total	C	N	O	S	0	3	0
			2045	1304	341	386	14			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	115	GLY	-	LINKER	UNP P19491
A	116	THR	-	LINKER	UNP P19491
B	115	GLY	-	LINKER	UNP P19491
B	116	THR	-	LINKER	UNP P19491

- Molecule 2 is (5R)-3-hydroxy-4,5,6,7-tetrahydroisoxazolo[5,4-c]pyridine-5-carboxylic acid (three-letter code: HA5) (formula: C₇H₈N₂O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			13	7	2	4		
2	B	1	Total	C	N	O	0	0
			13	7	2	4		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Cl 1 1	0	0
5	A	3	Total Cl 3 3	0	0

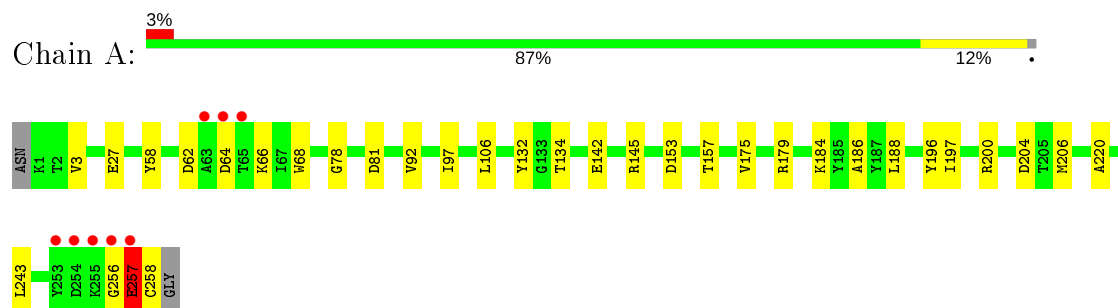
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	171	Total O 171 171	0	0
6	B	190	Total O 190 190	0	0

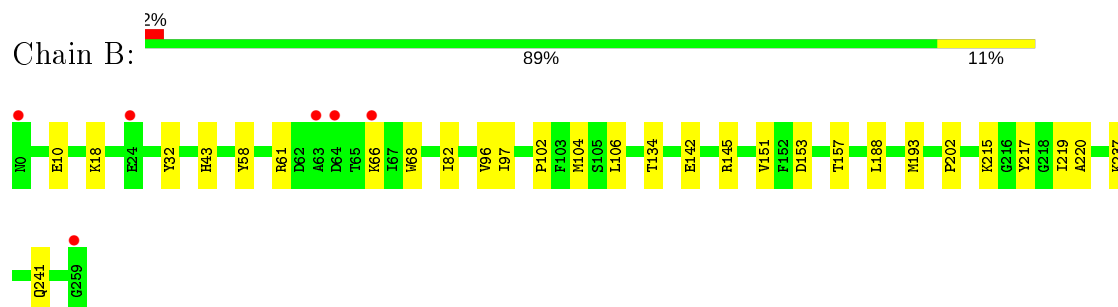
3 Residue-property plots

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: Glutamate receptor 2



- Molecule 1: Glutamate receptor 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	99.39 Å 121.25 Å 47.55 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.41 – 2.10 29.42 – 2.10	Depositor EDS
% Data completeness (in resolution range)	93.4 (29.41-2.10) 99.0 (29.42-2.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.86 (at 2.10 Å)	Xtriage
Refinement program	PHENIX 1.5_2	Depositor
R, R_{free}	0.177 , 0.233 0.179 , 0.233	Depositor DCC
R_{free} test set	1713 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	21.5	Xtriage
Anisotropy	0.388	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 58.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4540	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 24.14 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.0646e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² 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: GOL, CL, HA5, SO4

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	0.36	0/2097	0.51	0/2820
1	B	0.38	0/2091	0.51	0/2812
All	All	0.37	0/4188	0.51	0/5632

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2054	0	2092	20	0
1	B	2045	0	2085	22	0
2	A	13	0	6	1	0
2	B	13	0	6	1	0
3	A	15	0	0	0	0
3	B	5	0	0	0	0
4	A	12	0	16	0	0
4	B	18	0	24	6	0
5	A	3	0	0	0	0
5	B	1	0	0	0	0
6	A	171	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	190	0	0	3	0
All	All	4540	0	4229	42	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 5.

All (42) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:VAL:HG21	1:A:197:ILE:HD13	1.70	0.73
1:A:134:THR:HG22	1:A:188[A]:LEU:HB2	1.72	0.70
1:B:61:ARG:NH2	1:B:66:LYS:HD2	2.07	0.70
1:A:27:GLU:HG2	6:A:473:HOH:O	2.01	0.59
1:B:96:VAL:CB	4:B:264:GOL:H11	2.34	0.58
1:B:215:LYS:HA	4:B:263:GOL:H31	1.85	0.58
1:A:134:THR:HG22	1:A:188[B]:LEU:HB2	1.87	0.57
1:A:78:GLY:HA2	6:A:355:HOH:O	2.07	0.55
1:B:142:GLU:OE1	1:B:145:ARG:NH1	2.39	0.55
1:B:32:TYR:CZ	1:B:104:MET:HE3	2.42	0.54
1:B:43[B]:HIS:HD2	6:B:413:HOH:O	1.91	0.54
1:A:179:ARG:HG2	1:A:204:ASP:OD2	2.08	0.53
1:B:134:THR:HG22	1:B:188:LEU:HB2	1.90	0.52
1:A:175:VAL:CG2	1:A:197:ILE:HD13	2.41	0.51
1:B:237:LYS:O	1:B:241:GLN:HG3	2.12	0.50
1:B:96:VAL:HA	4:B:264:GOL:H11	1.93	0.50
1:B:96:VAL:HB	4:B:264:GOL:H11	1.94	0.50
1:A:175:VAL:HG21	1:A:197:ILE:CD1	2.40	0.49
1:A:97:ILE:HD12	1:A:220:ALA:HB1	1.96	0.48
1:B:96:VAL:CA	4:B:264:GOL:H11	2.44	0.48
1:A:62:ASP:O	1:A:66:LYS:HA	2.13	0.47
1:B:151:VAL:HG23	6:B:338:HOH:O	2.15	0.47
1:A:58:TYR:CZ	2:A:260:HA5:H4A	2.49	0.47
1:B:58:TYR:CZ	2:B:260:HA5:H4A	2.51	0.46
1:A:256:GLY:O	1:A:258:CYS:N	2.49	0.46
1:B:145:ARG:HH12	4:B:262:GOL:H31	1.81	0.46
1:B:97:ILE:HD12	1:B:220:ALA:HB1	1.98	0.46
1:B:10:GLU:HG2	1:B:193:MET:HE3	1.98	0.46
1:A:153:ASP:O	1:A:157:THR:HG23	2.17	0.45
1:B:82:ILE:HD11	1:B:219:ILE:HG21	1.97	0.44
1:A:196:TYR:O	1:A:200:ARG:HG2	2.17	0.44
1:A:256:GLY:O	1:A:257:GLU:C	2.56	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:18:LYS:NZ	6:B:436:HOH:O	2.49	0.43
1:B:102:PRO:HA	1:B:217:TYR:O	2.19	0.43
1:A:68:TRP:HH2	1:A:92:VAL:HG12	1.83	0.42
1:A:132:TYR:HA	1:A:186:ALA:O	2.20	0.41
1:A:142:GLU:OE1	1:A:145:ARG:NH1	2.52	0.41
1:B:61:ARG:HD2	1:B:68:TRP:NE1	2.35	0.41
1:B:82:ILE:HD11	1:B:219:ILE:CG2	2.50	0.41
1:B:153:ASP:O	1:B:157:THR:HG23	2.20	0.41
1:A:184:LYS:HD3	1:A:184:LYS:HA	1.87	0.41
1:A:3:VAL:HG13	1:A:81:ASP:HB2	2.03	0.41

There are no symmetry-related clashes.

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	261/260 (100%)	255 (98%)	4 (2%)	2 (1%)	19	15
1	B	261/260 (100%)	257 (98%)	4 (2%)	0	100	100
All	All	522/520 (100%)	512 (98%)	8 (2%)	2 (0%)	34	32

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	64	ASP
1	A	257	GLU

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	222/218 (102%)	217 (98%)	5 (2%)	50	55
1	B	221/218 (101%)	219 (99%)	2 (1%)	78	84
All	All	443/436 (102%)	436 (98%)	7 (2%)	67	69

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	106	LEU
1	A	206	MET
1	A	243[A]	LEU
1	A	243[B]	LEU
1	A	257	GLU
1	B	106	LEU
1	B	202	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	199	GLN
1	B	199	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 15 ligands modelled in this entry, 4 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
2	HA5	A	260	-	5,14,14	2.65	3 (60%)	2,20,20	2.62	1 (50%)
3	SO4	A	263	-	4,4,4	0.14	0	6,6,6	0.14	0
4	GOL	A	265	-	5,5,5	0.66	0	5,5,5	0.63	0
4	GOL	B	264	-	5,5,5	0.70	0	5,5,5	0.46	0
3	SO4	A	261	-	4,4,4	0.11	0	6,6,6	0.19	0
4	GOL	B	263	-	5,5,5	0.56	0	5,5,5	0.78	0
3	SO4	B	261	-	4,4,4	0.14	0	6,6,6	0.17	0
3	SO4	A	262	-	4,4,4	0.12	0	6,6,6	0.18	0
4	GOL	B	262	-	5,5,5	0.60	0	5,5,5	0.40	0
4	GOL	A	264	-	5,5,5	0.65	0	5,5,5	0.23	0
2	HA5	B	260	-	5,14,14	3.17	2 (40%)	2,20,20	2.22	1 (50%)

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
2	HA5	A	260	-	-	0/0/13/13	0/2/2/2
2	HA5	B	260	-	-	0/0/13/13	0/2/2/2
4	GOL	A	265	-	-	2/4/4/4	-
4	GOL	B	264	-	-	2/4/4/4	-
4	GOL	B	263	-	-	2/4/4/4	-
4	GOL	B	262	-	-	2/4/4/4	-
4	GOL	A	264	-	-	4/4/4/4	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	260	HA5	C6-N5	5.42	1.52	1.47
2	A	260	HA5	C6-N5	4.18	1.51	1.47
2	B	260	HA5	C4-N5	3.88	1.51	1.46
2	A	260	HA5	C4-N5	3.39	1.51	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	260	HA5	C4-C3	-2.29	1.49	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	260	HA5	C3-C4-N5	-3.48	104.97	113.27
2	B	260	HA5	C3-C4-N5	-3.06	105.97	113.27

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	265	GOL	O1-C1-C2-C3
4	B	264	GOL	C1-C2-C3-O3
4	B	263	GOL	O1-C1-C2-O2
4	B	262	GOL	C1-C2-C3-O3
4	A	264	GOL	C1-C2-C3-O3
4	A	265	GOL	O1-C1-C2-O2
4	B	264	GOL	O2-C2-C3-O3
4	A	264	GOL	O2-C2-C3-O3
4	B	263	GOL	O1-C1-C2-C3
4	A	264	GOL	O1-C1-C2-C3
4	B	262	GOL	O2-C2-C3-O3
4	A	264	GOL	O1-C1-C2-O2

There are no ring outliers.

5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	260	HA5	1	0
4	B	264	GOL	4	0
4	B	263	GOL	1	0
4	B	262	GOL	1	0
2	B	260	HA5	1	0

5.7 Other polymers [i](#)

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	258/260 (99%)	0.06	8 (3%) 49 55	12, 23, 45, 65	0
1	B	260/260 (100%)	0.04	6 (2%) 60 65	12, 20, 41, 69	0
All	All	518/520 (99%)	0.05	14 (2%) 54 60	12, 21, 42, 69	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	64	ASP	6.1
1	B	63	ALA	5.0
1	A	64	ASP	4.2
1	A	256	GLY	4.1
1	A	63	ALA	4.0
1	B	259	GLY	3.3
1	A	254	ASP	3.3
1	A	255	LYS	3.2
1	A	257	GLU	3.1
1	A	253	TYR	3.1
1	B	0	ASN	2.8
1	A	65	THR	2.4
1	B	24	GLU	2.1
1	B	66	LYS	2.0

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

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

6.3 Carbohydrates ⓘ

There are no monosaccharides 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	GOL	B	264	6/6	0.67	0.35	35,37,41,43	0
4	GOL	A	265	6/6	0.76	0.29	37,41,46,49	0
3	SO4	A	263	5/5	0.80	0.38	50,59,84,97	0
5	CL	A	267	1/1	0.80	0.09	64,64,64,64	0
5	CL	A	268	1/1	0.83	0.12	51,51,51,51	0
3	SO4	A	262	5/5	0.88	0.24	49,56,68,75	0
4	GOL	B	262	6/6	0.89	0.17	29,37,41,52	0
3	SO4	B	261	5/5	0.90	0.29	53,56,68,80	0
4	GOL	A	264	6/6	0.90	0.22	45,51,52,53	0
4	GOL	B	263	6/6	0.92	0.18	21,31,37,45	0
5	CL	A	266	1/1	0.93	0.05	54,54,54,54	0
5	CL	B	265	1/1	0.93	0.12	55,55,55,55	0
2	HA5	A	260	13/13	0.95	0.17	14,18,23,26	0
3	SO4	A	261	5/5	0.96	0.21	43,48,58,65	0
2	HA5	B	260	13/13	0.96	0.16	12,16,21,25	0

6.5 Other polymers [i](#)

There are no such residues in this entry.