



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2018 – 11:14 am GMT

PDB ID : 5GX7
Title : Crystal structure of solute-binding protein complexed with unsaturated chondroitin disaccharide with a sulfate group at C-6 position of GalNAc
Authors : Oiki, S.; Mikami, B.; Murata, K.; Hashimoto, W.
Deposited on : 2016-09-15
Resolution : 1.99 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 : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk30967
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) : trunk30967

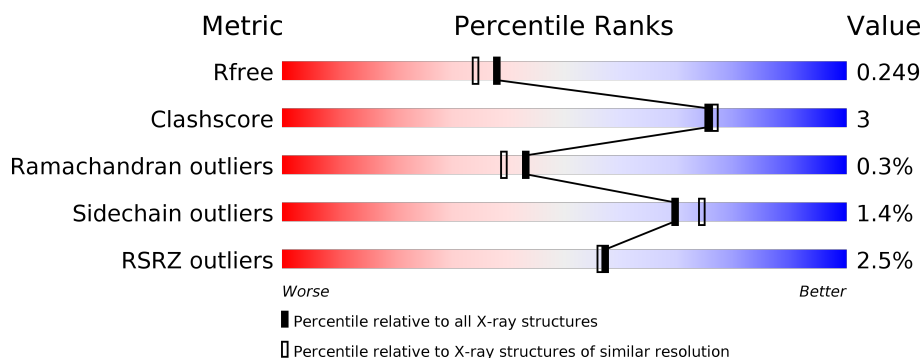
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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	7193 (2.00-2.00)
Clashscore	122126	8267 (2.00-2.00)
Ramachandran outliers	120053	8166 (2.00-2.00)
Sidechain outliers	120020	8165 (2.00-2.00)
RSRZ outliers	108989	7011 (2.00-2.00)

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. 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	483	<div> <div>%</div> <div> <div></div> <div>91%</div> <div>6% ..</div> </div> </div>
1	B	483	<div> <div>3%</div> <div> <div></div> <div>88%</div> <div>8% ..</div> </div> </div>
1	C	483	<div> <div>3%</div> <div> <div></div> <div>88%</div> <div>9% ..</div> </div> </div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 12349 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.

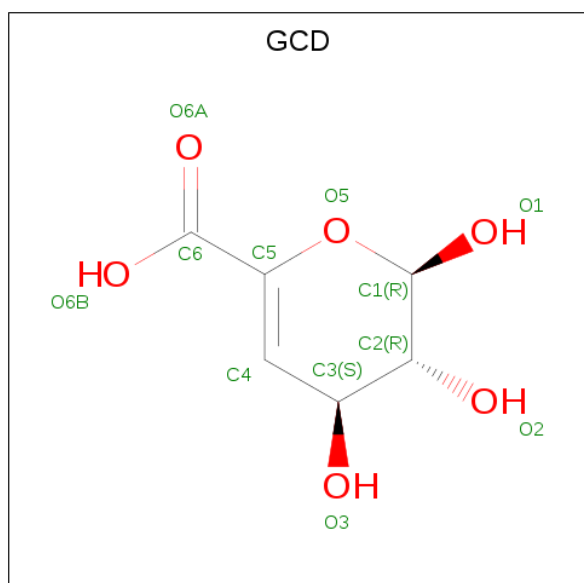
- Molecule 1 is a protein called Extracellular solute-binding protein family 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	474	Total	C	N	O	S	0	0	0
			3833	2466	633	728	6			
1	B	474	Total	C	N	O	S	0	0	0
			3833	2466	633	728	6			
1	C	474	Total	C	N	O	S	0	0	0
			3833	2466	633	728	6			

There are 3 discrepancies between the modelled and reference sequences:

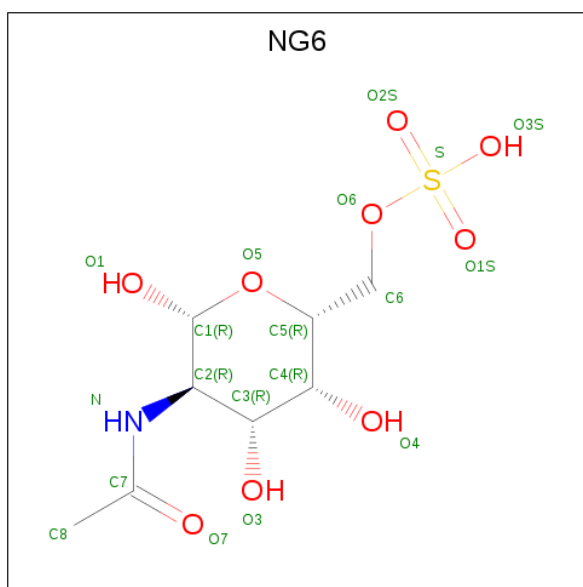
Chain	Residue	Modelled	Actual	Comment	Reference
A	18	MET	-	expression tag	UNP D1AWE0
B	18	MET	-	expression tag	UNP D1AWE0
C	18	MET	-	expression tag	UNP D1AWE0

- Molecule 2 is 4,5-DEHYDRO-D-GLUCURONIC ACID (three-letter code: GCD) (formula: $C_6H_8O_6$).



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

- Molecule 3 is N-ACETYL-D-GALACTOSAMINE 6-SULFATE (three-letter code: NG6) (formula: $C_8H_{15}NO_9S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			19	8	1	9	1		
3	B	1	Total	C	N	O	S	0	0
			19	8	1	9	1		
3	C	1	Total	C	N	O	S	0	0
			19	8	1	9	1		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Ca	0	0
			1	1		
4	A	1	Total	Ca	0	0
			1	1		
4	C	1	Total	Ca	0	0
			1	1		

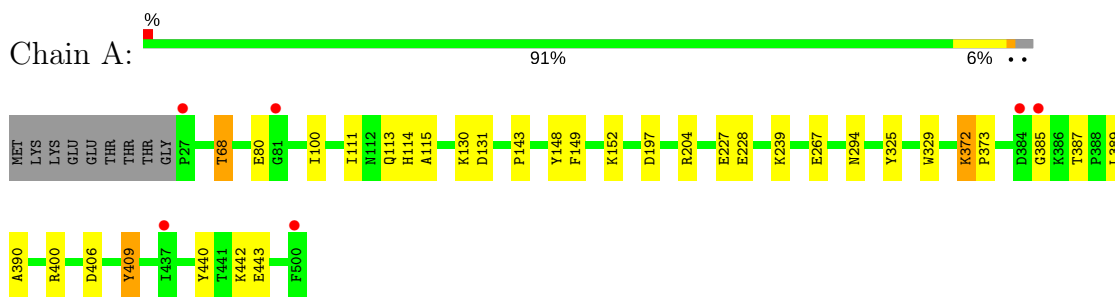
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	294	Total 294	O 294	0	0
5	B	260	Total 260	O 260	0	0
5	C	203	Total 203	O 203	0	0

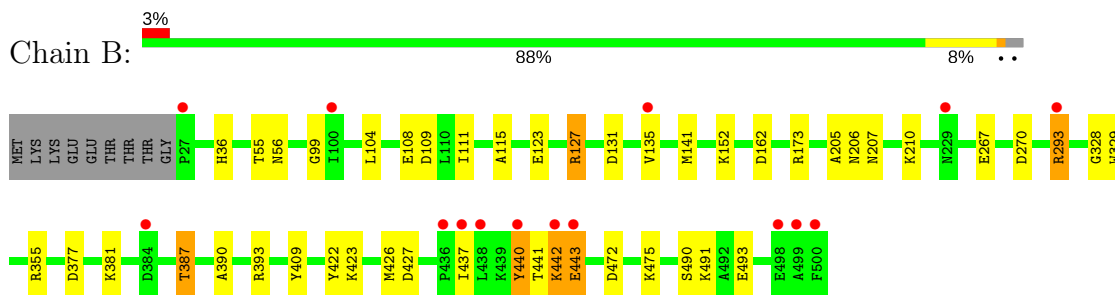
3 Residue-property plots [i](#)

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.

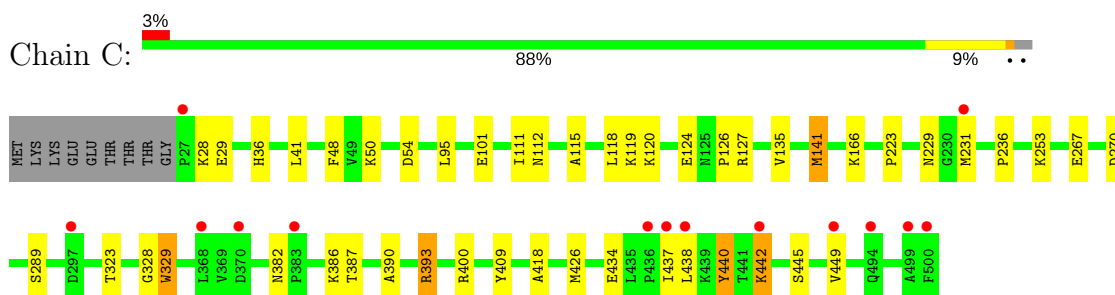
- Molecule 1: Extracellular solute-binding protein family 1



- Molecule 1: Extracellular solute-binding protein family 1



- Molecule 1: Extracellular solute-binding protein family 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	80.28Å 112.44Å 166.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.67 – 1.99 46.60 – 1.99	Depositor EDS
% Data completeness (in resolution range)	97.2 (45.67-1.99) 97.3 (46.60-1.99)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.21 (at 2.00Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.197 , 0.249 0.197 , 0.249	Depositor DCC
R_{free} test set	5068 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	22.0	Xtriage
Anisotropy	0.479	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 35.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12349	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.70% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NG6, CA, GCD

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	0.98	4/3923 (0.1%)	0.88	7/5308 (0.1%)
1	B	0.93	4/3923 (0.1%)	0.87	6/5308 (0.1%)
1	C	0.94	6/3923 (0.2%)	0.87	6/5308 (0.1%)
All	All	0.95	14/11769 (0.1%)	0.87	19/15924 (0.1%)

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	127	ARG	CZ-NH2	-6.50	1.24	1.33
1	A	68	THR	CB-CG2	-6.23	1.31	1.52
1	A	409	TYR	CD1-CE1	6.09	1.48	1.39
1	C	127	ARG	CZ-NH2	-6.07	1.25	1.33
1	C	101	GLU	CG-CD	5.68	1.60	1.51
1	C	329	TRP	CB-CG	5.65	1.60	1.50
1	C	101	GLU	CB-CG	5.61	1.62	1.52
1	A	267	GLU	CG-CD	5.58	1.60	1.51
1	C	267	GLU	CG-CD	5.58	1.60	1.51
1	C	267	GLU	CB-CG	5.35	1.62	1.52
1	B	491	LYS	CB-CG	-5.35	1.38	1.52
1	B	293	ARG	CB-CG	-5.30	1.38	1.52
1	A	372	LYS	CE-NZ	5.20	1.62	1.49
1	B	267	GLU	CB-CG	5.10	1.61	1.52

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	127	ARG	NE-CZ-NH2	-8.99	115.81	120.30
1	A	197	ASP	CB-CG-OD2	-6.85	112.14	118.30
1	B	173	ARG	NE-CZ-NH2	-6.67	116.97	120.30
1	B	442	LYS	CB-CG-CD	-6.38	95.02	111.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	406	ASP	CB-CG-OD1	6.17	123.85	118.30
1	A	409	TYR	OH-CZ-CE2	-6.01	103.86	120.10
1	C	127	ARG	NE-CZ-NH2	-5.98	117.31	120.30
1	B	173	ARG	NE-CZ-NH1	5.93	123.27	120.30
1	C	141	MET	CG-SD-CE	-5.84	90.86	100.20
1	C	426	MET	CG-SD-CE	-5.78	90.95	100.20
1	A	204	ARG	NE-CZ-NH1	5.67	123.13	120.30
1	A	400	ARG	NE-CZ-NH1	-5.66	117.47	120.30
1	B	355	ARG	NE-CZ-NH2	-5.66	117.47	120.30
1	A	409	TYR	CE1-CZ-OH	5.63	135.30	120.10
1	C	118	LEU	CB-CG-CD2	-5.45	101.74	111.00
1	B	162	ASP	CB-CG-OD1	5.38	123.14	118.30
1	C	393	ARG	NE-CZ-NH1	5.04	122.82	120.30
1	C	393	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	A	406	ASP	CB-CG-OD2	-5.01	113.79	118.30

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	3833	0	3788	21	0
1	B	3833	0	3788	31	0
1	C	3833	0	3788	28	0
2	A	11	0	5	0	0
2	B	11	0	5	0	0
2	C	11	0	5	0	0
3	A	19	0	13	0	0
3	B	19	0	14	5	0
3	C	19	0	13	4	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
5	A	294	0	0	1	0
5	B	260	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	203	0	0	3	0
All	All	12349	0	11419	79	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 3.

All (79) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:387:THR:HG22	1:B:390:ALA:H	1.18	1.05
1:B:393:ARG:HH22	3:B:602:NG6:H82	1.39	0.87
1:B:36:HIS:CE1	3:B:602:NG6:H83	2.14	0.82
1:C:253:LYS:HE3	5:C:883:HOH:O	1.79	0.81
1:C:393:ARG:HH22	3:C:602:NG6:H82	1.49	0.78
1:B:442:LYS:HE2	1:B:443:GLU:OE1	1.85	0.75
1:C:382:ASN:OD1	1:C:386:LYS:HG3	1.90	0.72
1:C:36:HIS:NE2	3:C:602:NG6:H83	2.06	0.69
1:B:127:ARG:NH2	1:B:131:ASP:OD1	2.27	0.67
1:B:293:ARG:HG3	1:B:293:ARG:HH11	1.58	0.66
1:B:387:THR:CG2	1:B:390:ALA:H	2.04	0.66
1:C:445:SER:O	1:C:449:VAL:HG22	1.98	0.64
1:B:387:THR:HG22	1:B:390:ALA:N	2.02	0.63
1:B:36:HIS:HE1	3:B:602:NG6:H83	1.60	0.63
1:A:113:GLN:HG2	1:A:114:HIS:CD2	2.33	0.63
1:B:135:VAL:HG11	1:B:440:TYR:O	2.00	0.61
1:C:438:LEU:HA	5:C:852:HOH:O	2.00	0.61
1:C:111:ILE:HA	1:C:115:ALA:HB3	1.83	0.60
1:A:68:THR:HG22	5:A:920:HOH:O	2.00	0.59
1:C:135:VAL:HG11	1:C:440:TYR:O	2.03	0.59
1:C:36:HIS:CE1	1:C:400:ARG:HB2	2.37	0.59
1:A:387:THR:HG22	1:A:389:LEU:N	2.18	0.58
1:A:372:LYS:HE3	1:A:373:PRO:HD2	1.87	0.57
1:B:293:ARG:HG3	1:B:293:ARG:NH1	2.17	0.56
1:B:293:ARG:HG2	5:B:770:HOH:O	2.06	0.55
1:B:36:HIS:CE1	3:B:602:NG6:C8	2.89	0.55
1:C:36:HIS:CE1	3:C:602:NG6:H83	2.42	0.54
1:A:294:ASN:HD21	1:A:385:GLY:CA	2.21	0.54
1:B:123:GLU:O	1:C:126:PRO:HG2	2.08	0.53
1:A:149:PHE:HA	1:A:152:LYS:HE3	1.91	0.53
1:B:377:ASP:OD1	1:B:381:LYS:HE2	2.09	0.53
1:A:111:ILE:HA	1:A:115:ALA:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:387:THR:HG23	5:B:903:HOH:O	2.09	0.52
1:B:36:HIS:HE1	3:B:602:NG6:C8	2.24	0.51
1:C:50:LYS:HE2	1:C:54:ASP:OD1	2.09	0.51
1:C:229:ASN:C	1:C:231:MET:H	2.13	0.51
1:C:393:ARG:NH2	3:C:602:NG6:H82	2.22	0.50
1:C:41:LEU:HD11	1:C:48:PHE:CE2	2.47	0.49
1:B:207:ASN:ND2	1:B:210:LYS:HE2	2.28	0.48
1:A:387:THR:HG22	1:A:390:ALA:H	1.77	0.48
1:A:387:THR:HG22	1:A:389:LEU:H	1.77	0.48
1:C:28:LYS:HD2	5:C:723:HOH:O	2.12	0.48
1:A:143:PRO:HB3	1:A:325:TYR:CD2	2.49	0.48
1:A:294:ASN:HD21	1:A:385:GLY:HA2	1.79	0.48
1:A:148:TYR:O	1:A:152:LYS:HG3	2.13	0.48
1:B:206:ASN:OD1	1:B:210:LYS:HE3	2.14	0.48
1:B:108:GLU:HG2	1:B:109:ASP:N	2.28	0.47
1:C:141:MET:HE1	1:C:328:GLY:HA3	1.97	0.47
1:B:141:MET:CE	1:B:328:GLY:HA3	2.44	0.47
1:C:229:ASN:O	1:C:231:MET:N	2.48	0.47
1:B:99:GLY:HA2	1:B:104:LEU:HB2	1.96	0.46
1:B:423:LYS:NZ	1:B:427:ASP:OD2	2.44	0.46
1:C:289:SER:HB2	1:C:418:ALA:HB2	1.98	0.46
1:A:113:GLN:HG2	1:A:114:HIS:NE2	2.31	0.46
1:A:100:ILE:CG2	1:A:442:LYS:HG3	2.46	0.46
1:C:223:PRO:HA	1:C:236:PRO:HG3	1.97	0.45
1:C:141:MET:CE	1:C:328:GLY:HA3	2.47	0.45
1:C:323:THR:HG22	1:C:434:GLU:HG2	1.98	0.45
1:B:472:ASP:HB3	1:B:475:LYS:HG3	1.99	0.44
1:A:239:LYS:HE3	5:B:919:HOH:O	2.16	0.44
1:B:36:HIS:HD2	5:B:830:HOH:O	1.99	0.44
1:C:387:THR:HG23	1:C:390:ALA:CB	2.47	0.44
1:A:148:TYR:CZ	1:A:152:LYS:HG2	2.52	0.44
1:A:113:GLN:O	1:A:113:GLN:HG3	2.17	0.43
1:A:227:GLU:HG2	1:A:228:GLU:N	2.32	0.43
1:C:442:LYS:HG3	1:C:442:LYS:H	1.58	0.43
1:C:166:LYS:HB2	1:C:166:LYS:HE3	1.87	0.42
1:A:131:ASP:HB3	1:A:325:TYR:CE1	2.55	0.41
1:C:120:LYS:HE2	1:C:124:GLU:OE2	2.19	0.41
1:A:148:TYR:O	1:A:152:LYS:HE3	2.21	0.41
1:B:55:THR:O	1:B:56:ASN:HB2	2.21	0.41
1:C:112:ASN:O	1:C:119:LYS:NZ	2.54	0.41
1:B:490:SER:HA	1:B:493:GLU:OE2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:442:LYS:HE3	1:A:443:GLU:OE2	2.21	0.40
1:B:205:ALA:HB1	1:B:210:LYS:HB2	2.03	0.40
1:C:95:LEU:HD12	1:C:95:LEU:HA	1.82	0.40
1:B:111:ILE:HA	1:B:115:ALA:HB3	2.03	0.40
1:B:141:MET:HE2	1:B:328:GLY:HA3	2.04	0.40
1:B:422:TYR:O	1:B:426:MET:HG2	2.21	0.40

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	472/483 (98%)	463 (98%)	8 (2%)	1 (0%)	49	46
1	B	472/483 (98%)	459 (97%)	12 (2%)	1 (0%)	49	46
1	C	472/483 (98%)	459 (97%)	11 (2%)	2 (0%)	36	31
All	All	1416/1449 (98%)	1381 (98%)	31 (2%)	4 (0%)	43	39

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	442	LYS
1	A	80	GLU
1	C	437	ILE
1	B	437	ILE

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	408/416 (98%)	404 (99%)	4 (1%)	78	83
1	B	408/416 (98%)	400 (98%)	8 (2%)	58	61
1	C	408/416 (98%)	403 (99%)	5 (1%)	74	78
All	All	1224/1248 (98%)	1207 (99%)	17 (1%)	69	74

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	130	LYS
1	A	329	TRP
1	A	409	TYR
1	A	440	TYR
1	B	152	LYS
1	B	270	ASP
1	B	329	TRP
1	B	387	THR
1	B	409	TYR
1	B	440	TYR
1	B	441	THR
1	B	443	GLU
1	C	29	GLU
1	C	270	ASP
1	C	329	TRP
1	C	409	TYR
1	C	440	TYR

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	294	ASN
1	B	36	HIS

5.3.3 RNA ⓘ

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 [i](#)

Of 9 ligands modelled in this entry, 3 are monoatomic - leaving 6 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	GCD	A	601	3	7,11,12	2.80	4 (57%)	7,15,17	2.35	2 (28%)
3	NG6	A	602	2	19,19,19	1.56	2 (10%)	26,28,28	2.01	8 (30%)
2	GCD	B	601	3	7,11,12	1.88	2 (28%)	7,15,17	0.92	0
3	NG6	B	602	2	19,19,19	1.24	2 (10%)	26,28,28	2.07	4 (15%)
2	GCD	C	601	3	7,11,12	1.95	2 (28%)	7,15,17	1.71	2 (28%)
3	NG6	C	602	2	19,19,19	1.57	3 (15%)	26,28,28	1.54	4 (15%)

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	GCD	A	601	3	-	0/0/17/20	0/1/1/1
3	NG6	A	602	2	-	0/10/30/30	0/1/1/1
2	GCD	B	601	3	-	0/0/17/20	0/1/1/1
3	NG6	B	602	2	-	0/10/30/30	0/1/1/1
2	GCD	C	601	3	-	0/0/17/20	0/1/1/1
3	NG6	C	602	2	-	0/10/30/30	0/1/1/1

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	602	NG6	C8-C7	-3.09	1.43	1.50
3	A	602	NG6	O6-S	-3.00	1.48	1.56
2	A	601	GCD	O5-C1	-2.72	1.41	1.45
3	B	602	NG6	C8-C7	-2.21	1.45	1.50
2	A	601	GCD	C4-C5	2.05	1.35	1.32
2	B	601	GCD	O5-C5	2.24	1.40	1.37
3	C	602	NG6	O7-C7	2.52	1.29	1.23
2	C	601	GCD	C3-C4	2.71	1.54	1.50
3	B	602	NG6	O3S-S	2.95	1.66	1.50
2	C	601	GCD	O5-C5	3.14	1.41	1.37
2	A	601	GCD	C3-C4	3.72	1.55	1.50
2	B	601	GCD	C4-C5	3.76	1.37	1.32
3	C	602	NG6	O2S-S	4.72	1.63	1.45
2	A	601	GCD	O5-C5	5.05	1.44	1.37
3	A	602	NG6	O2S-S	5.33	1.65	1.45

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	602	NG6	O6-C6-C5	-7.87	92.61	107.64
3	A	602	NG6	O6-S-O2S	-5.44	90.40	106.88
2	A	601	GCD	O5-C5-C4	-5.32	120.25	124.84
3	A	602	NG6	O6-C6-C5	-5.23	97.66	107.64
3	C	602	NG6	C6-C5-C4	-3.44	104.68	112.08
3	B	602	NG6	O6-S-O2S	-3.36	96.70	106.88
2	C	601	GCD	O5-C5-C4	-2.95	122.29	124.84
3	C	602	NG6	O1-C1-O5	-2.44	103.08	110.44
3	A	602	NG6	O1-C1-C2	-2.34	104.35	109.22
3	C	602	NG6	C1-O5-C5	-2.20	109.46	113.69
3	A	602	NG6	C1-O5-C5	-2.13	109.60	113.69
2	A	601	GCD	C1-C2-C3	-2.07	107.04	109.66
3	A	602	NG6	O5-C1-C2	-2.06	107.44	109.52
3	A	602	NG6	O3-C3-C2	-2.03	105.54	109.62
3	B	602	NG6	O2S-S-O1S	2.17	121.64	112.25
3	B	602	NG6	O7-C7-N	2.34	126.35	121.94
3	A	602	NG6	O6-S-O1S	2.37	114.06	106.88
2	C	601	GCD	C3-C4-C5	2.44	125.73	121.60
3	C	602	NG6	O6-C6-C5	3.00	113.37	107.64
3	A	602	NG6	O3S-S-O2S	3.03	119.51	108.79

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	602	NG6	5	0
3	C	602	NG6	4	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

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	474/483 (98%)	-0.12	6 (1%) 77 76	13, 20, 34, 56	0
1	B	474/483 (98%)	-0.08	15 (3%) 47 47	15, 22, 41, 60	3 (0%)
1	C	474/483 (98%)	-0.01	14 (2%) 50 49	14, 23, 46, 62	2 (0%)
All	All	1422/1449 (98%)	-0.07	35 (2%) 57 56	13, 21, 41, 62	5 (0%)

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	27	PRO	10.2
1	B	499	ALA	7.4
1	C	437	ILE	6.0
1	C	500	PHE	5.7
1	B	437	ILE	5.1
1	C	438	LEU	4.7
1	A	437	ILE	4.3
1	B	500	PHE	4.1
1	B	442	LYS	3.9
1	C	499	ALA	3.6
1	C	383	PRO	3.5
1	B	440	TYR	3.4
1	C	449	VAL	3.3
1	B	436	PRO	3.3
1	C	231	MET	3.2
1	C	27	PRO	3.2
1	A	385	GLY	3.2
1	C	494	GLN	2.7
1	B	27	PRO	2.6
1	A	384	ASP	2.6
1	A	81	GLY	2.6
1	B	100	ILE	2.5
1	B	443	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	370	ASP	2.4
1	C	442	LYS	2.4
1	C	368	LEU	2.3
1	B	498	GLU	2.3
1	B	384	ASP	2.3
1	B	293	ARG	2.3
1	A	500	PHE	2.2
1	B	135	VAL	2.2
1	C	297	ASP	2.1
1	B	438	LEU	2.1
1	C	436	PRO	2.1
1	B	229	ASN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no 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, 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
3	NG6	B	602	19/19	0.91	0.12	9,17,38,48	0
3	NG6	C	602	19/19	0.93	0.12	13,21,35,39	0
3	NG6	A	602	19/19	0.95	0.11	13,16,38,40	0
2	GCD	C	601	11/12	0.96	0.09	16,18,20,20	0
2	GCD	A	601	11/12	0.97	0.08	15,16,17,18	0
2	GCD	B	601	11/12	0.97	0.08	15,17,18,19	0
4	CA	A	603	1/1	0.98	0.04	22,22,22,22	0
4	CA	C	603	1/1	0.99	0.09	25,25,25,25	0
4	CA	B	603	1/1	1.00	0.04	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.