



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:49 PM GMT

PDB ID : 4GBZ  
Title : The structure of the MFS (major facilitator superfamily) proton:xylose symporter XylE bound to D-glucose  
Authors : Sun, L.F.; Zeng, X.; Yan, C.Y.; Yan, N.  
Deposited on : 2012-07-28  
Resolution : 2.89 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

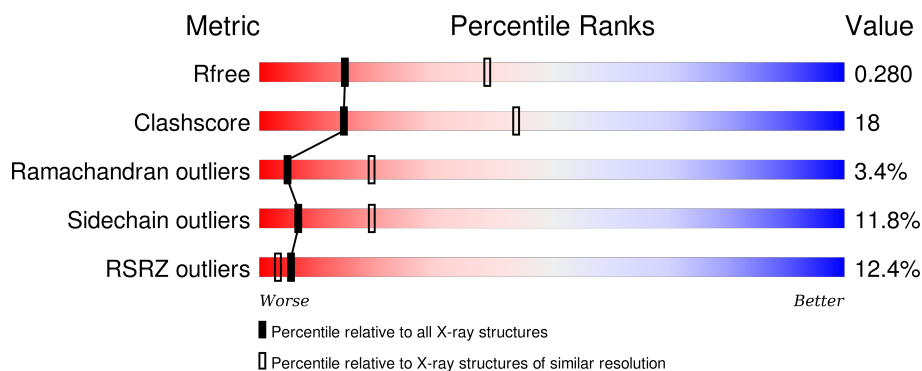
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.89 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))
$R_{free}$	91344	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)

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	491	<div> <div>12%</div> <div>63%</div> <div>27%</div> <div>6%</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
2	BGC	A	501	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	BNG	A	502	-	-	-	X
3	BNG	A	504	-	-	-	X
3	BNG	A	505	-	-	-	X

## 2 Entry composition [i](#)

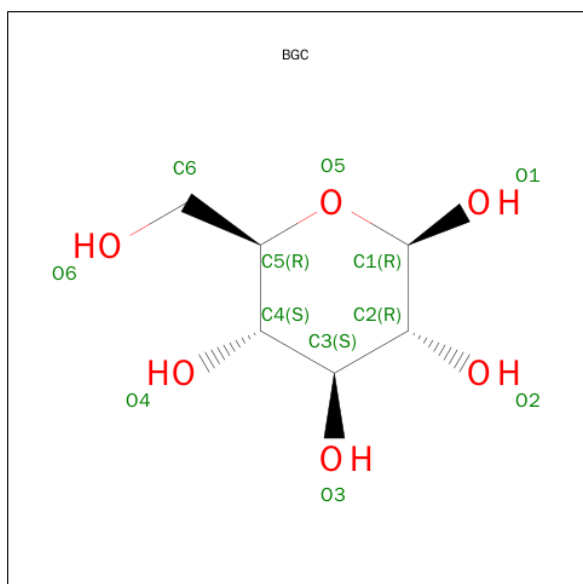
There are 4 unique types of molecules in this entry. The entry contains 3677 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 D-xylose-proton symporter.

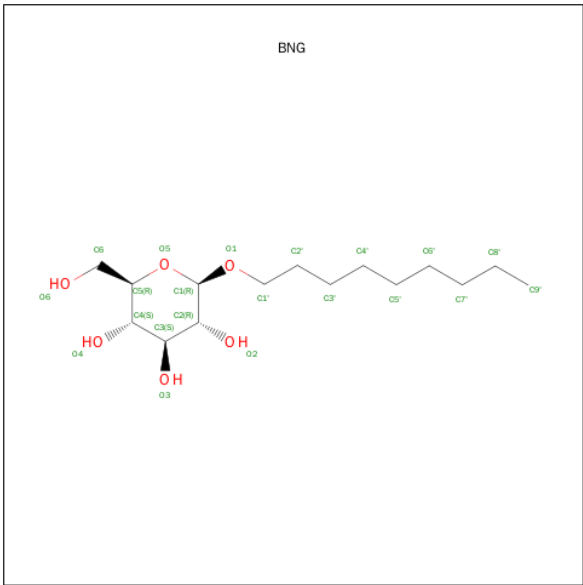
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	475	3579	2369	565	622	23	0	0	0

- Molecule 2 is SUGAR (BETA-D-GLUCOSE) (three-letter code: BGC) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	12	6	6	0	0

- Molecule 3 is SUGAR (B-NONYLGLUCOSIDE) (three-letter code: BNG) (formula: C<sub>15</sub>H<sub>30</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			21	15	6		
3	A	1	Total	C	O	0	0
			21	15	6		
3	A	1	Total	C	O	0	0
			21	15	6		
3	A	1	Total	C	O	0	0
			21	15	6		

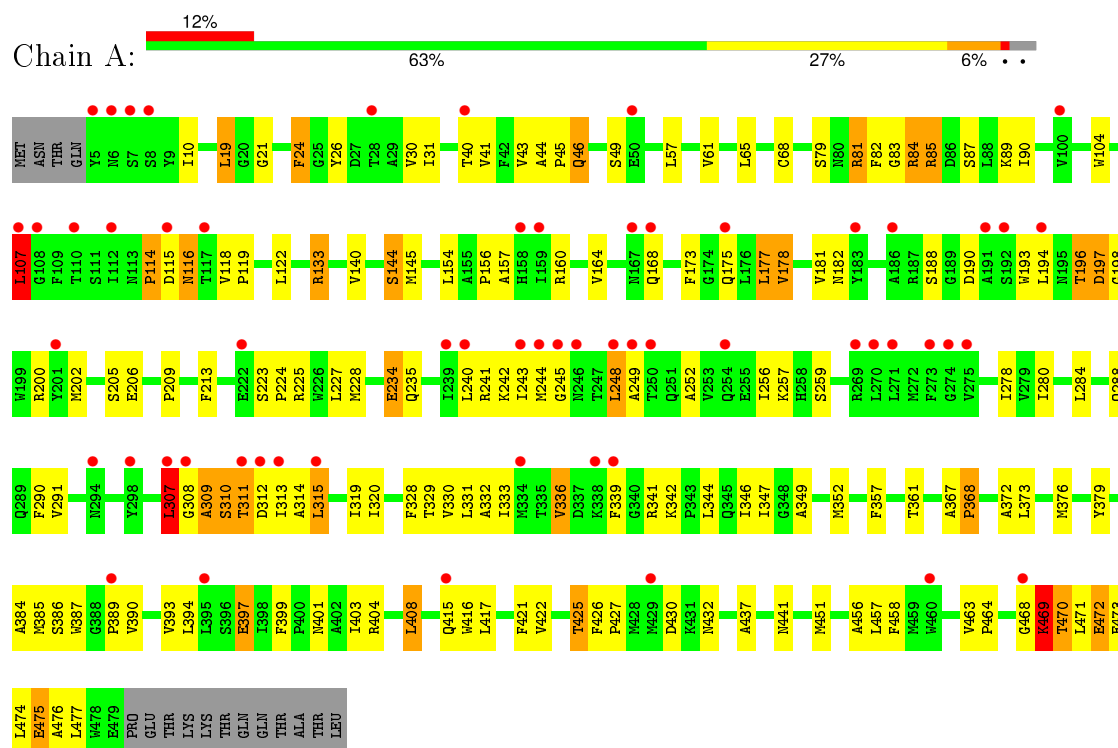
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	O	0	0
			2	2		

### 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 errors 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 ( $\text{RSRZ} > 2$ ). 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: D-xylose-proton symporter



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	95.04Å 95.04Å 168.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.52 – 2.89 38.52 – 2.89	Depositor EDS
% Data completeness (in resolution range)	98.1 (38.52-2.89) 98.1 (38.52-2.89)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.03 (at 2.90Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, $R_{free}$	0.247 , 0.289 0.244 , 0.280	Depositor DCC
$R_{free}$ test set	899 reflections (5.40%)	DCC
Wilson B-factor (Å <sup>2</sup> )	86.6	Xtriage
Anisotropy	0.456	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 77.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 17553 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	3677	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	93.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.31% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: BGC, BNG

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	0.44	0/3672	0.59	1/5008 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	30	VAL	CB-CA-C	-5.35	101.23	111.40

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	3579	0	3586	133	0
2	A	12	0	12	2	0
3	A	84	0	120	11	0
4	A	2	0	0	0	0
All	All	3677	0	3718	133	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 18.

All (133) 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:310:SER:CB	1:A:313:ILE:HB	1.72	1.18
1:A:310:SER:HB3	1:A:313:ILE:CB	1.79	1.12
1:A:372:ALA:HB3	3:A:505:BNG:H2'2	1.41	1.01
1:A:372:ALA:CB	3:A:505:BNG:H2'2	1.98	0.93
1:A:470:THR:HG22	1:A:473:GLU:H	1.38	0.88
1:A:182:ASN:OD1	1:A:202:MET:HG2	1.75	0.86
1:A:197:ASP:OD1	3:A:504:BNG:H61	1.83	0.77
1:A:421:PHE:HA	1:A:425:THR:HG23	1.67	0.75
1:A:310:SER:HB3	1:A:313:ILE:HB	0.84	0.73
1:A:244:MET:SD	1:A:249:ALA:HA	2.32	0.70
1:A:244:MET:HB2	1:A:248:LEU:HB3	1.74	0.70
1:A:310:SER:O	1:A:314:ALA:N	2.22	0.68
1:A:307:LEU:HD23	1:A:307:LEU:N	2.10	0.66
1:A:307:LEU:CD2	1:A:307:LEU:N	2.58	0.66
1:A:307:LEU:H	1:A:307:LEU:HD23	1.62	0.65
1:A:244:MET:HG3	1:A:249:ALA:HB2	1.79	0.64
1:A:234:GLU:CG	1:A:235:GLN:N	2.60	0.64
1:A:79:SER:O	1:A:83:GLY:HA2	1.98	0.64
1:A:307:LEU:HD11	3:A:505:BNG:O2	1.99	0.62
1:A:332:ALA:O	1:A:336:VAL:HG22	2.01	0.61
1:A:157:ALA:HB1	1:A:469:LYS:O	2.02	0.60
1:A:234:GLU:HG2	1:A:235:GLN:N	2.16	0.60
1:A:193:TRP:HA	1:A:196:THR:HG22	1.84	0.60
1:A:116:ASN:ND2	1:A:116:ASN:O	2.31	0.59
1:A:470:THR:H	1:A:473:GLU:HB2	1.67	0.58
1:A:441:ASN:ND2	3:A:503:BNG:O4	2.36	0.58
1:A:160:ARG:HE	1:A:397:GLU:HG2	1.67	0.58
1:A:311:THR:HG22	1:A:312:ASP:N	2.16	0.58
1:A:315:LEU:HD22	1:A:319:ILE:HG13	1.86	0.57
1:A:164:VAL:HB	1:A:393:VAL:HG22	1.87	0.57
1:A:341:ARG:NE	1:A:397:GLU:OE1	2.28	0.57
1:A:249:ALA:O	1:A:252:ALA:HB3	2.06	0.56
1:A:390:VAL:O	1:A:394:LEU:HG	2.05	0.56
1:A:31:ILE:HD12	1:A:133:ARG:HD2	1.88	0.56
1:A:104:TRP:HE1	3:A:504:BNG:HO6	1.54	0.55
1:A:194:LEU:HA	1:A:198:GLY:HA3	1.88	0.55
1:A:437:ALA:HA	1:A:441:ASN:HB2	1.88	0.55
1:A:19:LEU:HB3	1:A:213:PHE:CD2	2.42	0.55
1:A:26:TYR:CE2	1:A:206:GLU:HB3	2.43	0.54
1:A:26:TYR:OH	1:A:205:SER:OG	2.25	0.54
1:A:234:GLU:HG2	1:A:235:GLN:H	1.70	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:LEU:HD11	1:A:200:ARG:NH2	2.23	0.54
1:A:404:ARG:NH1	1:A:471:LEU:HD13	2.23	0.54
1:A:367:ALA:O	3:A:505:BNG:H62	2.09	0.53
1:A:280:ILE:O	1:A:284:LEU:HB2	2.08	0.53
1:A:307:LEU:CD1	3:A:505:BNG:O2	2.57	0.52
1:A:309:ALA:O	1:A:310:SER:CB	2.57	0.52
1:A:470:THR:HG22	1:A:473:GLU:N	2.18	0.52
1:A:228:MET:HE1	1:A:257:LYS:HG3	1.90	0.52
1:A:349:ALA:HB3	1:A:456:ALA:HB2	1.92	0.51
1:A:386:SER:HG	1:A:387:TRP:HD1	1.51	0.51
1:A:386:SER:OG	1:A:387:TRP:CD1	2.62	0.51
1:A:206:GLU:HA	1:A:209:PRO:HD2	1.92	0.51
1:A:224:PRO:HA	1:A:227:LEU:HD12	1.92	0.51
1:A:426:PHE:HB3	1:A:427:PRO:HD3	1.93	0.51
1:A:342:LYS:O	1:A:346:ILE:HG13	2.11	0.51
1:A:342:LYS:NZ	1:A:463:VAL:O	2.38	0.51
1:A:309:ALA:O	1:A:310:SER:OG	2.29	0.50
1:A:245:GLY:O	1:A:249:ALA:HB3	2.11	0.50
1:A:330:VAL:HA	1:A:333:ILE:HD12	1.94	0.50
1:A:284:LEU:HD13	1:A:458:PHE:HE1	1.77	0.50
1:A:308:GLY:O	1:A:309:ALA:O	2.30	0.50
1:A:470:THR:HB	1:A:473:GLU:OE1	2.11	0.49
1:A:332:ALA:HB2	1:A:385:MET:HA	1.94	0.49
1:A:114:PRO:HG2	1:A:115:ASP:H	1.77	0.49
1:A:225:ARG:HD3	1:A:401:ASN:ND2	2.27	0.49
1:A:310:SER:CB	1:A:313:ILE:CB	2.59	0.49
1:A:140:VAL:O	1:A:144:SER:HB3	2.13	0.49
1:A:288:GLN:NE2	2:A:501:BGC:O1	2.46	0.48
1:A:256:ILE:O	1:A:259:SER:HB3	2.14	0.48
1:A:310:SER:O	1:A:311:THR:C	2.52	0.47
1:A:372:ALA:HB2	3:A:505:BNG:O6	2.14	0.47
1:A:329:THR:HA	1:A:384:ALA:O	2.15	0.47
1:A:352:MET:HB2	1:A:379:TYR:CD2	2.49	0.47
1:A:468:GLY:O	1:A:469:LYS:O	2.31	0.47
1:A:315:LEU:HD22	1:A:319:ILE:CD1	2.44	0.47
1:A:357:PHE:O	1:A:361:THR:HG23	2.14	0.47
1:A:244:MET:HB2	1:A:248:LEU:HD13	1.97	0.47
1:A:241:ARG:C	1:A:243:ILE:H	2.18	0.47
1:A:85:ARG:HD3	1:A:89:LYS:HE3	1.97	0.47
1:A:175:GLN:O	1:A:178:VAL:HG23	2.16	0.46
1:A:399:PHE:O	1:A:404:ARG:NH2	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:404:ARG:O	1:A:408:LEU:HB2	2.14	0.46
1:A:241:ARG:C	1:A:243:ILE:N	2.68	0.45
1:A:244:MET:CB	1:A:248:LEU:HD13	2.46	0.45
1:A:223:SER:HA	1:A:224:PRO:HD2	1.79	0.45
1:A:202:MET:O	1:A:205:SER:HB3	2.17	0.45
1:A:31:ILE:HD13	1:A:61:VAL:HA	1.98	0.45
1:A:469:LYS:HG2	1:A:473:GLU:HB3	1.99	0.45
1:A:154:LEU:HD11	1:A:223:SER:HA	1.98	0.45
1:A:415:GLN:NE2	2:A:501:BGC:O2	2.49	0.45
1:A:399:PHE:O	1:A:404:ARG:NE	2.48	0.45
1:A:240:LEU:O	1:A:243:ILE:HB	2.15	0.45
1:A:26:TYR:HE1	1:A:177:LEU:HD13	1.82	0.45
1:A:367:ALA:HB1	1:A:368:PRO:HD2	1.98	0.45
1:A:248:LEU:O	1:A:248:LEU:HD22	2.17	0.44
1:A:122:LEU:HD11	1:A:200:ARG:HH22	1.82	0.44
1:A:107:LEU:HD22	3:A:502:BNG:H3'2	2.00	0.44
1:A:84:ARG:CD	1:A:84:ARG:H	2.31	0.44
1:A:43:VAL:HG21	1:A:57:LEU:HB2	2.00	0.44
1:A:315:LEU:HD22	1:A:319:ILE:CG1	2.48	0.44
1:A:26:TYR:CZ	1:A:178:VAL:HG13	2.52	0.44
1:A:352:MET:HE2	1:A:379:TYR:CE2	2.53	0.44
1:A:160:ARG:O	1:A:164:VAL:HG23	2.18	0.44
1:A:469:LYS:NZ	1:A:477:LEU:HD11	2.34	0.43
1:A:404:ARG:HH12	1:A:471:LEU:HD13	1.82	0.43
1:A:241:ARG:O	1:A:243:ILE:N	2.51	0.43
1:A:244:MET:HB2	1:A:248:LEU:CD1	2.48	0.43
1:A:408:LEU:HD23	1:A:408:LEU:HA	1.75	0.43
1:A:118:VAL:HA	1:A:119:PRO:HD3	1.71	0.43
1:A:87:SER:HA	1:A:90:ILE:HD12	2.00	0.43
1:A:404:ARG:HH22	1:A:471:LEU:HB3	1.84	0.43
1:A:470:THR:HG23	1:A:472:GLU:HG2	2.00	0.42
1:A:474:LEU:O	1:A:476:ALA:N	2.53	0.42
1:A:197:ASP:OD1	3:A:504:BNG:C6	2.60	0.42
1:A:65:LEU:HA	1:A:68:CYS:HB2	2.01	0.42
1:A:81:ARG:HD2	1:A:82:PHE:CZ	2.55	0.42
1:A:26:TYR:CE2	1:A:178:VAL:HG13	2.54	0.42
1:A:177:LEU:O	1:A:181:VAL:HG23	2.20	0.42
1:A:385:MET:HE2	1:A:385:MET:O	2.20	0.42
1:A:243:ILE:HG22	1:A:243:ILE:O	2.19	0.41
1:A:344:LEU:HD23	1:A:344:LEU:HA	1.85	0.41
1:A:41:VAL:HG13	1:A:122:LEU:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:310:SER:CB	1:A:313:ILE:CG2	2.99	0.41
1:A:463:VAL:HA	1:A:464:PRO:HD3	1.82	0.41
1:A:10:ILE:HD11	1:A:154:LEU:O	2.21	0.41
1:A:114:PRO:C	1:A:116:ASN:H	2.23	0.41
1:A:290:PHE:HB3	1:A:451:MET:HG3	2.03	0.41
1:A:21:GLY:O	1:A:24:PHE:HB3	2.21	0.41
1:A:44:ALA:C	1:A:46:GLN:H	2.24	0.41
1:A:173:PHE:O	1:A:177:LEU:HB2	2.20	0.40
1:A:328:PHE:HB2	1:A:384:ALA:HB3	2.02	0.40
1:A:68:CYS:HB3	1:A:416:TRP:CD2	2.56	0.40

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	473/491 (96%)	410 (87%)	47 (10%)	16 (3%)	5 19

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	107	LEU
1	A	156	PRO
1	A	307	LEU
1	A	309	ALA
1	A	310	SER
1	A	469	LYS
1	A	311	THR
1	A	430	ASP
1	A	475	GLU
1	A	114	PRO
1	A	242	LYS

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Mol	Chain	Res	Type
1	A	368	PRO
1	A	84	ARG
1	A	389	PRO
1	A	397	GLU
1	A	45	PRO

### 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	365/396 (92%)	322 (88%)	43 (12%)	6 19

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	LEU
1	A	24	PHE
1	A	40	THR
1	A	46	GLN
1	A	49	SER
1	A	81	ARG
1	A	85	ARG
1	A	107	LEU
1	A	116	ASN
1	A	133	ARG
1	A	144	SER
1	A	145	MET
1	A	168	GLN
1	A	177	LEU
1	A	178	VAL
1	A	188	SER
1	A	190	ASP
1	A	196	THR
1	A	197	ASP
1	A	234	GLU
1	A	248	LEU

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Mol	Chain	Res	Type
1	A	278	ILE
1	A	291	VAL
1	A	307	LEU
1	A	315	LEU
1	A	320	ILE
1	A	331	LEU
1	A	336	VAL
1	A	339	PHE
1	A	347	ILE
1	A	373	LEU
1	A	376	MET
1	A	403	ILE
1	A	408	LEU
1	A	417	LEU
1	A	422	VAL
1	A	425	THR
1	A	432	ASN
1	A	457	LEU
1	A	469	LYS
1	A	470	THR
1	A	472	GLU
1	A	475	GLU

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	415	GLN
1	A	441	ASN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry

5 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	BGC	A	501	-	12,12,12	0.43	0	17,17,17	0.51	0
3	BNG	A	502	-	21,21,21	0.44	0	26,26,26	0.63	0
3	BNG	A	503	-	21,21,21	0.44	0	26,26,26	0.64	0
3	BNG	A	504	-	21,21,21	0.43	0	26,26,26	0.63	0
3	BNG	A	505	-	21,21,21	0.46	0	26,26,26	0.62	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
2	BGC	A	501	-	-	0/2/22/22	0/1/1/1
3	BNG	A	502	-	-	0/12/32/32	0/1/1/1
3	BNG	A	503	-	-	0/12/32/32	0/1/1/1
3	BNG	A	504	-	-	0/12/32/32	0/1/1/1
3	BNG	A	505	-	-	0/12/32/32	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	BGC	2	0
3	A	502	BNG	1	0
3	A	503	BNG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	504	BNG	3	0
3	A	505	BNG	6	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, 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	475/491 (96%)	0.58	59 (12%) 5 3	50, 84, 162, 278	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	245	GLY	7.3
1	A	244	MET	6.8
1	A	273	PHE	6.7
1	A	5	TYR	6.5
1	A	115	ASP	5.3
1	A	192	SER	5.3
1	A	312	ASP	5.0
1	A	249	ALA	4.9
1	A	275	VAL	4.8
1	A	274	GLY	4.5
1	A	334	MET	4.3
1	A	339	PHE	4.3
1	A	271	LEU	4.1
1	A	7	SER	4.0
1	A	468	GLY	4.0
1	A	313	ILE	3.8
1	A	270	LEU	3.8
1	A	112	ILE	3.7
1	A	338	LYS	3.6
1	A	159	ILE	3.6
1	A	246	ASN	3.6
1	A	389	PRO	3.3
1	A	460	TRP	3.1
1	A	175	GLN	3.0
1	A	40	THR	3.0
1	A	243	ILE	2.9
1	A	110	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	6	ASN	2.8
1	A	28	THR	2.8
1	A	191	ALA	2.8
1	A	117	THR	2.7
1	A	107	LEU	2.7
1	A	158	HIS	2.7
1	A	250	THR	2.7
1	A	108	GLY	2.7
1	A	298	TYR	2.6
1	A	168	GLN	2.6
1	A	183	TYR	2.6
1	A	239	ILE	2.6
1	A	269	ARG	2.6
1	A	194	LEU	2.5
1	A	308	GLY	2.5
1	A	186	ALA	2.5
1	A	254	GLN	2.5
1	A	429	MET	2.4
1	A	248	LEU	2.4
1	A	222	GLU	2.4
1	A	307	LEU	2.3
1	A	100	VAL	2.3
1	A	315	LEU	2.3
1	A	415	GLN	2.2
1	A	395	LEU	2.2
1	A	201	TYR	2.2
1	A	294	ASN	2.1
1	A	167	ASN	2.1
1	A	311	THR	2.1
1	A	50	GLU	2.0
1	A	240	LEU	2.0
1	A	8	SER	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 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	BNG	A	505	21/21	0.87	0.64	5.89	108,121,122,123	0
2	BGC	A	501	12/12	0.89	0.64	4.71	74,75,78,80	0
3	BNG	A	504	21/21	0.87	0.68	3.47	117,128,136,138	0
3	BNG	A	503	21/21	0.76	0.34	1.84	134,136,140,142	0
3	BNG	A	502	21/21	0.79	0.47	1.24	144,151,156,157	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.