



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 21, 2025 – 12:10 PM EDT

PDB ID : 9MNE / pdb\_00009mne  
Title : Crystal structure of enteropathogenic Escherichia coli EspC  
Authors : Pilapitiya, A.U.; Heras, B.; Paxman, J.J.  
Deposited on : 2024-12-21  
Resolution : 2.94 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

<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>.

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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	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
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)	:	2.46

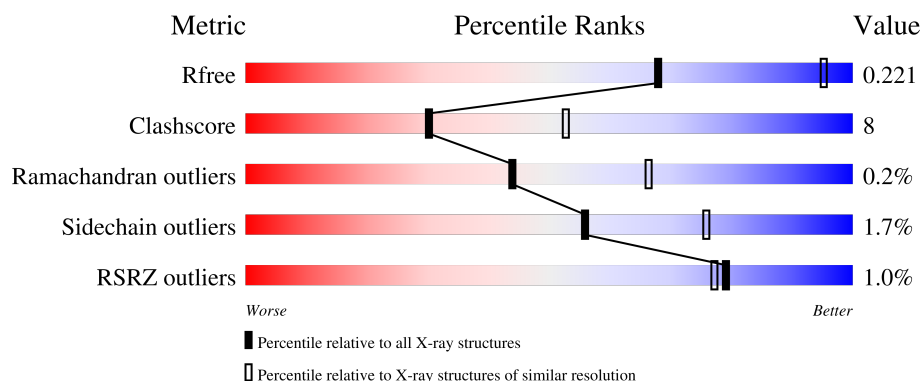
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.94 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))
$R_{free}$	164625	1067 (2.96-2.92)
Clashscore	180529	1122 (2.96-2.92)
Ramachandran outliers	177936	1075 (2.96-2.92)
Sidechain outliers	177891	1075 (2.96-2.92)
RSRZ outliers	164620	1067 (2.96-2.92)

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  $\geq 3$ , 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	975	
1	B	975	

## 2 Entry composition [i](#)

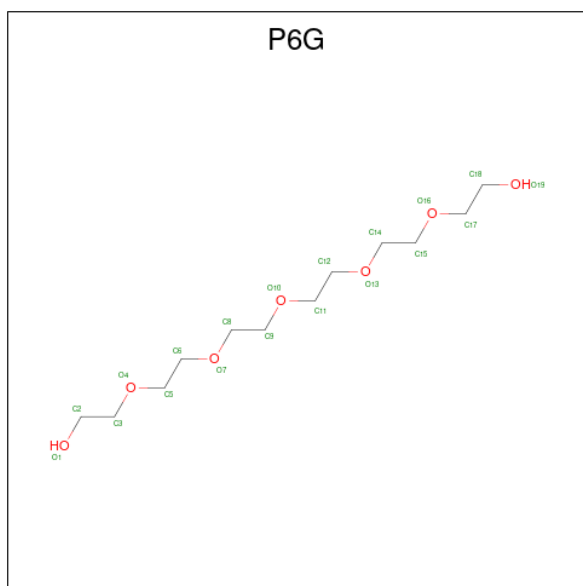
There are 6 unique types of molecules in this entry. The entry contains 14482 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Serine protease EspC.

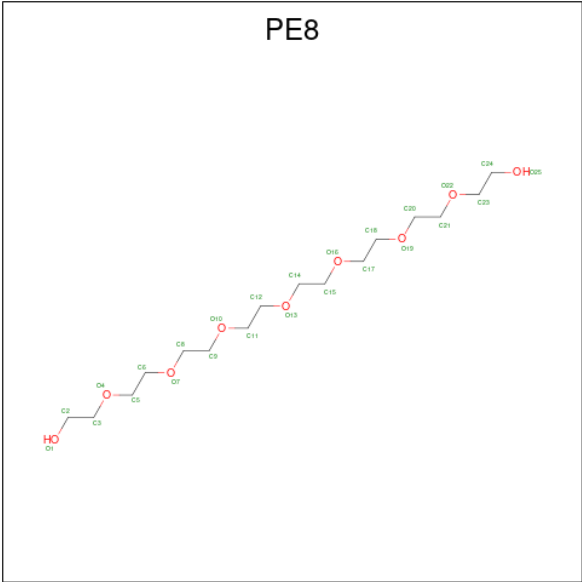
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	937	Total	C	N	O	S	0	0	0
			7096	4393	1225	1461	17			
1	A	934	Total	C	N	O	S	0	0	0
			7071	4377	1221	1457	16			

- Molecule 2 is HEXAETHYLENE GLYCOL (CCD ID: P6G) (formula: C<sub>12</sub>H<sub>26</sub>O<sub>7</sub>).



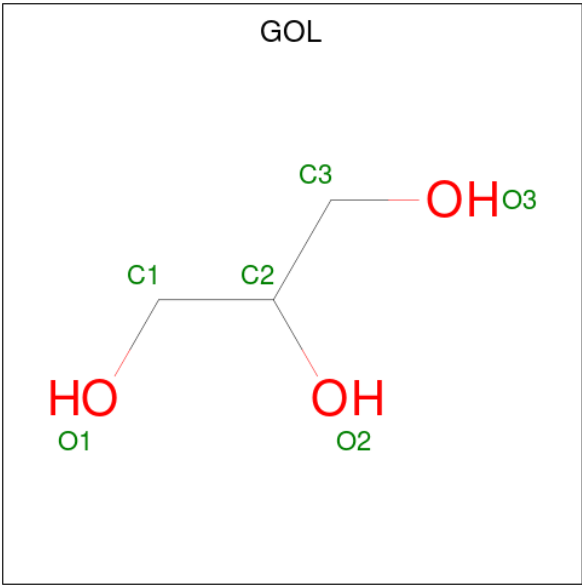
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 3 is 3,6,9,12,15,18,21-HEPTAOXATRICOSANE-1,23-DIOL (CCD ID: PE8) (formula: C<sub>16</sub>H<sub>34</sub>O<sub>9</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			25	16	9		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



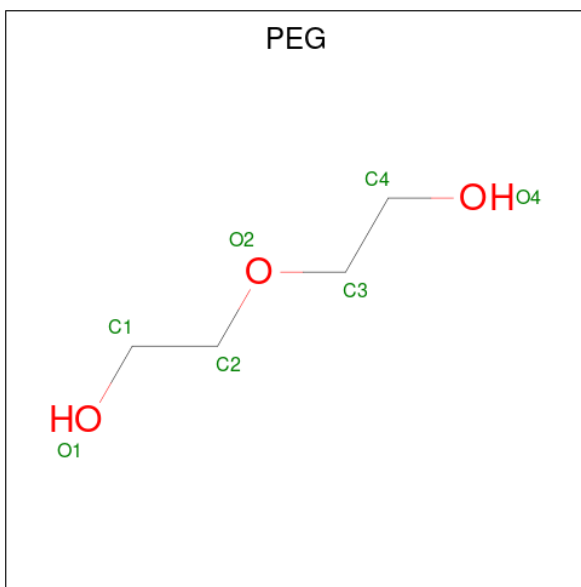
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		

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

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			7	4	3		

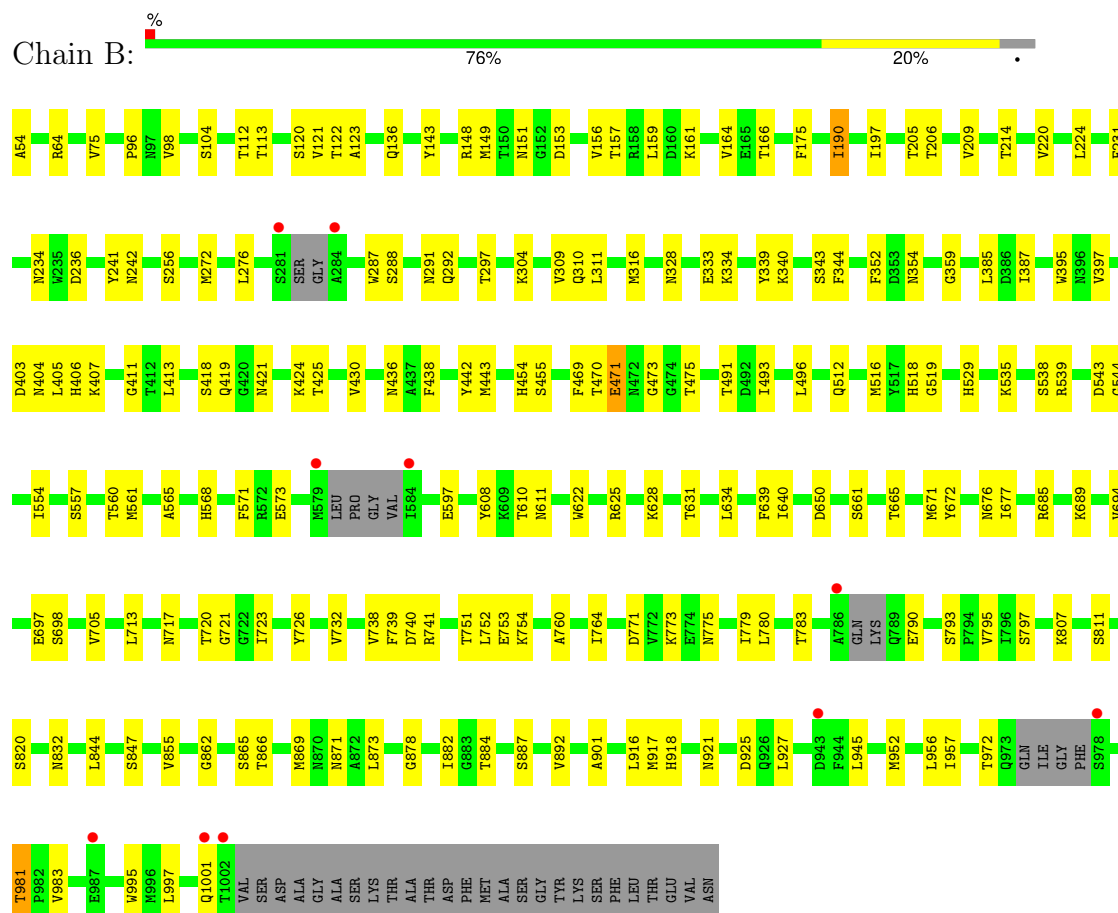
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	98	Total	O	0	0
			98	98		
6	A	58	Total	O	0	0
			58	58		

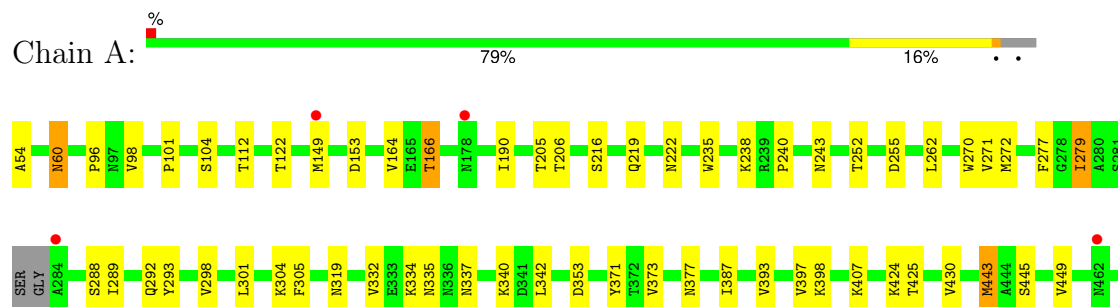
### 3 Residue-property plots

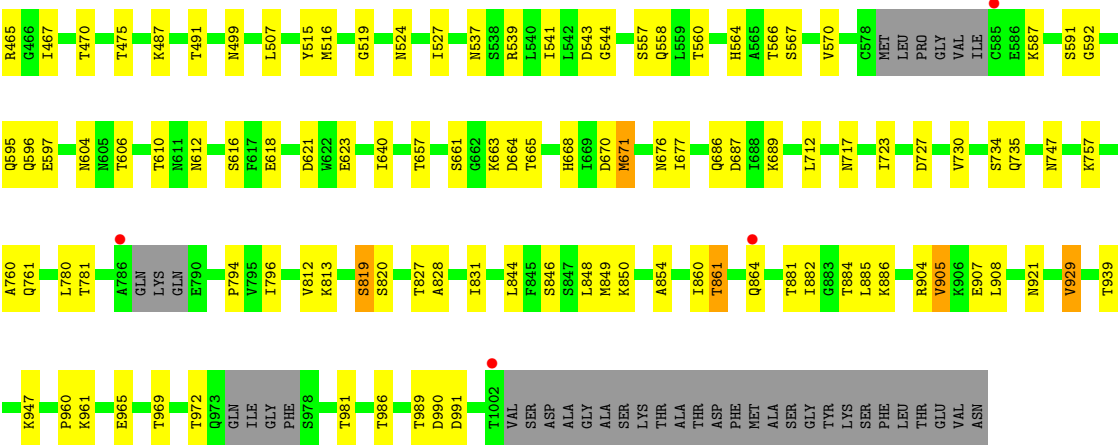
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Serine protease EspC



#### • Molecule 1: Serine protease EspC







## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	213.47Å 94.35Å 139.83Å 90.00° 108.16° 90.00°	Depositor
Resolution (Å)	48.20 – 2.94 48.20 – 2.94	Depositor EDS
% Data completeness (in resolution range)	97.4 (48.20-2.94) 98.2 (48.20-2.94)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.66 (at 2.96Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, $R_{free}$	0.163 , 0.223 0.163 , 0.221	Depositor DCC
$R_{free}$ test set	2930 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	54.6	Xtriage
Anisotropy	0.629	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 57.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	14482	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.13% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, P6G, PE8, PEG

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	0.33	0/7187	0.53	0/9750
1	B	0.35	2/7212 (0.0%)	0.54	2/9783 (0.0%)
All	All	0.34	2/14399 (0.0%)	0.53	2/19533 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	694	VAL	C-N	5.36	1.48	1.33
1	B	790	GLU	CD-OE2	5.16	1.35	1.25

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	694	VAL	CA-C-N	-5.41	106.31	122.71
1	B	694	VAL	C-N-CA	-5.41	106.31	122.71

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	7071	0	6771	108	0
1	B	7096	0	6801	125	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	7	0	9	0	0
3	B	25	0	34	0	0
4	A	48	0	64	5	0
4	B	72	0	96	7	0
5	B	7	0	10	1	0
6	A	58	0	0	1	0
6	B	98	0	0	0	0
All	All	14482	0	13785	233	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 8.

All (233) 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:560:THR:HG22	1:B:640:ILE:HB	1.38	1.05
1:B:491:THR:HG22	1:B:676:ASN:HB2	1.50	0.93
1:A:407:LYS:HB3	1:A:425:THR:HG22	1.55	0.88
1:B:539:ARG:HD3	1:B:560:THR:HG23	1.59	0.84
1:B:151:ASN:HB2	1:B:297:THR:HG21	1.57	0.84
1:B:96:PRO:HB3	1:B:190:ILE:HG12	1.60	0.82
1:A:491:THR:HG22	1:A:676:ASN:HB2	1.64	0.78
1:A:54:ALA:HB1	1:A:206:THR:HG22	1.67	0.76
1:A:972:THR:HG22	1:A:981:THR:HG22	1.67	0.75
1:A:387:ILE:HD12	1:A:407:LYS:HE2	1.73	0.71
1:B:844:LEU:HA	1:B:847:SER:HB2	1.73	0.70
1:A:149:MET:HG2	1:A:301:LEU:HD13	1.74	0.69
1:B:764:ILE:H	1:B:797:SER:HB3	1.58	0.69
1:B:121:VAL:HG21	1:B:272:MET:HE2	1.75	0.69
1:A:640:ILE:HG23	1:A:665:THR:HG22	1.75	0.69
1:B:720:THR:HG22	1:B:738:VAL:HB	1.75	0.68
1:A:425:THR:HG21	1:A:430:VAL:HG21	1.74	0.68
1:A:449:VAL:HG22	1:A:475:THR:HB	1.76	0.68
1:A:794:PRO:HB3	1:A:849:MET:HE3	1.76	0.67
1:A:827:THR:HG23	6:A:1208:HOH:O	1.94	0.67
1:B:112:THR:HA	1:B:122:THR:HG22	1.76	0.66
1:A:882:ILE:HG13	1:A:905:VAL:HG13	1.76	0.66
1:B:316:MET:HE1	1:B:344:PHE:HE2	1.60	0.66
1:B:661:SER:HB2	1:B:717:ASN:HB3	1.80	0.64
1:A:240:PRO:HG2	1:A:288:SER:HB2	1.79	0.64
1:B:753:GLU:O	1:B:773:LYS:HB2	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:554:ILE:HB	1:B:634:LEU:HD23	1.79	0.63
1:B:561:MET:HE2	1:B:639:PHE:HZ	1.66	0.61
1:B:395:TRP:HB2	1:B:413:LEU:HD11	1.84	0.60
1:B:866:THR:HG23	1:B:884:THR:HB	1.83	0.60
1:A:252:THR:HG22	1:A:255:ASP:OD2	2.03	0.59
1:B:753:GLU:O	1:B:754:LYS:HG3	2.02	0.58
1:A:101:PRO:HG3	1:A:270:TRP:CE2	2.38	0.58
1:B:470:THR:O	1:B:471:GLU:HB2	2.03	0.57
1:A:657:THR:HG22	1:A:712:LEU:HD12	1.85	0.57
1:B:470:THR:HA	1:B:677:ILE:HG13	1.87	0.57
1:B:697:GLU:HG3	4:B:1103:GOL:H11	1.85	0.57
1:B:475:THR:HG22	1:B:496:LEU:HB3	1.87	0.56
1:A:618:GLU:CD	1:A:618:GLU:H	2.13	0.56
1:B:471:GLU:C	1:B:473:GLY:H	2.11	0.56
1:B:640:ILE:HG23	1:B:665:THR:HG22	1.86	0.56
1:B:149:MET:SD	1:B:304:LYS:NZ	2.79	0.56
1:B:597:GLU:OE1	1:B:610:THR:HG21	2.04	0.56
1:B:205:THR:HG22	1:B:220:VAL:HB	1.85	0.56
1:A:812:VAL:HG12	1:A:854:ALA:HB1	1.87	0.56
1:B:256:SER:HA	1:B:276:LEU:HD23	1.88	0.56
1:B:352:PHE:CE2	1:B:397:VAL:HG21	2.40	0.55
1:A:908:LEU:HD12	1:A:929:VAL:HG22	1.89	0.55
1:A:334:LYS:HD3	1:A:337:ASN:HA	1.88	0.55
1:B:310:GLN:OE1	1:B:310:GLN:N	2.34	0.55
1:B:539:ARG:HH11	1:B:560:THR:HG23	1.72	0.54
1:A:661:SER:HB2	1:A:717:ASN:HB3	1.90	0.54
1:B:136:GLN:HE22	1:B:157:THR:HG21	1.73	0.54
1:A:570:VAL:HG13	1:A:612:ASN:OD1	2.07	0.54
1:A:470:THR:HG22	1:A:677:ILE:HG13	1.90	0.54
1:B:454:HIS:HA	4:B:1111:GOL:H11	1.89	0.54
1:A:597:GLU:OE1	1:A:610:THR:HG21	2.08	0.54
1:A:819:SER:O	1:A:819:SER:OG	2.24	0.53
1:B:96:PRO:HG3	1:B:190:ILE:HD11	1.89	0.53
1:B:631:THR:HG22	1:B:650:ASP:HB2	1.89	0.53
1:A:235:TRP:O	1:A:238:LYS:NZ	2.33	0.53
1:B:529:HIS:HB3	1:B:554:ILE:HD12	1.90	0.53
1:A:219:GLN:HG2	1:A:222:ASN:HD22	1.74	0.53
1:B:538:SER:OG	1:B:557:SER:HB2	2.08	0.53
1:A:881:THR:HG22	1:A:904:ARG:HB3	1.90	0.53
1:B:918:HIS:HB3	1:B:945:LEU:HD11	1.91	0.53
1:A:558:GLN:HG2	4:A:1107:GOL:H31	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:404:ASN:HD22	4:B:1104:GOL:H32	1.73	0.52
1:A:153:ASP:OD2	1:A:277:PHE:HD1	1.92	0.52
1:A:760:ALA:HB3	1:A:780:LEU:HD23	1.90	0.52
1:B:751:THR:HG23	1:B:771:ASP:HB2	1.90	0.52
1:B:190:ILE:CD1	1:B:197:ILE:HG13	2.40	0.52
1:B:869:MET:HB2	1:B:887:SER:HA	1.92	0.52
1:B:983:VAL:HG22	1:B:1001:GLN:HG3	1.90	0.52
1:A:519:GLY:O	1:A:544:GLY:HA3	2.10	0.52
1:B:104:SER:C	1:B:166:THR:HG21	2.35	0.51
1:B:571:PHE:CZ	1:B:610:THR:HG22	2.45	0.51
1:B:956:LEU:HD11	1:B:997:LEU:HB2	1.92	0.51
1:B:425:THR:HG21	1:B:430:VAL:HG21	1.91	0.51
1:B:732:VAL:HB	1:B:752:LEU:HD23	1.93	0.51
1:A:831:ILE:HD12	1:A:860:ILE:HD13	1.92	0.51
1:B:241:TYR:CE1	1:B:287:TRP:HB3	2.46	0.51
1:B:927:LEU:HD23	1:B:957:ILE:HG23	1.93	0.51
1:A:491:THR:CG2	1:A:677:ILE:HG12	2.40	0.51
1:A:54:ALA:HB3	1:A:252:THR:HG21	1.93	0.50
1:B:316:MET:HE1	1:B:344:PHE:CE2	2.45	0.50
1:B:855:VAL:HG22	1:B:873:LEU:HB3	1.94	0.50
1:B:161:LYS:HD3	1:B:406:HIS:CD2	2.46	0.50
1:B:387:ILE:HG22	1:B:411:GLY:HA3	1.92	0.50
1:B:760:ALA:HB3	1:B:780:LEU:HD23	1.94	0.50
1:A:965:GLU:HB3	1:A:986:THR:HG21	1.93	0.50
1:B:404:ASN:ND2	4:B:1104:GOL:H32	2.27	0.50
1:B:871:ASN:OD1	4:A:1103:GOL:H11	2.12	0.50
1:B:406:HIS:NE2	4:B:1104:GOL:H31	2.27	0.49
1:B:726:TYR:OH	5:B:1115:PEG:H22	2.11	0.49
1:A:921:ASN:ND2	1:A:947:LYS:O	2.45	0.49
1:A:104:SER:O	1:A:166:THR:HG21	2.12	0.49
1:B:561:MET:HE2	1:B:639:PHE:CZ	2.48	0.49
1:B:112:THR:CG2	1:B:120:SER:HB2	2.42	0.49
1:B:112:THR:HG21	1:B:136:GLN:OE1	2.12	0.49
1:A:98:VAL:HG11	1:A:270:TRP:CZ2	2.48	0.49
1:A:319:ASN:HB3	1:A:353:ASP:HB3	1.93	0.49
1:A:820:SER:HA	4:A:1102:GOL:H31	1.94	0.49
1:B:443:MET:HE2	1:B:469:PHE:CE2	2.48	0.48
1:B:443:MET:O	1:B:470:THR:HG22	2.13	0.48
1:A:272:MET:HG2	1:A:293:TYR:CD2	2.49	0.48
1:A:661:SER:HA	1:A:665:THR:HG21	1.96	0.48
1:B:352:PHE:CD2	1:B:397:VAL:HG21	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:884:THR:HG22	1:A:907:GLU:HB3	1.94	0.48
1:B:407:LYS:HB3	1:B:425:THR:HG22	1.95	0.48
1:A:663:LYS:HE2	1:A:664:ASP:OD1	2.13	0.48
1:A:761:GLN:HG2	1:A:781:THR:OG1	2.13	0.48
1:B:175:PHE:CZ	1:B:292:GLN:HB3	2.49	0.48
1:B:190:ILE:HD11	1:B:197:ILE:HG13	1.96	0.48
1:A:885:LEU:HB3	1:A:908:LEU:HD23	1.96	0.48
1:A:537:ASN:HA	4:A:1107:GOL:H11	1.96	0.47
1:B:385:LEU:HG	1:B:405:LEU:HD11	1.96	0.47
1:B:403:ASP:O	1:B:421:ASN:HB2	2.14	0.47
1:A:828:ALA:HA	1:A:864:GLN:O	2.14	0.47
1:A:972:THR:HG22	1:A:981:THR:CG2	2.39	0.47
1:B:209:VAL:HG22	1:B:214:THR:HG23	1.97	0.47
1:B:419:GLN:HG3	1:B:438:PHE:CE1	2.50	0.47
1:B:519:GLY:O	1:B:544:GLY:HA3	2.14	0.47
1:A:671:MET:HB2	1:A:687:ASP:HB3	1.95	0.47
1:B:783:THR:HG23	1:B:795:VAL:HG21	1.96	0.47
1:B:512:GLN:OE1	1:B:535:LYS:NZ	2.48	0.46
1:B:878:GLY:O	1:B:901:ALA:HB1	2.16	0.46
1:B:705:VAL:HG11	1:B:713:LEU:HD22	1.97	0.46
1:B:334:LYS:HE2	1:B:339:TYR:CZ	2.50	0.46
1:B:981:THR:OG1	1:B:1001:GLN:HB2	2.16	0.46
1:A:293:TYR:CZ	1:A:298:VAL:HG21	2.50	0.46
1:A:487:LYS:HB3	1:A:515:TYR:CE1	2.50	0.46
1:B:418:SER:OG	1:B:436:ASN:O	2.31	0.46
1:A:371:TYR:HB2	1:A:393:VAL:HG22	1.98	0.46
1:B:917:MET:HG2	1:B:925:ASP:O	2.16	0.45
1:A:153:ASP:CG	1:A:277:PHE:HD1	2.24	0.45
1:A:939:THR:HA	1:A:969:THR:O	2.16	0.45
1:B:957:ILE:HB	1:B:995:TRP:HB2	1.97	0.45
1:A:96:PRO:HG3	1:A:190:ILE:HD12	1.98	0.45
1:B:671:MET:HG2	1:B:689:LYS:HE2	1.99	0.45
1:A:566:THR:HG22	1:A:623:GLU:HG3	1.99	0.45
1:A:104:SER:HB3	1:A:166:THR:CG2	2.46	0.45
1:A:796:ILE:HD11	1:A:848:LEU:HD21	1.99	0.45
1:B:148:ARG:HA	1:B:156:VAL:O	2.17	0.45
1:A:516:MET:HG2	1:A:541:ILE:HB	1.99	0.45
1:A:929:VAL:O	1:A:960:PRO:HD3	2.17	0.45
1:B:205:THR:CG2	1:B:220:VAL:HB	2.47	0.45
1:B:491:THR:CG2	1:B:677:ILE:HG12	2.47	0.45
1:A:332:VAL:HG13	1:A:342:LEU:HD21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:557:SER:OG	1:A:558:GLN:N	2.45	0.44
1:B:740:ASP:OD1	1:B:741:ARG:HG3	2.17	0.44
1:A:566:THR:HG22	1:A:623:GLU:CG	2.47	0.44
1:A:961:LYS:HD2	1:A:990:ASP:O	2.16	0.44
1:B:608:TYR:HA	1:B:611:ASN:ND2	2.32	0.44
1:A:164:VAL:HG21	1:A:424:LYS:HB3	2.00	0.44
1:B:779:ILE:HG12	1:B:811:SER:OG	2.18	0.44
1:B:518:HIS:HA	1:B:543:ASP:OD1	2.18	0.44
1:B:820:SER:HA	4:B:1106:GOL:H2	1.99	0.44
1:A:470:THR:HG22	1:A:677:ILE:HB	2.00	0.44
1:B:471:GLU:C	1:B:473:GLY:N	2.76	0.43
1:A:723:ILE:HG21	1:A:730:VAL:HG21	1.99	0.43
1:B:104:SER:O	1:B:166:THR:HG21	2.19	0.43
1:A:262:LEU:O	1:A:271:VAL:HG22	2.18	0.43
1:B:54:ALA:HB1	1:B:206:THR:HA	1.99	0.43
1:B:516:MET:HE2	1:B:516:MET:HB3	1.96	0.43
1:A:470:THR:HG22	1:A:677:ILE:CG1	2.49	0.43
1:B:811:SER:HB3	1:B:832:ASN:HB2	2.01	0.43
1:A:54:ALA:O	1:A:206:THR:HA	2.19	0.43
1:A:539:ARG:HD3	1:A:560:THR:OG1	2.18	0.43
1:A:205:THR:O	1:A:252:THR:HG21	2.18	0.43
1:B:869:MET:HE2	1:B:892:VAL:CG2	2.49	0.43
1:B:164:VAL:HG13	1:B:406:HIS:HD1	1.84	0.43
1:A:989:THR:C	1:A:991:ASP:H	2.26	0.43
1:A:470:THR:HG22	1:A:677:ILE:CB	2.48	0.43
1:A:671:MET:HE2	1:A:689:LYS:HG3	2.01	0.43
1:B:565:ALA:HB2	1:B:622:TRP:CH2	2.53	0.43
1:A:112:THR:HB	1:A:122:THR:HG22	2.00	0.43
1:A:591:SER:O	1:A:595:GLN:HG3	2.19	0.43
1:B:143:TYR:HB3	1:B:159:LEU:HB3	2.01	0.42
1:B:862:GLY:O	1:B:882:ILE:HA	2.18	0.42
1:A:846:SER:O	1:A:850:LYS:HD2	2.19	0.42
1:B:120:SER:OG	1:B:157:THR:HB	2.19	0.42
1:B:234:ASN:OD1	1:B:236:ASP:HB2	2.19	0.42
1:B:529:HIS:HB3	1:B:554:ILE:CD1	2.49	0.42
1:B:672:TYR:CD2	1:B:685:ARG:HG3	2.54	0.42
1:A:216:SER:O	1:A:587:LYS:NZ	2.47	0.42
1:A:491:THR:HG21	1:A:677:ILE:HG12	2.01	0.42
1:B:543:ASP:O	1:B:625:ARG:NE	2.48	0.42
1:B:921:ASN:HA	1:B:952:MET:HE1	2.00	0.42
1:A:499:ASN:ND2	1:A:524:ASN:O	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:THR:HG22	1:A:122:THR:HG21	2.02	0.42
1:A:112:THR:HA	1:A:122:THR:HG22	2.00	0.42
1:A:507:LEU:O	1:A:527:ILE:HA	2.19	0.42
1:A:592:GLY:O	1:A:596:GLN:HG3	2.19	0.42
1:A:670:ASP:OD2	1:A:686:GLN:HG3	2.19	0.42
1:B:123:ALA:HA	1:B:153:ASP:O	2.20	0.42
1:B:705:VAL:HB	1:B:723:ILE:HD13	2.01	0.42
1:A:377:ASN:OD1	1:A:398:LYS:HE2	2.20	0.42
1:A:305:PHE:HA	1:A:340:LYS:HG2	2.02	0.42
1:A:373:VAL:HG12	1:A:397:VAL:CG2	2.49	0.42
1:B:304:LYS:O	1:B:340:LYS:HD3	2.20	0.42
1:B:424:LYS:HE2	1:B:442:TYR:CD2	2.54	0.42
1:A:844:LEU:HD23	1:A:844:LEU:HA	1.88	0.42
1:B:214:THR:HG21	4:B:1109:GOL:H2	2.02	0.41
1:A:604:ASN:O	1:A:606:THR:HG23	2.20	0.41
1:A:60:ASN:HD22	1:A:60:ASN:HA	1.64	0.41
1:A:616:SER:HB3	1:A:618:GLU:OE2	2.21	0.41
1:A:238:LYS:HG3	1:A:292:GLN:OE1	2.20	0.41
1:B:224:LEU:HD11	1:B:573:GLU:HG3	2.02	0.41
1:A:304:LYS:HE3	1:A:335:ASN:OD1	2.19	0.41
1:A:727:ASP:OD1	1:A:747:ASN:HB3	2.20	0.41
1:B:775:ASN:OD1	1:B:807:LYS:HE3	2.21	0.41
1:B:333:GLU:OE1	1:B:340:LYS:NZ	2.34	0.41
1:A:861:THR:O	1:A:861:THR:OG1	2.37	0.41
1:B:628:LYS:HE3	1:B:628:LYS:HB2	1.87	0.41
1:B:64:ARG:HD2	1:B:568:HIS:HB3	2.03	0.41
1:B:311:LEU:HD13	1:B:316:MET:CE	2.51	0.41
1:B:311:LEU:HD13	1:B:316:MET:HE3	2.02	0.41
1:B:493:ILE:HD13	1:B:625:ARG:NH2	2.35	0.41
1:A:734:SER:HB2	4:A:1101:GOL:H32	2.02	0.41
1:A:543:ASP:OD2	1:A:564:HIS:HD2	2.03	0.41
1:B:231:PHE:HB3	1:B:242:ASN:OD1	2.20	0.40
1:B:869:MET:HE2	1:B:892:VAL:HG23	2.03	0.40
1:A:279:ILE:N	1:A:289:ILE:HD12	2.36	0.40
1:A:541:ILE:HD13	1:A:668:HIS:CG	2.56	0.40
1:A:735:GLN:O	1:A:757:LYS:HB3	2.21	0.40
1:B:309:VAL:N	1:B:343:SER:O	2.50	0.40
1:B:721:GLY:O	1:B:739:PHE:HA	2.20	0.40
1:A:104:SER:C	1:A:166:THR:HG21	2.46	0.40
1:A:443:MET:HE3	1:A:443:MET:HB3	1.92	0.40
1:A:813:LYS:HA	1:A:854:ALA:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:153:ASP:HB3	1:B:291:ASN:OD1	2.21	0.40
1:A:566:THR:HG23	1:A:621:ASP:O	2.22	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	924/975 (95%)	877 (95%)	47 (5%)	0	100	100
1	B	927/975 (95%)	862 (93%)	61 (7%)	4 (0%)	30	55
All	All	1851/1950 (95%)	1739 (94%)	108 (6%)	4 (0%)	44	66

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	698	SER
1	B	471	GLU
1	B	328	ASN
1	B	359	GLY

### 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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	781/813 (96%)	766 (98%)	15 (2%)	52 73
1	B	784/813 (96%)	772 (98%)	12 (2%)	60 78
All	All	1565/1626 (96%)	1538 (98%)	27 (2%)	56 76

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	75	VAL
1	B	98	VAL
1	B	113	THR
1	B	190	ILE
1	B	288	SER
1	B	354	ASN
1	B	455	SER
1	B	793	SER
1	B	865	SER
1	B	916	LEU
1	B	972	THR
1	B	981	THR
1	A	60	ASN
1	A	166	THR
1	A	243	ASN
1	A	279	ILE
1	A	443	MET
1	A	445	SER
1	A	465	ARG
1	A	467	ILE
1	A	567	SER
1	A	671	MET
1	A	819	SER
1	A	861	THR
1	A	886	LYS
1	A	905	VAL
1	A	929	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	55	GLN
1	B	151	ASN
1	B	249	ASN
1	B	292	GLN
1	B	329	ASN
1	B	335	ASN
1	B	369	HIS
1	B	486	ASN
1	B	655	ASN
1	B	668	HIS
1	B	704	ASN
1	B	710	HIS
1	B	937	ASN
1	A	57	ASN
1	A	137	ASN
1	A	234	ASN
1	A	310	GLN
1	A	376	ASN
1	A	396	ASN
1	A	414	ASN
1	A	472	ASN
1	A	479	ASN
1	A	537	ASN
1	A	704	ASN
1	A	735	GLN
1	A	823	HIS
1	A	864	GLN
1	A	879	ASN
1	A	912	ASN
1	A	918	HIS
1	A	937	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 [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

23 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	$\# Z  > 2$
4	GOL	A	1104	-	5,5,5	0.44	0	5,5,5	0.60	0
4	GOL	B	1109	-	5,5,5	0.29	0	5,5,5	0.58	0
4	GOL	B	1103	-	5,5,5	0.23	0	5,5,5	0.82	0
4	GOL	B	1107	-	5,5,5	0.35	0	5,5,5	0.85	0
4	GOL	A	1105	-	5,5,5	0.24	0	5,5,5	0.38	0
4	GOL	B	1113	-	5,5,5	0.32	0	5,5,5	0.46	0
2	P6G	B	1101	-	6,6,18	0.31	0	5,5,17	0.77	0
4	GOL	B	1105	-	5,5,5	0.46	0	5,5,5	0.62	0
4	GOL	B	1112	-	5,5,5	0.33	0	5,5,5	0.36	0
4	GOL	B	1106	-	5,5,5	0.39	0	5,5,5	0.11	0
4	GOL	A	1102	-	5,5,5	0.38	0	5,5,5	0.72	0
5	PEG	B	1115	-	6,6,6	0.27	0	5,5,5	0.28	0
4	GOL	A	1103	-	5,5,5	0.34	0	5,5,5	0.60	0
4	GOL	A	1108	-	5,5,5	0.33	0	5,5,5	0.50	0
4	GOL	B	1104	-	5,5,5	0.47	0	5,5,5	0.69	0
3	PE8	B	1102	-	24,24,24	0.37	0	23,23,23	0.61	0
4	GOL	B	1108	-	5,5,5	0.35	0	5,5,5	0.39	0
4	GOL	A	1106	-	5,5,5	0.37	0	5,5,5	0.35	0
4	GOL	B	1111	-	5,5,5	0.28	0	5,5,5	0.70	0
4	GOL	B	1110	-	5,5,5	0.35	0	5,5,5	0.38	0
4	GOL	A	1101	-	5,5,5	0.30	0	5,5,5	0.49	0
4	GOL	B	1114	-	5,5,5	0.34	0	5,5,5	0.38	0
4	GOL	A	1107	-	5,5,5	0.39	0	5,5,5	0.31	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	GOL	A	1104	-	-	1/4/4/4	-
4	GOL	B	1109	-	-	2/4/4/4	-
4	GOL	B	1103	-	-	3/4/4/4	-
4	GOL	B	1107	-	-	4/4/4/4	-
4	GOL	A	1105	-	-	3/4/4/4	-
4	GOL	B	1113	-	-	1/4/4/4	-
2	P6G	B	1101	-	-	3/4/4/16	-
4	GOL	B	1105	-	-	2/4/4/4	-
4	GOL	B	1112	-	-	2/4/4/4	-
4	GOL	B	1106	-	-	0/4/4/4	-
4	GOL	A	1102	-	-	4/4/4/4	-
5	PEG	B	1115	-	-	2/4/4/4	-
4	GOL	A	1103	-	-	0/4/4/4	-
4	GOL	A	1108	-	-	3/4/4/4	-
4	GOL	B	1104	-	-	2/4/4/4	-
3	PE8	B	1102	-	-	14/22/22/22	-
4	GOL	B	1108	-	-	2/4/4/4	-
4	GOL	A	1106	-	-	0/4/4/4	-
4	GOL	B	1111	-	-	4/4/4/4	-
4	GOL	B	1110	-	-	1/4/4/4	-
4	GOL	A	1101	-	-	0/4/4/4	-
4	GOL	B	1114	-	-	0/4/4/4	-
4	GOL	A	1107	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (53) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1103	GOL	O1-C1-C2-C3
4	B	1105	GOL	C1-C2-C3-O3
4	B	1107	GOL	O1-C1-C2-C3
4	B	1107	GOL	C1-C2-C3-O3
4	B	1108	GOL	C1-C2-C3-O3
4	B	1111	GOL	C1-C2-C3-O3
4	B	1111	GOL	O2-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
4	B	1112	GOL	C1-C2-C3-O3
4	B	1112	GOL	O2-C2-C3-O3
4	A	1102	GOL	O1-C1-C2-C3
4	A	1102	GOL	C1-C2-C3-O3
3	B	1102	PE8	O16-C17-C18-O19
5	B	1115	PEG	O1-C1-C2-O2
4	B	1104	GOL	C1-C2-C3-O3
4	B	1109	GOL	C1-C2-C3-O3
4	B	1111	GOL	O1-C1-C2-C3
4	A	1104	GOL	O1-C1-C2-C3
4	A	1105	GOL	C1-C2-C3-O3
4	A	1108	GOL	O1-C1-C2-C3
4	B	1105	GOL	O2-C2-C3-O3
4	B	1111	GOL	O1-C1-C2-O2
4	A	1102	GOL	O1-C1-C2-O2
4	A	1102	GOL	O2-C2-C3-O3
2	B	1101	P6G	O1-C2-C3-O4
2	B	1101	P6G	O4-C5-C6-O7
4	B	1108	GOL	O2-C2-C3-O3
4	B	1109	GOL	O2-C2-C3-O3
4	A	1108	GOL	O2-C2-C3-O3
4	A	1105	GOL	O1-C1-C2-O2
4	A	1105	GOL	O2-C2-C3-O3
5	B	1115	PEG	C4-C3-O2-C2
4	B	1110	GOL	O2-C2-C3-O3
3	B	1102	PE8	C5-C6-O7-C8
3	B	1102	PE8	C11-C12-O13-C14
3	B	1102	PE8	C6-C5-O4-C3
4	B	1104	GOL	O2-C2-C3-O3
4	B	1107	GOL	O1-C1-C2-O2
4	B	1107	GOL	O2-C2-C3-O3
2	B	1101	P6G	C6-C5-O4-C3
3	B	1102	PE8	C2-C3-O4-C5
3	B	1102	PE8	C15-C14-O13-C12
4	B	1103	GOL	O1-C1-C2-O2
3	B	1102	PE8	C18-C17-O16-C15
3	B	1102	PE8	O22-C23-C24-O25
3	B	1102	PE8	C14-C15-O16-C17
3	B	1102	PE8	C8-C9-O10-C11
3	B	1102	PE8	O4-C5-C6-O7
3	B	1102	PE8	C12-C11-O10-C9
3	B	1102	PE8	C24-C23-O22-C21

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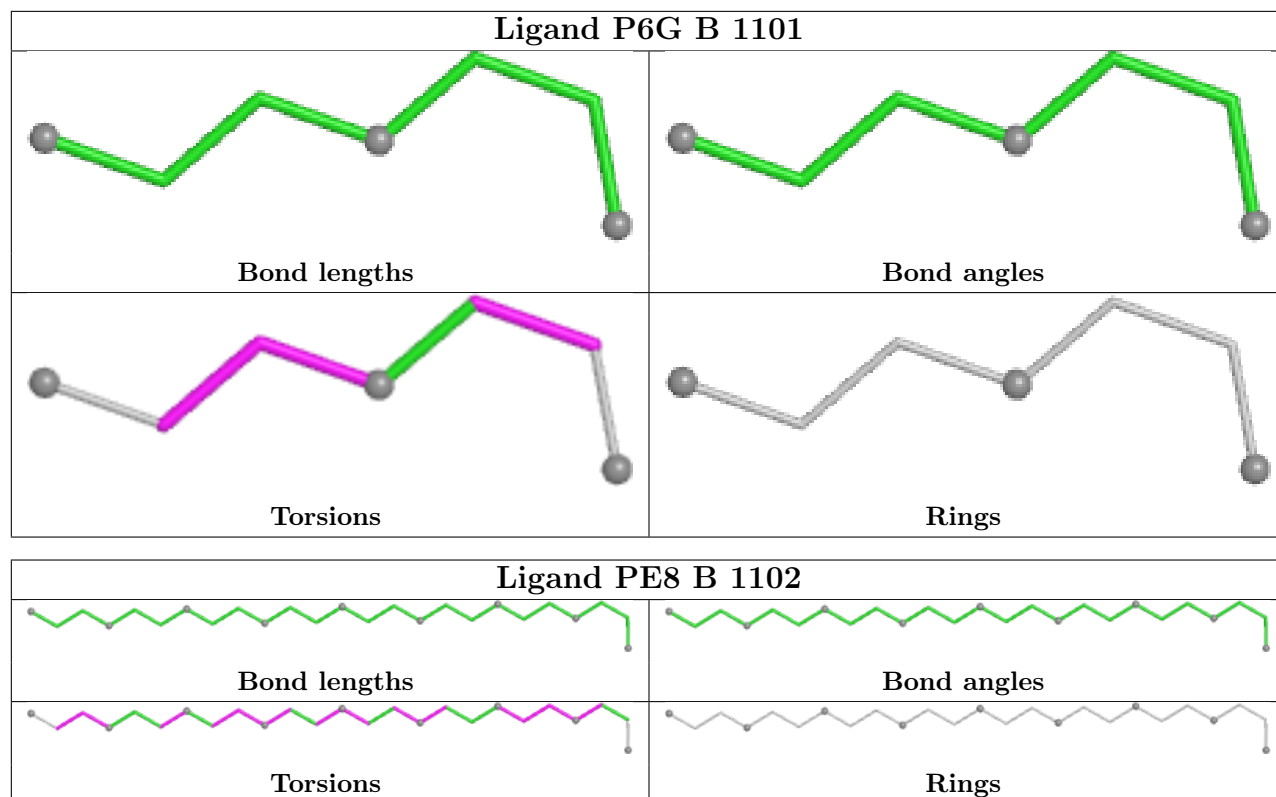
Mol	Chain	Res	Type	Atoms
3	B	1102	PE8	C21-C20-O19-C18
4	A	1108	GOL	C1-C2-C3-O3
4	B	1103	GOL	O2-C2-C3-O3
4	B	1113	GOL	O1-C1-C2-O2

There are no ring outliers.

10 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1109	GOL	1	0
4	B	1103	GOL	1	0
4	B	1106	GOL	1	0
4	A	1102	GOL	1	0
5	B	1115	PEG	1	0
4	A	1103	GOL	1	0
4	B	1104	GOL	3	0
4	B	1111	GOL	1	0
4	A	1101	GOL	1	0
4	A	1107	GOL	2	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, 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	934/975 (95%)	-0.44	8 (0%) 81 79	37, 64, 101, 151	0
1	B	937/975 (96%)	-0.47	10 (1%) 77 75	38, 61, 92, 134	0
All	All	1871/1950 (95%)	-0.46	18 (0%) 79 77	37, 62, 96, 151	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	281	SER	3.5
1	A	786	ALA	3.4
1	B	786	ALA	3.3
1	B	584	ILE	3.0
1	A	284	ALA	3.0
1	A	1002	THR	2.7
1	A	462	ASN	2.5
1	B	579	MET	2.5
1	A	149	MET	2.4
1	B	943	ASP	2.4
1	A	864	GLN	2.3
1	B	1002	THR	2.3
1	B	978	SER	2.2
1	B	284	ALA	2.2
1	B	987	GLU	2.2
1	A	178	ASN	2.1
1	A	585	CYS	2.1
1	B	1001	GLN	2.1

### 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

There are no oligosaccharides in this entry.

## 6.4 Ligands

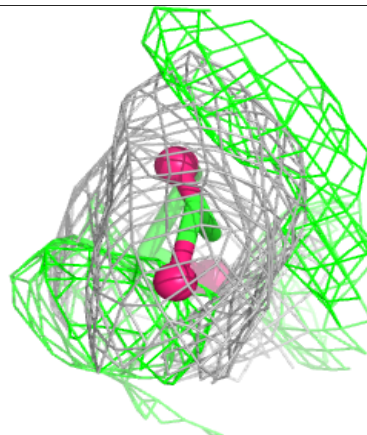
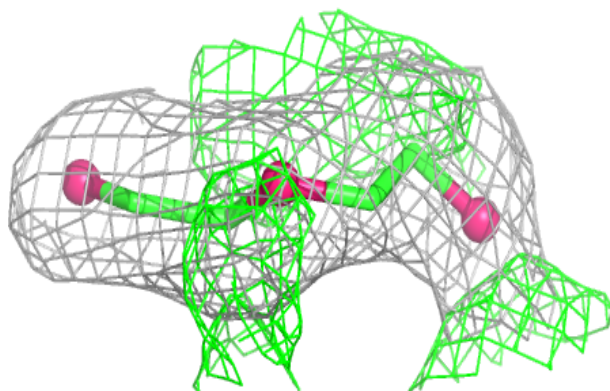
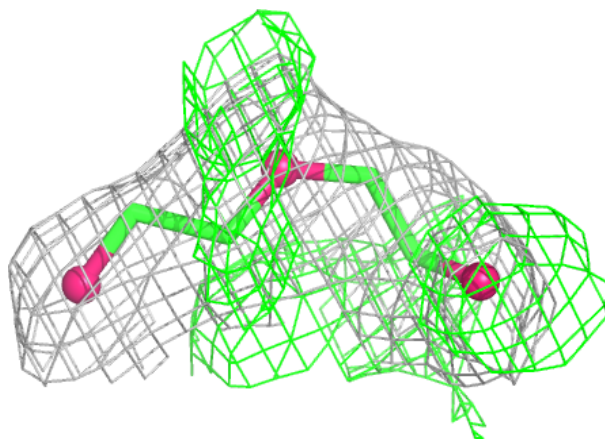
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	GOL	B	1112	6/6	0.75	0.17	82,91,100,103	0
4	GOL	B	1106	6/6	0.79	0.15	60,73,92,96	0
4	GOL	B	1111	6/6	0.82	0.14	82,90,96,102	0
4	GOL	B	1109	6/6	0.82	0.18	83,87,96,98	0
4	GOL	A	1106	6/6	0.82	0.13	83,92,104,107	0
4	GOL	B	1110	6/6	0.83	0.21	60,81,90,93	0
4	GOL	A	1104	6/6	0.84	0.17	59,70,75,92	0
2	P6G	B	1101	7/19	0.85	0.21	58,67,74,77	0
4	GOL	B	1108	6/6	0.85	0.13	68,79,89,96	0
4	GOL	B	1104	6/6	0.86	0.17	59,70,74,75	0
4	GOL	B	1105	6/6	0.86	0.16	45,63,70,75	0
4	GOL	B	1103	6/6	0.88	0.12	48,67,75,83	0
4	GOL	A	1105	6/6	0.88	0.18	68,72,78,84	0
4	GOL	B	1113	6/6	0.88	0.14	86,90,94,101	0
4	GOL	A	1107	6/6	0.89	0.14	71,78,82,85	0
3	PE8	B	1102	25/25	0.91	0.13	53,67,83,85	0
4	GOL	B	1114	6/6	0.91	0.14	66,83,94,95	0
4	GOL	A	1102	6/6	0.91	0.11	43,66,74,79	0
4	GOL	A	1103	6/6	0.91	0.11	59,74,87,91	0
4	GOL	B	1107	6/6	0.93	0.13	58,67,71,77	0
5	PEG	B	1115	7/7	0.93	0.13	50,59,74,84	0
4	GOL	A	1108	6/6	0.94	0.10	74,81,86,92	0
4	GOL	A	1101	6/6	0.96	0.08	55,70,78,81	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.

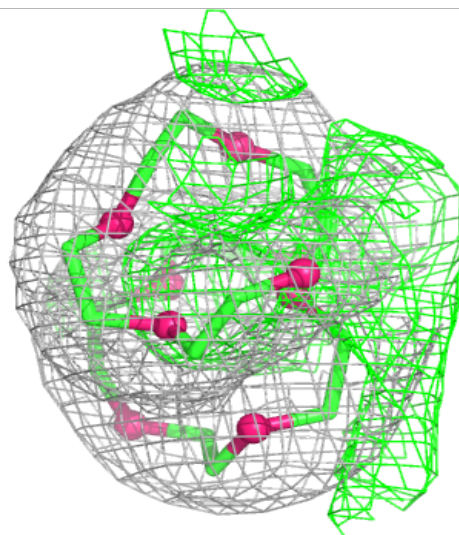
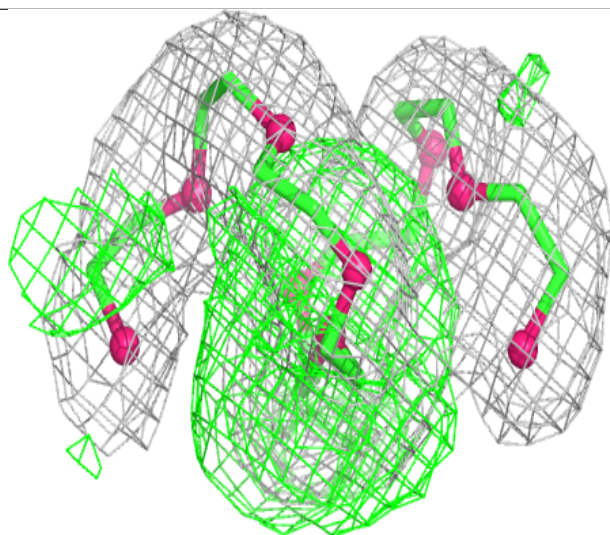
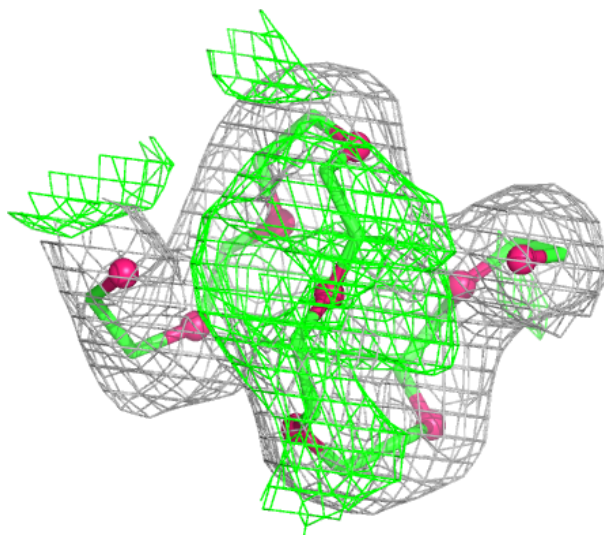
**Electron density around P6G B 1101:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around PE8 B 1102:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.