



# Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 07:58 pm BST

PDB ID : 5ZFJ  
Title : Crystal structure of a cyclase Filc from Fischerella sp. in complex with 4-(1H-Indol-3-yl)butan-2-one  
Authors : Hu, X.Y.; Liu, W.D.; Chen, C.C.; Guo, R.T.  
Deposited on : 2018-03-06  
Resolution : 1.86 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.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
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) : 2.11

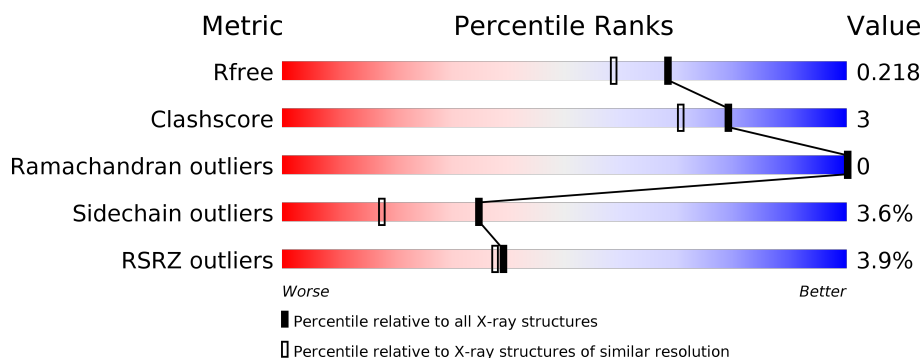
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.86 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	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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 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	227	<div> <div>2%</div> <div> <div></div> <div>79%</div> <div>8%</div> <div>12%</div> </div> </div>
1	B	227	<div> <div>2%</div> <div> <div></div> <div>80%</div> <div>7%</div> <div>12%</div> </div> </div>
1	C	227	<div> <div>5%</div> <div> <div></div> <div>80%</div> <div>7%</div> <div>12%</div> </div> </div>
1	D	227	<div> <div>4%</div> <div> <div></div> <div>81%</div> <div>7%</div> <div>12%</div> </div> </div>

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6998 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 acyclase.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	199	Total	C	N	O	0	0	0
			1533	980	250	303			
1	B	199	Total	C	N	O	0	0	0
			1533	980	250	303			
1	C	199	Total	C	N	O	0	0	0
			1533	980	250	303			
1	D	199	Total	C	N	O	0	0	0
			1533	980	250	303			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

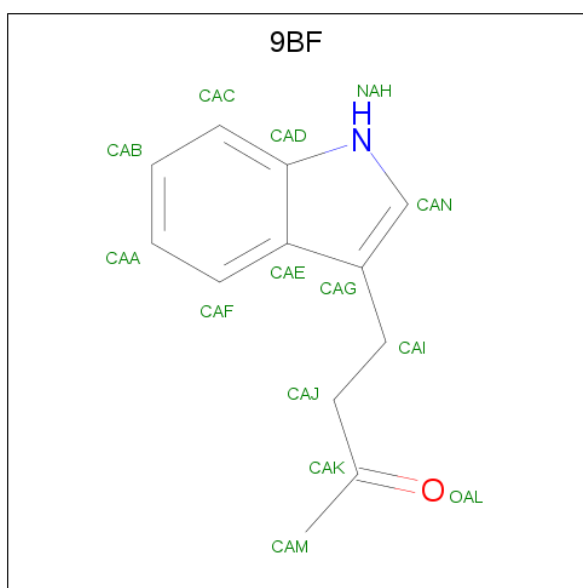
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Ca	0	0
			2	2		
2	A	2	Total	Ca	0	0
			2	2		
2	D	2	Total	Ca	0	0
			2	2		
2	C	2	Total	Ca	0	0
			2	2		

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C<sub>4</sub>H<sub>12</sub>NO<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			8	4	1	3		
3	D	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 4 is 4-(1 {H}-indol-3-yl)butan-2-one (three-letter code: 9BF) (formula: C<sub>12</sub>H<sub>13</sub>NO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	12	1	1		
4	B	1	Total	C	N	O	0	0
			14	12	1	1		

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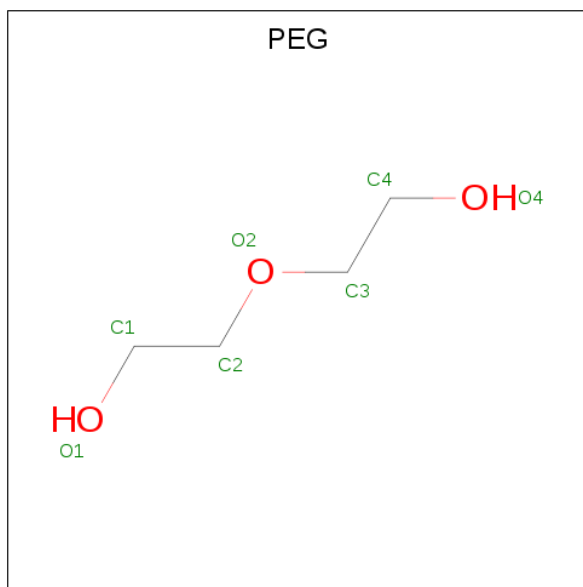
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	C	1	Total	C	N	O	0	0
			14	12	1	1		
4	D	1	Total	C	N	O	0	0
			14	12	1	1		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



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

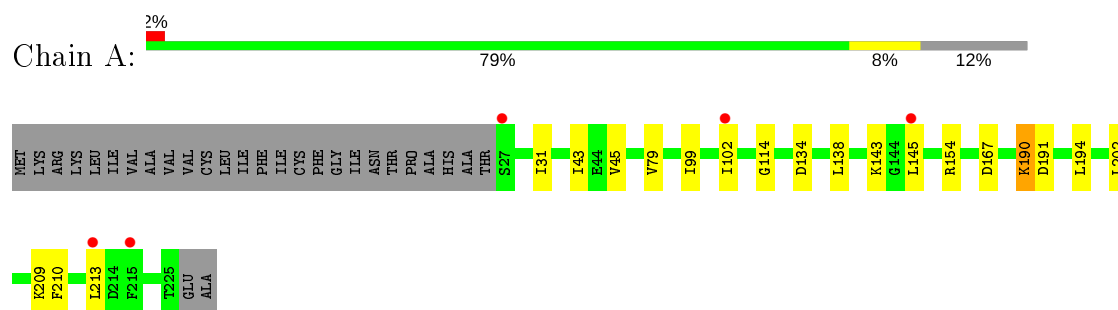
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	226	Total	O	0	0
			226	226		
7	B	190	Total	O	0	0
			190	190		
7	C	173	Total	O	0	0
			173	173		
7	D	184	Total	O	0	0
			184	184		

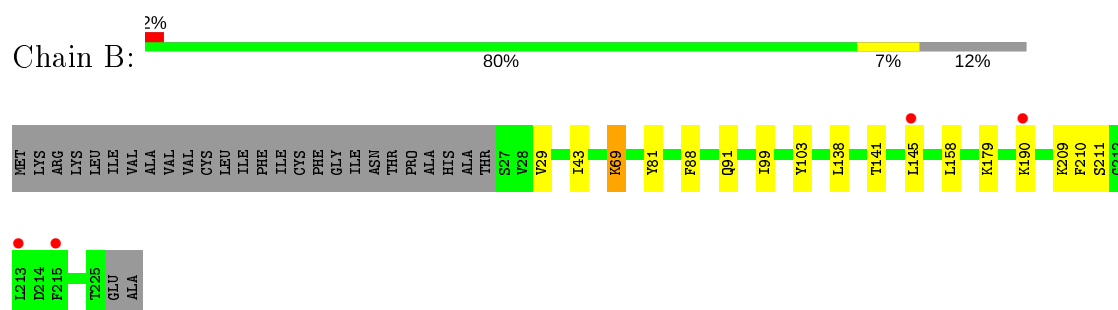
### 3 Residue-property plots [i](#)

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.

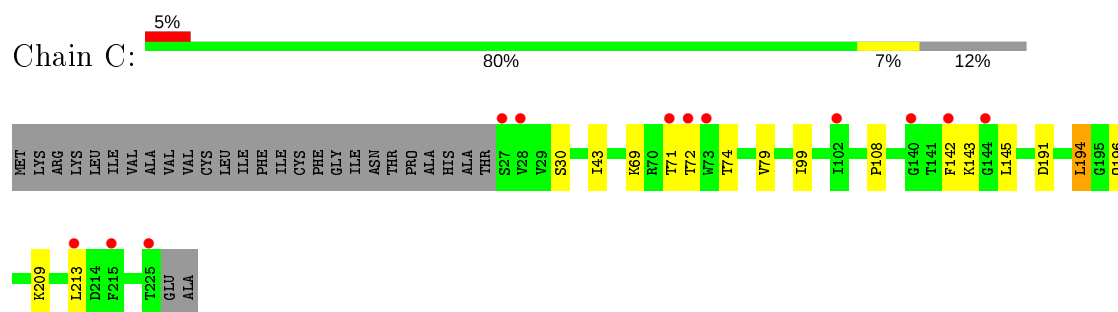
- Molecule 1: acyclase



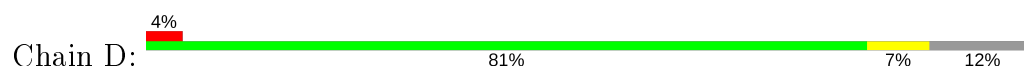
- Molecule 1: acyclase

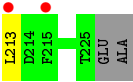
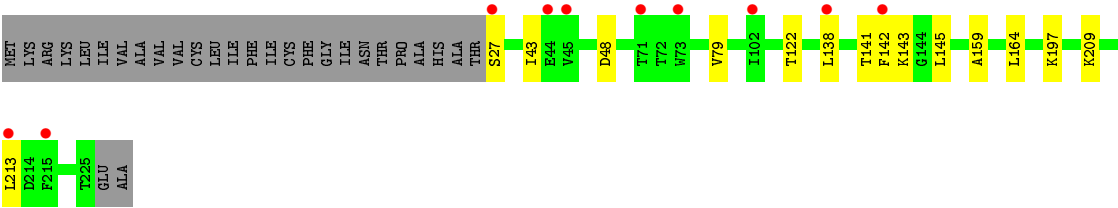


- Molecule 1: acyclase



- Molecule 1: acyclase







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	88.20 Å   255.06 Å   36.18 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	24.66 – 1.86 24.65 – 1.86	Depositor EDS
% Data completeness (in resolution range)	99.3 (24.66-1.86) 99.4 (24.65-1.86)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.75 (at 1.86 Å)	Xtriage
Refinement program	REFMAC 5.8.0230	Depositor
R, $R_{free}$	0.169   ,   0.201 0.184   ,   0.218	Depositor DCC
$R_{free}$ test set	3548 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.9	Xtriage
Anisotropy	0.201	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 52.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	6998	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	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 39.68 % 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 3.0607e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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, CA, PEG, TRS, 9BF

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	0.48	0/1570	0.80	0/2145
1	B	0.49	0/1570	0.79	0/2145
1	C	0.45	0/1570	0.78	0/2145
1	D	0.45	0/1570	0.75	0/2145
All	All	0.47	0/6280	0.78	0/8580

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 [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	1533	0	1484	12	0
1	B	1533	0	1484	9	0
1	C	1533	0	1484	9	0
1	D	1533	0	1484	6	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	8	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	8	0	12	0	0
4	A	14	0	0	0	0
4	B	14	0	0	0	0
4	C	14	0	0	0	0
4	D	14	0	0	1	0
5	A	6	0	8	0	0
6	B	7	0	10	0	0
7	A	226	0	0	1	0
7	B	190	0	0	2	0
7	C	173	0	0	0	0
7	D	184	0	0	1	0
All	All	6998	0	5978	34	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 (34) 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:45:VAL:HG21	1:B:69:LYS:HG2	1.75	0.68
1:D:209:LYS:HD3	7:D:501:HOH:O	1.96	0.66
1:A:45:VAL:CG2	1:B:69:LYS:HG2	2.28	0.64
1:B:91:GLN:NE2	7:B:402:HOH:O	2.32	0.61
1:A:43:ILE:HD11	1:A:79:VAL:HG23	1.83	0.61
1:C:71:THR:HG22	1:C:74:THR:HG23	1.83	0.60
1:D:43:ILE:HD11	1:D:79:VAL:HG23	1.85	0.58
1:D:122:THR:HG22	1:D:197:LYS:HD3	1.86	0.58
1:B:99:ILE:C	1:B:99:ILE:HD12	2.25	0.56
1:A:143:LYS:NZ	7:A:403:HOH:O	2.43	0.51
1:A:102:ILE:HG12	1:A:114:GLY:HA2	1.93	0.51
1:A:143:LYS:HE3	1:B:103:TYR:OH	2.11	0.51
1:C:99:ILE:C	1:C:99:ILE:HD12	2.33	0.49
1:A:99:ILE:C	1:A:99:ILE:HD12	2.32	0.49
1:C:71:THR:CG2	1:C:74:THR:HG23	2.44	0.48
1:C:191:ASP:HB3	1:C:194:LEU:HD13	1.97	0.46
1:C:71:THR:OG1	1:C:72:THR:N	2.47	0.46
1:B:69:LYS:HE2	7:B:490:HOH:O	2.16	0.46
1:A:191:ASP:HB3	1:A:194:LEU:HD13	1.98	0.45
1:B:209:LYS:HA	1:B:210:PHE:C	2.37	0.45
1:D:141:THR:HA	1:D:145:LEU:O	2.17	0.45
1:C:108:PRO:HD3	1:C:209:LYS:HE2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:LYS:HB2	1:A:190:LYS:HE3	1.69	0.44
1:C:43:ILE:HD11	1:C:79:VAL:HG23	1.99	0.44
4:D:304:9BF:CAK	4:D:304:9BF:CAN	2.96	0.44
1:D:159:ALA:HB2	1:D:164:LEU:HD11	2.00	0.43
1:A:209:LYS:HA	1:A:210:PHE:C	2.40	0.42
1:C:142:PHE:O	1:C:143:LYS:HB2	2.20	0.42
1:C:71:THR:HG22	1:C:74:THR:CG2	2.50	0.41
1:B:43:ILE:HB	1:B:81:TYR:HB2	2.03	0.41
1:D:142:PHE:O	1:D:143:LYS:HB2	2.21	0.41
1:B:88:PHE:HB3	1:B:138:LEU:HG	2.02	0.41
1:A:114:GLY:HA3	1:A:202:LEU:O	2.21	0.40
1:A:154:ARG:HA	1:A:167:ASP:O	2.22	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	197/227 (87%)	194 (98%)	3 (2%)	0	100	100
1	B	197/227 (87%)	194 (98%)	3 (2%)	0	100	100
1	C	197/227 (87%)	193 (98%)	4 (2%)	0	100	100
1	D	197/227 (87%)	192 (98%)	5 (2%)	0	100	100
All	All	788/908 (87%)	773 (98%)	15 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar

resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	166/189 (88%)	160 (96%)	6 (4%)	35	18
1	B	166/189 (88%)	158 (95%)	8 (5%)	25	10
1	C	166/189 (88%)	160 (96%)	6 (4%)	35	18
1	D	166/189 (88%)	162 (98%)	4 (2%)	49	33
All	All	664/756 (88%)	640 (96%)	24 (4%)	35	18

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	ILE
1	A	134	ASP
1	A	138	LEU
1	A	145	LEU
1	A	190	LYS
1	A	213	LEU
1	B	29	VAL
1	B	69	LYS
1	B	141	THR
1	B	145	LEU
1	B	158	LEU
1	B	179	LYS
1	B	190	LYS
1	B	211	SER
1	C	30	SER
1	C	69	LYS
1	C	145	LEU
1	C	194	LEU
1	C	196	GLN
1	C	213	LEU
1	D	27	SER
1	D	48	ASP
1	D	138	LEU
1	D	213	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	91	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
4	9BF	A	304	-	14,15,15	1.89	3 (21%)	14,20,20	1.03	0
4	9BF	C	303	-	14,15,15	2.04	3 (21%)	14,20,20	1.37	1 (7%)
3	TRS	D	303	-	7,7,7	0.61	0	9,9,9	0.66	0
3	TRS	A	303	-	7,7,7	0.50	0	9,9,9	1.24	1 (11%)
4	9BF	B	303	-	14,15,15	1.95	4 (28%)	14,20,20	1.07	2 (14%)
6	PEG	B	304	-	6,6,6	0.48	0	5,5,5	0.63	0
4	9BF	D	304	-	14,15,15	1.96	3 (21%)	14,20,20	1.05	1 (7%)
5	GOL	A	305	-	5,5,5	0.21	0	5,5,5	0.67	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	9BF	A	304	-	-	4/5/5/5	0/2/2/2
4	9BF	C	303	-	-	3/5/5/5	0/2/2/2
3	TRS	D	303	-	-	0/9/9/9	-
3	TRS	A	303	-	-	3/9/9/9	-
4	9BF	B	303	-	-	2/5/5/5	0/2/2/2
6	PEG	B	304	-	-	1/4/4/4	-
4	9BF	D	304	-	-	2/5/5/5	0/2/2/2
5	GOL	A	305	-	-	2/4/4/4	-

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	303	9BF	CAC-CAD	-4.80	1.33	1.41
4	D	304	9BF	CAC-CAD	-4.25	1.34	1.41
4	A	304	9BF	CAC-CAD	-4.01	1.34	1.41
4	C	303	9BF	CAF-CAE	-3.98	1.34	1.42
4	D	304	9BF	CAF-CAE	-3.91	1.34	1.42
4	B	303	9BF	CAC-CAD	-3.69	1.35	1.41
4	A	304	9BF	CAF-CAE	-3.61	1.34	1.42
4	B	303	9BF	CAF-CAE	-3.49	1.35	1.42
4	B	303	9BF	CAE-CAD	-3.05	1.34	1.42
4	D	304	9BF	CAE-CAD	-2.92	1.34	1.42
4	C	303	9BF	CAE-CAD	-2.85	1.35	1.42
4	A	304	9BF	CAE-CAD	-2.67	1.35	1.42
4	B	303	9BF	CAB-CAC	2.20	1.41	1.36

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	303	9BF	CAF-CAE-CAD	3.45	122.74	118.17
4	D	304	9BF	CAF-CAE-CAD	2.62	121.64	118.17
3	A	303	TRS	C1-C-N	2.41	115.18	107.98
4	B	303	9BF	CAF-CAE-CAD	2.41	121.36	118.17
4	B	303	9BF	CAA-CAB-CAC	-2.29	117.23	120.44

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	303	TRS	N-C-C3-O3
4	C	303	9BF	CAE-CAG-CAI-CAJ

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Mol	Chain	Res	Type	Atoms
5	A	305	GOL	C1-C2-C3-O3
6	B	304	PEG	C4-C3-O2-C2
4	D	304	9BF	CAI-CAJ-CAK-OAL
4	D	304	9BF	CAI-CAJ-CAK-CAM
3	A	303	TRS	C2-C-C3-O3
4	C	303	9BF	CAI-CAJ-CAK-CAM
4	B	303	9BF	CAI-CAJ-CAK-OAL
5	A	305	GOL	O2-C2-C3-O3
4	A	304	9BF	CAI-CAJ-CAK-OAL
4	B	303	9BF	CAI-CAJ-CAK-CAM
4	A	304	9BF	CAI-CAJ-CAK-CAM
4	A	304	9BF	CAE-CAG-CAI-CAJ
4	C	303	9BF	CAI-CAJ-CAK-OAL
4	A	304	9BF	CAN-CAG-CAI-CAJ
3	A	303	TRS	C1-C-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	304	9BF	1	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	199/227 (87%)	0.05	5 (2%) 57 56	16, 25, 45, 67	0
1	B	199/227 (87%)	0.09	4 (2%) 65 64	18, 27, 45, 63	0
1	C	199/227 (87%)	0.23	12 (6%) 21 21	21, 31, 55, 100	0
1	D	199/227 (87%)	0.18	10 (5%) 28 27	21, 29, 50, 92	0
All	All	796/908 (87%)	0.14	31 (3%) 39 38	16, 28, 48, 100	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	73	TRP	5.8
1	D	73	TRP	5.6
1	A	213	LEU	3.2
1	B	213	LEU	3.2
1	C	27	SER	3.0
1	D	213	LEU	2.7
1	D	142	PHE	2.7
1	D	27	SER	2.6
1	B	215	PHE	2.6
1	C	28	VAL	2.5
1	D	138	LEU	2.5
1	B	190	LYS	2.4
1	C	72	THR	2.4
1	C	71	THR	2.4
1	B	145	LEU	2.3
1	A	215	PHE	2.3
1	C	102	ILE	2.3
1	D	102	ILE	2.3
1	D	44	GLU	2.2
1	D	215	PHE	2.2
1	C	144	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	45	VAL	2.2
1	C	142	PHE	2.1
1	C	140	GLY	2.1
1	A	102	ILE	2.1
1	C	213	LEU	2.1
1	C	225	THR	2.1
1	A	27	SER	2.1
1	A	145	LEU	2.1
1	C	215	PHE	2.1
1	D	71	THR	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, 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(Å <sup>2</sup> )	Q<0.9
6	PEG	B	304	7/7	0.63	0.21	51,54,60,62	0
4	9BF	D	304	14/14	0.77	0.29	51,58,67,68	0
4	9BF	C	303	14/14	0.78	0.21	48,58,76,81	0
5	GOL	A	305	6/6	0.82	0.22	44,47,51,53	0
4	9BF	B	303	14/14	0.86	0.18	32,35,40,45	0
4	9BF	A	304	14/14	0.87	0.18	23,28,38,47	0
3	TRS	A	303	8/8	0.89	0.11	30,32,35,35	0
3	TRS	D	303	8/8	0.91	0.11	32,33,36,36	0
2	CA	C	302	1/1	0.92	0.17	36,36,36,36	0
2	CA	D	302	1/1	0.96	0.12	36,36,36,36	0
2	CA	C	301	1/1	0.97	0.04	24,24,24,24	0
2	CA	A	301	1/1	0.97	0.04	18,18,18,18	0
2	CA	B	301	1/1	0.97	0.04	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	CA	B	302	1/1	0.98	0.13	30,30,30,30	0
2	CA	D	301	1/1	0.98	0.03	23,23,23,23	0
2	CA	A	302	1/1	0.98	0.08	30,30,30,30	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.