



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2020 – 08:09 AM BST

PDB ID : 6D5B  
Title : Structure of Caldicellulosiruptor danielii CBM3 module of glycoside hydrolase  
WP\_045175321  
Authors : Alahuhta, P.M.; Lunin, V.V.  
Deposited on : 2018-04-19  
Resolution : 2.00 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
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

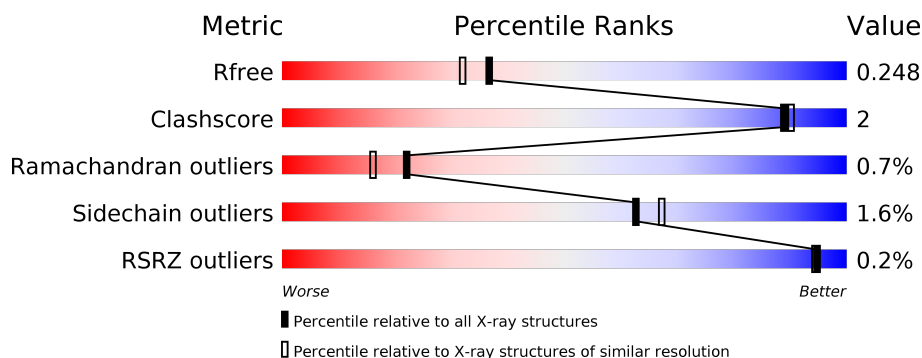
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (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  $\geq 3$ , 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	170	<div> <div>%</div> <div> <div></div> <div>83%</div> <div>7%</div> <div>10%</div> </div> </div>
1	B	170	<div> <div>%</div> <div> <div></div> <div>85%</div> <div>5%</div> <div>9%</div> </div> </div>
1	C	170	<div> <div>%</div> <div> <div></div> <div>85%</div> <div>5%</div> <div>10%</div> </div> </div>
1	D	170	<div> <div></div> <div> <div></div> <div>82%</div> <div>8%</div> <div>10%</div> </div> </div>
1	E	170	<div> <div></div> <div> <div></div> <div>83%</div> <div>6%</div> <div>10%</div> </div> </div>
1	F	170	<div> <div></div> <div> <div></div> <div>82%</div> <div>7%</div> <div>11%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	170	<div><div></div><div>84%</div><div>6%</div><div>10%</div></div>
1	H	170	<div><div></div><div>85%</div><div>5%</div><div>11%</div></div>
1	I	170	<div><div></div><div>85%</div><div>5%</div><div>10%</div></div>
1	J	170	<div><div></div><div>84%</div><div>6%</div><div>10%</div></div>
1	K	170	<div><div></div><div>%</div><div>85%</div><div>5%</div><div>10%</div></div>
1	L	170	<div><div></div><div>79%</div><div>11%</div><div>10%</div></div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 16774 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 glycoside hydrolase WP\_045175321.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	153	Total	C	N	O	S	0	1	0
			1208	762	204	241	1			
1	B	154	Total	C	N	O	S	0	0	0
			1209	763	204	241	1			
1	C	153	Total	C	N	O	S	0	1	0
			1208	762	204	241	1			
1	D	153	Total	C	N	O	S	0	0	0
			1202	759	203	239	1			
1	E	153	Total	C	N	O	S	0	2	0
			1214	765	205	243	1			
1	F	152	Total	C	N	O	S	0	0	0
			1196	756	202	237	1			
1	G	153	Total	C	N	O	S	0	1	0
			1208	762	204	241	1			
1	H	152	Total	C	N	O	S	0	0	0
			1196	756	202	237	1			
1	I	153	Total	C	N	O	S	0	0	0
			1202	759	203	239	1			
1	J	153	Total	C	N	O	S	0	3	0
			1223	771	207	244	1			
1	K	153	Total	C	N	O	S	0	0	0
			1202	759	203	239	1			
1	L	153	Total	C	N	O	S	0	2	0
			1216	766	205	244	1			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	1	Total	Ca	0	0
			1	1		
2	J	1	Total	Ca	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total 1	Ca 1	0	0
2	K	1	Total 1	Ca 1	0	0
2	E	1	Total 1	Ca 1	0	0
2	H	1	Total 1	Ca 1	0	0
2	B	1	Total 1	Ca 1	0	0
2	I	1	Total 1	Ca 1	0	0
2	C	1	Total 1	Ca 1	0	0
2	A	1	Total 1	Ca 1	0	0
2	L	1	Total 1	Ca 1	0	0
2	F	1	Total 1	Ca 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	182	Total 182	O 182	0	0
3	B	186	Total 186	O 186	0	0
3	C	172	Total 172	O 172	0	0
3	D	189	Total 189	O 189	0	0
3	E	223	Total 223	O 223	0	0
3	F	209	Total 209	O 209	0	0
3	G	181	Total 181	O 181	0	0
3	H	198	Total 198	O 198	0	0
3	I	189	Total 189	O 189	0	0

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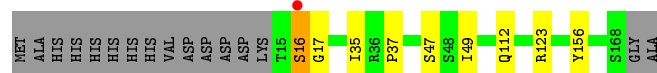
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	J	146	Total 146	O 146	0	0
3	K	215	Total 215	O 215	0	0
3	L	188	Total 188	O 188	0	0




- Molecule 1: glycoside hydrolase WP 045175321



- Chain B:  85% 5% 9%



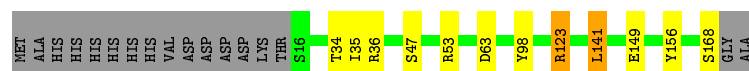
- Chain C:  %




- Chain D:  82% 8% 10%

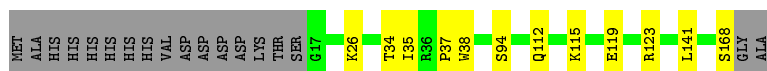


- Chain E:  83% 6% • 10%




- WORLDWIDE  
**PDB**  
PROTEIN DATA BANK

Chain F:  82% 7% 11%




- Molecule 1: glycoside hydrolase WP\_045175321

Chain G:  84% 6% 10%




- Molecule 1: glycoside hydrolase WP\_045175321

Chain H:  85% 5% 11%




- Molecule 1: glycoside hydrolase WP\_045175321

Chain I:  85% 5% 10%




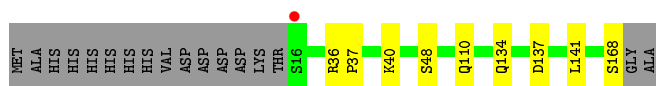
- Molecule 1: glycoside hydrolase WP\_045175321

Chain J:  84% 6% 10%




- Molecule 1: glycoside hydrolase WP\_045175321

Chain K:  85% 5% 10%



- Molecule 1: glycoside hydrolase WP\_045175321

Chain L:  79% 11% 10%





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	86.17Å 86.20Å 86.57Å 83.87° 83.93° 60.55°	Depositor
Resolution (Å)	85.91 – 2.00 58.32 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.5 (85.91-2.00) 98.5 (58.32-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.71 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.178 , 0.243 0.185 , 0.248	Depositor DCC
$R_{free}$ test set	7170 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.2	Xtriage
Anisotropy	0.249	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 37.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.034 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	16774	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.92% 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: CA

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	0.82	0/1236	0.86	1/1680 (0.1%)
1	B	0.87	1/1237 (0.1%)	0.87	0/1682
1	C	0.78	0/1236	0.87	1/1680 (0.1%)
1	D	0.86	0/1230	0.89	3/1672 (0.2%)
1	E	0.93	0/1242	0.91	5/1688 (0.3%)
1	F	0.90	0/1224	0.91	0/1664
1	G	0.85	0/1236	0.84	0/1680
1	H	0.90	0/1224	0.86	0/1664
1	I	0.83	0/1230	0.83	1/1672 (0.1%)
1	J	0.85	0/1251	0.86	0/1699
1	K	0.90	0/1230	0.89	2/1672 (0.1%)
1	L	0.89	0/1244	0.93	3/1691 (0.2%)
All	All	0.87	1/14820 (0.0%)	0.88	16/20144 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	E	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	156	TYR	CE1-CZ	-5.67	1.31	1.38

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	36	ARG	NE-CZ-NH1	6.94	123.77	120.30
1	A	123	ARG	NE-CZ-NH2	6.80	123.70	120.30
1	E	36	ARG	NE-CZ-NH1	6.61	123.60	120.30
1	L	123	ARG	NE-CZ-NH1	-6.59	117.01	120.30
1	D	53	ARG	NE-CZ-NH1	6.48	123.54	120.30
1	L	123	ARG	NE-CZ-NH2	5.89	123.25	120.30
1	D	158	ASP	CB-CG-OD1	5.76	123.49	118.30
1	E	63	ASP	CB-CG-OD1	5.72	123.45	118.30
1	I	53	ARG	NE-CZ-NH1	5.61	123.10	120.30
1	L	57	ARG	NE-CZ-NH1	-5.54	117.53	120.30
1	E	53	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	K	36	ARG	NE-CZ-NH2	-5.37	117.61	120.30
1	E	53	ARG	NE-CZ-NH2	-5.19	117.71	120.30
1	D	36	ARG	NE-CZ-NH1	5.17	122.89	120.30
1	C	66	ARG	NE-CZ-NH1	-5.17	117.72	120.30
1	E	123	ARG	NE-CZ-NH2	5.14	122.87	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	98	TYR	Peptide

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1208	0	1155	6	0
1	B	1209	0	1158	3	0
1	C	1208	0	1155	3	0
1	D	1202	0	1151	6	0
1	E	1214	0	1159	6	0
1	F	1196	0	1146	5	0
1	G	1208	0	1155	5	0
1	H	1196	0	1146	2	0
1	I	1202	0	1151	4	0
1	J	1223	0	1171	5	0
1	K	1202	0	1151	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L	1216	0	1158	9	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
3	A	182	0	0	0	0
3	B	186	0	0	1	0
3	C	172	0	0	1	0
3	D	189	0	0	0	0
3	E	223	0	0	2	0
3	F	209	0	0	1	0
3	G	181	0	0	1	0
3	H	198	0	0	1	0
3	I	189	0	0	0	0
3	J	146	0	0	1	0
3	K	215	0	0	1	0
3	L	188	0	0	1	0
All	All	16774	0	13856	53	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 2.

All (53) 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:C:97:ASP:OD2	3:C:301:HOH:O	2.05	0.73
1:F:112:GLN:HB2	1:F:115:LYS:HG3	1.80	0.63
1:K:110:GLN:NE2	3:K:303:HOH:O	2.35	0.60
1:D:155:ALA:HB3	1:D:163:TRP:HB3	1.85	0.57
1:E:47:SER:HB3	3:E:403:HOH:O	2.04	0.56
1:G:26:LYS:HG3	1:G:38:TRP:CE2	2.41	0.55
1:B:112:GLN:NE2	3:B:303:HOH:O	2.40	0.54
1:A:21:VAL:HG21	1:A:155:ALA:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:119:GLU:HG3	1:G:147:TYR:OH	2.12	0.49
1:C:155:ALA:HB3	1:C:163:TRP:HB3	1.95	0.48
1:A:155:ALA:HB3	1:A:163:TRP:HB3	1.96	0.48
1:L:112:GLN:HB2	1:L:115:LYS:HG3	1.96	0.47
1:K:134:GLN:HA	1:K:137:ASP:OD2	2.15	0.47
1:J:112:GLN:HB2	1:J:115[A]:LYS:HD3	1.97	0.46
1:L:156:TYR:CD1	1:L:156:TYR:N	2.83	0.46
1:J:66:ARG:NH2	3:J:312:HOH:O	2.49	0.45
1:L:21:VAL:HG21	1:L:155:ALA:HB2	1.99	0.45
1:E:141:LEU:HG	3:E:316:HOH:O	2.16	0.45
1:C:149:GLU:OE1	1:D:119:GLU:OE1	2.35	0.45
1:A:57:ARG:HG2	1:A:99:TYR:CD1	2.51	0.45
1:I:156:TYR:CD1	1:I:156:TYR:N	2.85	0.45
3:F:309:HOH:O	1:L:131:ASN:HB2	2.15	0.45
1:I:21:VAL:HG21	1:I:155:ALA:HB2	1.99	0.45
1:J:119:GLU:HG3	1:J:147:TYR:OH	2.17	0.44
1:J:156:TYR:HA	1:J:160:VAL:O	2.17	0.44
1:I:60:TYR:HB2	1:I:137:ASP:CG	2.38	0.44
1:B:16:SER:OG	1:B:17:GLY:N	2.50	0.44
1:L:155:ALA:HB3	1:L:163:TRP:HB3	2.01	0.43
1:L:26:LYS:HG3	1:L:38:TRP:CE2	2.54	0.43
1:E:149:GLU:OE1	1:F:119:GLU:OE1	2.37	0.43
1:G:158:ASP:HA	3:G:347:HOH:O	2.17	0.43
1:G:155:ALA:HB3	1:G:163:TRP:HB3	2.01	0.43
1:G:126:LYS:HE2	1:G:132:TYR:CE1	2.54	0.43
1:J:66:ARG:HD2	1:J:128:ASP:OD2	2.19	0.43
1:A:112:GLN:HB2	1:A:115:LYS:HE3	2.02	0.42
1:D:51:LEU:HD23	1:D:51:LEU:HA	1.93	0.42
1:D:93:VAL:HG21	1:D:167:PRO:HB2	2.02	0.42
1:E:156:TYR:N	1:E:156:TYR:CD1	2.87	0.42
1:F:35:ILE:O	1:F:123:ARG:HA	2.19	0.42
1:E:35:ILE:O	1:E:123:ARG:HA	2.20	0.41
1:A:26:LYS:HG3	1:A:38:TRP:CE2	2.56	0.41
1:D:156:TYR:CD1	1:D:156:TYR:N	2.89	0.41
1:E:34:THR:CG2	1:E:123:ARG:HB2	2.50	0.41
1:H:88:LYS:HE3	3:H:458:HOH:O	2.21	0.41
1:L:39:LEU:HD13	1:L:56:ILE:HG21	2.02	0.41
1:A:20:LYS:HG3	1:A:163:TRP:CZ3	2.56	0.41
1:D:119:GLU:HG3	1:D:147:TYR:OH	2.21	0.40
1:L:112:GLN:NE2	3:L:303:HOH:O	2.38	0.40
1:B:35:ILE:O	1:B:123:ARG:HA	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:34:THR:CG2	1:F:123:ARG:HB2	2.50	0.40
1:H:119:GLU:OE1	1:I:149:GLU:OE1	2.39	0.40
1:L:53:ARG:NE	1:L:158:ASP:OD1	2.46	0.40
1:F:26:LYS:HG3	1:F:38:TRP:CE2	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	152/170 (89%)	146 (96%)	5 (3%)	1 (1%)	22	16
1	B	152/170 (89%)	145 (95%)	5 (3%)	2 (1%)	12	6
1	C	152/170 (89%)	146 (96%)	5 (3%)	1 (1%)	22	16
1	D	151/170 (89%)	146 (97%)	4 (3%)	1 (1%)	22	16
1	E	153/170 (90%)	146 (95%)	7 (5%)	0	100	100
1	F	150/170 (88%)	147 (98%)	1 (1%)	2 (1%)	12	6
1	G	152/170 (89%)	147 (97%)	4 (3%)	1 (1%)	22	16
1	H	150/170 (88%)	145 (97%)	4 (3%)	1 (1%)	22	16
1	I	151/170 (89%)	148 (98%)	2 (1%)	1 (1%)	22	16
1	J	154/170 (91%)	149 (97%)	5 (3%)	0	100	100
1	K	151/170 (89%)	149 (99%)	1 (1%)	1 (1%)	22	16
1	L	153/170 (90%)	149 (97%)	3 (2%)	1 (1%)	22	16
All	All	1821/2040 (89%)	1763 (97%)	46 (2%)	12 (1%)	22	16

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	16	SER
1	F	94	SER
1	A	37	PRO
1	B	37	PRO
1	G	37	PRO
1	H	37	PRO
1	L	37	PRO
1	F	37	PRO
1	C	37	PRO
1	I	37	PRO
1	D	37	PRO
1	K	37	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	132/145 (91%)	132 (100%)	0	100	100
1	B	132/145 (91%)	130 (98%)	2 (2%)	65	69
1	C	132/145 (91%)	130 (98%)	2 (2%)	65	69
1	D	131/145 (90%)	129 (98%)	2 (2%)	65	69
1	E	133/145 (92%)	131 (98%)	2 (2%)	65	69
1	F	130/145 (90%)	128 (98%)	2 (2%)	65	69
1	G	132/145 (91%)	131 (99%)	1 (1%)	81	86
1	H	130/145 (90%)	125 (96%)	5 (4%)	33	31
1	I	131/145 (90%)	130 (99%)	1 (1%)	81	86
1	J	134/145 (92%)	132 (98%)	2 (2%)	65	69
1	K	131/145 (90%)	127 (97%)	4 (3%)	40	40
1	L	133/145 (92%)	131 (98%)	2 (2%)	65	69
All	All	1581/1740 (91%)	1556 (98%)	25 (2%)	62	67

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	47	SER
1	B	49	ILE
1	C	47	SER
1	C	141	LEU
1	D	40	LYS
1	D	141	LEU
1	E	141	LEU
1	E	168	SER
1	F	141	LEU
1	F	168	SER
1	G	141	LEU
1	H	47	SER
1	H	69	SER
1	H	115	LYS
1	H	141	LEU
1	H	168	SER
1	I	141	LEU
1	J	94	SER
1	J	141	LEU
1	K	40	LYS
1	K	48	SER
1	K	141	LEU
1	K	168	SER
1	L	141	LEU
1	L	168	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	76	GLN
1	F	18	GLN
1	L	29	ASN

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 12 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

## 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	153/170 (90%)	-0.51	1 (0%) 87 87	19, 27, 39, 71	0
1	B	154/170 (90%)	-0.48	1 (0%) 89 88	19, 27, 40, 71	0
1	C	153/170 (90%)	-0.41	1 (0%) 87 87	21, 30, 44, 79	0
1	D	153/170 (90%)	-0.50	0 100 100	16, 26, 38, 64	0
1	E	153/170 (90%)	-0.54	0 100 100	16, 23, 35, 58	0
1	F	152/170 (89%)	-0.51	0 100 100	17, 25, 36, 50	0
1	G	153/170 (90%)	-0.36	0 100 100	19, 29, 46, 66	0
1	H	152/170 (89%)	-0.49	0 100 100	17, 24, 39, 50	0
1	I	153/170 (90%)	-0.53	0 100 100	20, 27, 43, 67	0
1	J	153/170 (90%)	-0.47	0 100 100	20, 29, 49, 64	0
1	K	153/170 (90%)	-0.46	1 (0%) 87 87	16, 23, 39, 67	0
1	L	153/170 (90%)	-0.49	0 100 100	17, 25, 39, 60	0
All	All	1835/2040 (89%)	-0.48	4 (0%) 95 94	16, 26, 41, 79	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	16	SER	2.3
1	C	16	SER	2.2
1	B	16	SER	2.1
1	A	16	SER	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 monosaccharides in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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
2	CA	J	201	1/1	0.96	0.06	36,36,36,36	0
2	CA	G	201	1/1	0.97	0.06	32,32,32,32	0
2	CA	L	201	1/1	0.98	0.07	30,30,30,30	0
2	CA	D	201	1/1	0.98	0.06	25,25,25,25	0
2	CA	C	201	1/1	0.98	0.06	33,33,33,33	0
2	CA	A	201	1/1	0.99	0.06	31,31,31,31	0
2	CA	I	201	1/1	0.99	0.05	33,33,33,33	0
2	CA	B	201	1/1	0.99	0.05	29,29,29,29	0
2	CA	K	201	1/1	1.00	0.06	23,23,23,23	0
2	CA	F	201	1/1	1.00	0.05	22,22,22,22	0
2	CA	E	201	1/1	1.00	0.05	21,21,21,21	0
2	CA	H	201	1/1	1.00	0.07	23,23,23,23	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.