



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 08:23 AM UTC

PDB ID : 8FYM / pdb\_00008fym  
Title : Crystal structure of Fab235 in complex with MPER peptide  
Authors : Tan, K.; Kim, M.; Reinherz, E.L.  
Deposited on : 2023-01-26  
Resolution : 2.45 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
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) : 2.49

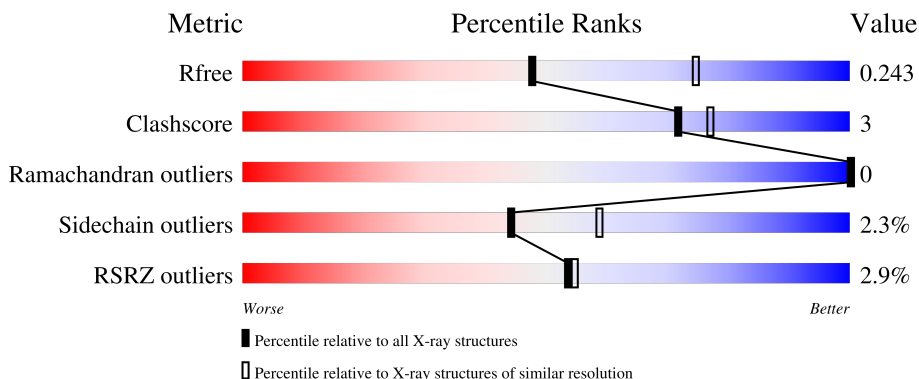
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.45 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.



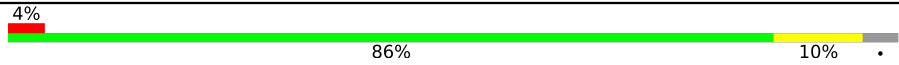

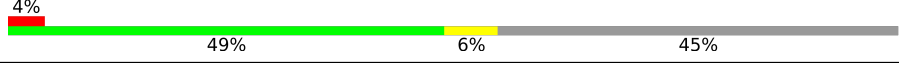
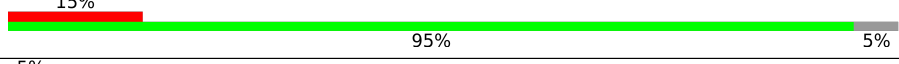
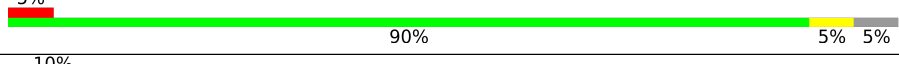
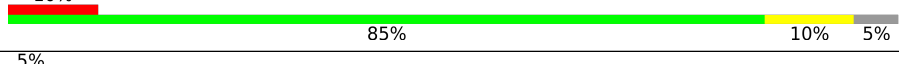
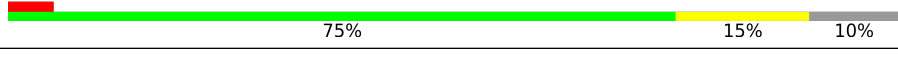
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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	220	92% 8%
1	D	220	87% 12%
1	G	220	46% 5% 48%
1	L	220	90% 10%
2	B	228	90% 6%

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Mol	Chain	Length	Quality of chain
2	E	228	 <p>4% 86% 10%</p>
2	H	228	 <p>1% 87% 11%</p>
2	I	228	 <p>4% 49% 6% 45%</p>
3	C	20	 <p>15% 95% 5%</p>
3	F	20	 <p>5% 90% 5% 5%</p>
3	J	20	 <p>10% 85% 10% 5%</p>
3	P	20	 <p>5% 75% 15% 10%</p>

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 13145 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 Fab235, L chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	L	220	Total 1708	C 1072	N 282	O 346	S 8	0	1	0
1	A	220	Total 1699	C 1067	N 280	O 344	S 8	0	0	0
1	D	219	Total 1693	C 1064	N 279	O 343	S 7	0	0	0
1	G	114	Total 878	C 557	N 141	O 175	S 5	0	0	0

- Molecule 2 is a protein called Fab235, H chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	225	Total 1686	C 1074	N 273	O 334	S 5	0	0	0
2	B	221	Total 1658	C 1059	N 268	O 326	S 5	0	0	0
2	E	220	Total 1654	C 1056	N 267	O 326	S 5	0	0	0
2	I	126	Total 968	C 619	N 155	O 191	S 3	0	0	0

- Molecule 3 is a protein called ALA-SER-LEU-TRP-ASN-TRP-PHE-ASN-ILE-THR-ASN-TRP-LEU-TRP-TYR-ILE-LYS-LYS-LYS.

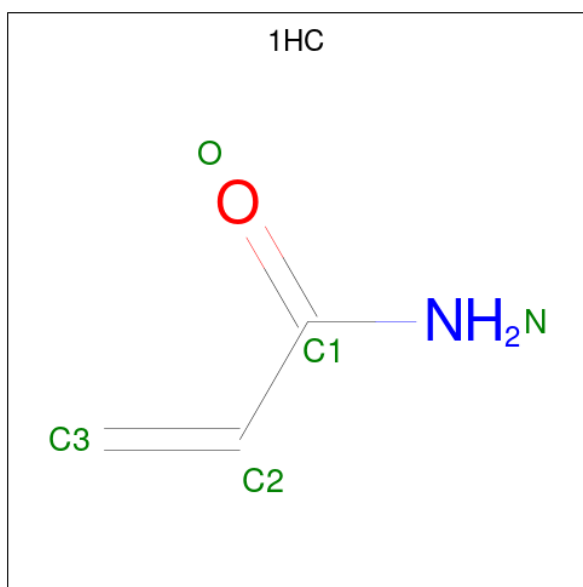
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	P	18	Total 176	C 123	N 28	O 25	0	0	0
3	C	19	Total 181	C 126	N 29	O 26	0	0	0
3	F	19	Total 181	C 126	N 29	O 26	0	0	0
3	J	19	Total 181	C 126	N 29	O 26	0	0	0

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula:  $C_3H_8O_3$ ).



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

- Molecule 5 is prop-2-enamide (CCD ID: 1HC) (formula:  $C_3H_5NO$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			5	3	1	1		
5	I	1	Total	C	N	O	0	0
			5	3	1	1		
5	J	1	Total	C	N	O	0	0
			5	3	1	1		

- Molecule 6 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	E	2	Total	Cl	0	0
			2	2		
6	G	1	Total	Cl	0	0
			1	1		
6	I	1	Total	Cl	0	0
			1	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	L	76	Total	O	0	0
			76	76		
7	H	91	Total	O	0	0
			91	91		
7	P	4	Total	O	0	0
			4	4		

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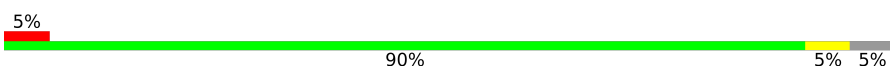
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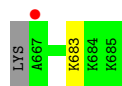
<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
7	A	71	Total 71	O 71	0	0
7	B	78	Total 78	O 78	0	0
7	C	4	Total 4	O 4	0	0
7	D	24	Total 24	O 24	0	0
7	E	29	Total 29	O 29	0	0
7	F	8	Total 8	O 8	0	0
7	G	21	Total 21	O 21	0	0
7	I	22	Total 22	O 22	0	0
7	J	5	Total 5	O 5	0	0






- Molecule 3: ALA-SER-LEU-TRP-ASN-TRP-PHE-ASN-ILE-THR-ASN-TRP-LEU-TRP-TYR-ILE-LYS-LYS-LYS

Chain F: 



- Molecule 3: ALA-SER-LEU-TRP-ASN-TRP-PHE-ASN-ILE-THR-ASN-TRP-LEU-TRP-TYR-ILE-LYS-LYS-LYS

Chain J: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	43.48Å 108.30Å 121.21Å 85.63° 82.95° 85.59°	Depositor
Resolution (Å)	47.95 – 2.45 47.95 – 2.45	Depositor EDS
% Data completeness (in resolution range)	95.7 (47.95-2.45) 95.7 (47.95-2.45)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.40 (at 2.45Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.200 , 0.243 0.200 , 0.243	Depositor DCC
$R_{free}$ test set	3853 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.4	Xtrriage
Anisotropy	0.194	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 41.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	13145	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% 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, 1HC, CL

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	0.08	0/1736	0.27	0/2355
1	D	0.08	0/1730	0.25	0/2347
1	G	0.09	0/898	0.27	0/1217
1	L	0.08	0/1745	0.25	0/2367
2	B	0.10	0/1703	0.30	0/2326
2	E	0.10	0/1699	0.28	0/2320
2	H	0.10	0/1732	0.29	0/2365
2	I	0.11	0/995	0.29	0/1356
3	C	0.07	0/190	0.19	0/258
3	F	0.11	0/190	0.28	0/258
3	J	0.09	0/190	0.23	0/258
3	P	0.08	0/185	0.19	0/251
All	All	0.09	0/12993	0.27	0/17678

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	1699	0	1651	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1693	0	1646	12	0
1	G	878	0	854	7	0
1	L	1708	0	1658	12	0
2	B	1658	0	1609	8	0
2	E	1654	0	1610	9	0
2	H	1686	0	1644	14	0
2	I	968	0	922	7	0
3	C	181	0	175	0	0
3	F	181	0	175	1	0
3	J	181	0	175	1	0
3	P	176	0	170	2	0
4	A	6	0	8	0	0
4	B	6	0	8	1	0
4	D	6	0	8	0	0
4	G	6	0	8	0	0
4	L	6	0	8	0	0
5	B	5	0	5	0	0
5	I	5	0	5	1	0
5	J	5	0	5	0	0
6	E	2	0	0	0	0
6	G	1	0	0	0	0
6	I	1	0	0	1	0
7	A	71	0	0	0	0
7	B	78	0	0	0	0
7	C	4	0	0	0	0
7	D	24	0	0	0	0
7	E	29	0	0	0	0
7	F	8	0	0	1	0
7	G	21	0	0	0	0
7	H	91	0	0	0	0
7	I	22	0	0	0	0
7	J	5	0	0	0	0
7	L	76	0	0	1	0
7	P	4	0	0	0	0
All	All	13145	0	12344	82	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.

The worst 5 of 82 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)
2:B:87:THR:HG22	2:B:89:ASP:H	1.49	0.76
1:L:43:GLN:HB2	1:L:53:LEU:HD11	1.72	0.71
1:L:45:LYS:NZ	1:L:87:GLU:O	2.26	0.68
1:L:129:GLU:OE2	2:H:219:LYS:NZ	2.24	0.64
1:A:43:GLN:HB2	1:A:53:LEU:HD11	1.79	0.63

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	218/220 (99%)	212 (97%)	6 (3%)	0	100	100
1	D	217/220 (99%)	211 (97%)	6 (3%)	0	100	100
1	G	112/220 (51%)	107 (96%)	5 (4%)	0	100	100
1	L	219/220 (100%)	215 (98%)	4 (2%)	0	100	100
2	B	217/228 (95%)	212 (98%)	5 (2%)	0	100	100
2	E	216/228 (95%)	208 (96%)	8 (4%)	0	100	100
2	H	223/228 (98%)	219 (98%)	4 (2%)	0	100	100
2	I	124/228 (54%)	120 (97%)	4 (3%)	0	100	100
3	C	17/20 (85%)	16 (94%)	1 (6%)	0	100	100
3	F	17/20 (85%)	16 (94%)	1 (6%)	0	100	100
3	J	17/20 (85%)	16 (94%)	1 (6%)	0	100	100
3	P	16/20 (80%)	15 (94%)	1 (6%)	0	100	100
All	All	1613/1872 (86%)	1567 (97%)	46 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	195/195 (100%)	194 (100%)	1 (0%)	81	87
1	D	194/195 (100%)	187 (96%)	7 (4%)	31	45
1	G	99/195 (51%)	97 (98%)	2 (2%)	48	63
1	L	196/195 (100%)	193 (98%)	3 (2%)	57	70
2	B	185/193 (96%)	181 (98%)	4 (2%)	45	60
2	E	186/193 (96%)	180 (97%)	6 (3%)	34	49
2	H	190/193 (98%)	187 (98%)	3 (2%)	55	69
2	I	104/193 (54%)	100 (96%)	4 (4%)	29	43
3	C	18/19 (95%)	18 (100%)	0	100	100
3	F	18/19 (95%)	18 (100%)	0	100	100
3	J	18/19 (95%)	17 (94%)	1 (6%)	19	27
3	P	18/19 (95%)	17 (94%)	1 (6%)	19	27
All	All	1421/1628 (87%)	1389 (98%)	32 (2%)	44	59

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	75	SER
2	I	88	SER
1	D	9	SER
2	B	148	LEU
2	I	123	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	174	HIS
1	G	27	GLN
1	G	35	GLN
2	B	202	GLN

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Mol	Chain	Res	Type
2	B	209	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 4 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	GOL	D	301	-	5,5,5	0.96	0	5,5,5	0.98	0
4	GOL	L	301	-	5,5,5	0.96	0	5,5,5	1.05	0
5	1HC	B	301	-	4,4,4	0.33	0	4,4,4	0.34	0
5	1HC	I	302	-	4,4,4	0.33	0	4,4,4	0.30	0
4	GOL	G	302	-	5,5,5	0.95	0	5,5,5	1.07	0
4	GOL	A	301	-	5,5,5	0.94	0	5,5,5	1.02	0
4	GOL	B	302	-	5,5,5	0.90	0	5,5,5	1.11	0
5	1HC	J	701	-	4,4,4	0.33	0	4,4,4	0.29	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	D	301	-	-	3/4/4/4	-
4	GOL	L	301	-	-	0/4/4/4	-
5	1HC	B	301	-	-	2/2/2/2	-
5	1HC	I	302	-	-	0/2/2/2	-
4	GOL	G	302	-	-	2/4/4/4	-
4	GOL	A	301	-	-	0/4/4/4	-
4	GOL	B	302	-	-	2/4/4/4	-
5	1HC	J	701	-	-	0/2/2/2	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	302	GOL	C1-C2-C3-O3
5	B	301	1HC	O-C1-C2-C3
4	B	302	GOL	O2-C2-C3-O3
4	D	301	GOL	C1-C2-C3-O3
4	G	302	GOL	O1-C1-C2-C3

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	I	302	1HC	1	0
4	B	302	GOL	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 [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	220/220 (100%)	0.02	3 (1%) 73 75	24, 38, 54, 89	0
1	D	219/220 (99%)	0.23	2 (0%) 81 82	25, 45, 67, 81	0
1	G	114/220 (51%)	0.49	7 (6%) 27 24	27, 51, 80, 97	0
1	L	220/220 (100%)	0.01	2 (0%) 81 82	20, 34, 54, 84	1 (0%)
2	B	221/228 (96%)	-0.05	7 (3%) 50 51	21, 31, 53, 97	0
2	E	220/228 (96%)	0.62	10 (4%) 38 37	23, 54, 90, 108	0
2	H	225/228 (98%)	-0.10	2 (0%) 81 82	19, 30, 44, 79	0
2	I	126/228 (55%)	0.48	8 (6%) 26 23	24, 43, 82, 113	0
3	C	19/20 (95%)	0.60	3 (15%) 5 3	23, 30, 87, 89	0
3	F	19/20 (95%)	0.10	1 (5%) 32 30	21, 26, 58, 70	0
3	J	19/20 (95%)	-0.07	2 (10%) 11 9	23, 28, 71, 82	0
3	P	18/20 (90%)	0.12	1 (5%) 30 27	23, 31, 64, 91	0
All	All	1640/1872 (87%)	0.18	48 (2%) 53 55	19, 37, 76, 113	1 (0%)

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	667	ALA	6.3
2	E	144	GLY	5.4
2	E	145	THR	4.8
1	L	220	CYS	4.7
2	E	138	SER	4.1

### 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 [i](#)

There are no oligosaccharides 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
4	GOL	B	302	6/6	0.83	0.14	38,39,43,45	0
5	1HC	I	302	5/5	0.83	0.18	50,56,61,61	0
5	1HC	B	301	5/5	0.84	0.14	34,34,39,40	0
4	GOL	A	301	6/6	0.86	0.16	40,43,49,51	0
5	1HC	J	701	5/5	0.90	0.16	43,43,44,46	0
4	GOL	D	301	6/6	0.91	0.11	35,36,45,49	0
4	GOL	L	301	6/6	0.91	0.12	43,46,48,48	0
4	GOL	G	302	6/6	0.94	0.09	36,39,42,45	0
6	CL	G	301	1/1	0.94	0.08	56,56,56,56	0
6	CL	E	302	1/1	0.97	0.15	50,50,50,50	0
6	CL	E	301	1/1	0.99	0.05	27,27,27,27	0
6	CL	I	301	1/1	0.99	0.07	23,23,23,23	0

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

There are no such residues in this entry.