wwPDB X-ray Structure Validation Summary Report (i)

Aug 19, 2023 – 08:13 PM EDT

PDB ID	:	2GTW
Title	:	Human Class I MHC HLA-A2 in complex with the nonameric Melan-A/MA RT-1(27-35) peptide having A27L substitution
Authors	:	Borbulevych, O.Y.; Baker, B.M.
Deposited on	:	2006-04-28
Resolution	:	1.55 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

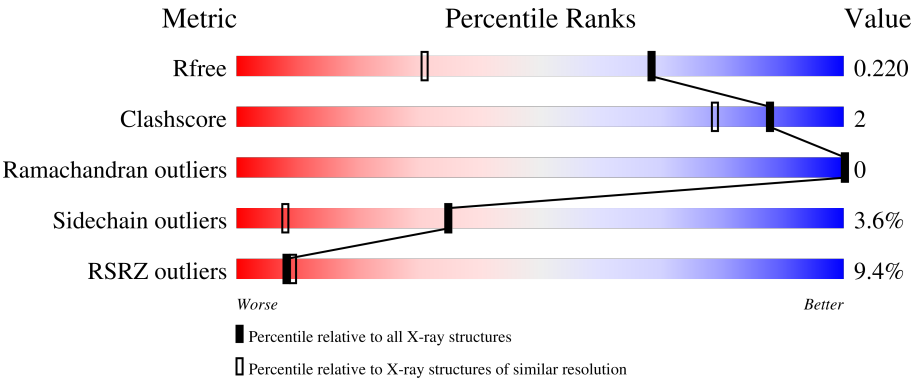
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.55 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	2556 (1.56-1.52)
Clashscore	141614	2634 (1.56-1.52)
Ramachandran outliers	138981	2580 (1.56-1.52)
Sidechain outliers	138945	2577 (1.56-1.52)
RSRZ outliers	127900	2524 (1.56-1.52)

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 >=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 <=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	275	9% 92% 7%
1	D	275	10% 92% 7%
2	B	100	8% 95% 5%
2	E	100	8% 95%
3	C	9	11% 89% 11%

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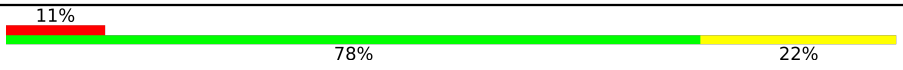
Mol	Chain	Length	Quality of chain
3	F	9	

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 7073 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 HLA-A*0201 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	275	Total	C	N	O	S	0	5	0
			2269	1418	413	428	10			
1	D	275	Total	C	N	O	S	0	7	0
			2271	1418	414	430	9			

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	100	Total	C	N	O	S	0	2	0
			843	537	141	160	5			
2	E	100	Total	C	N	O	S	0	2	0
			846	538	144	159	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P61769
E	0	MET	-	initiating methionine	UNP P61769

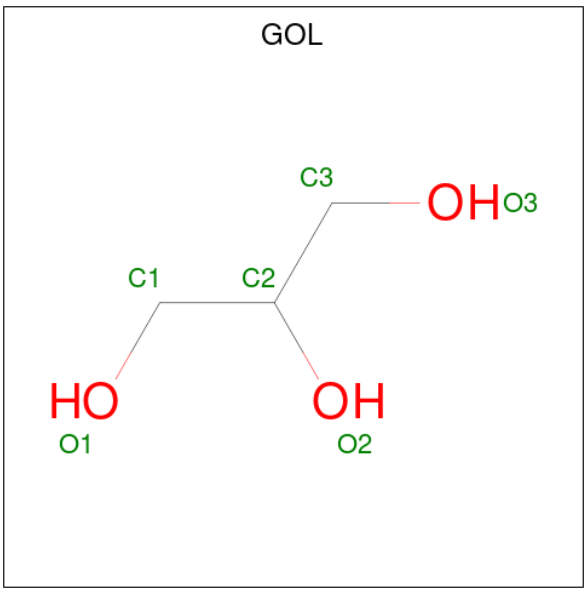
- Molecule 3 is a protein called octapeptide from Melan-A/MART-1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	0	1	0
			64	44	9	11			
3	F	9	Total	C	N	O	0	1	0
			64	44	9	11			

There are 2 discrepancies between the modelled and reference sequences:

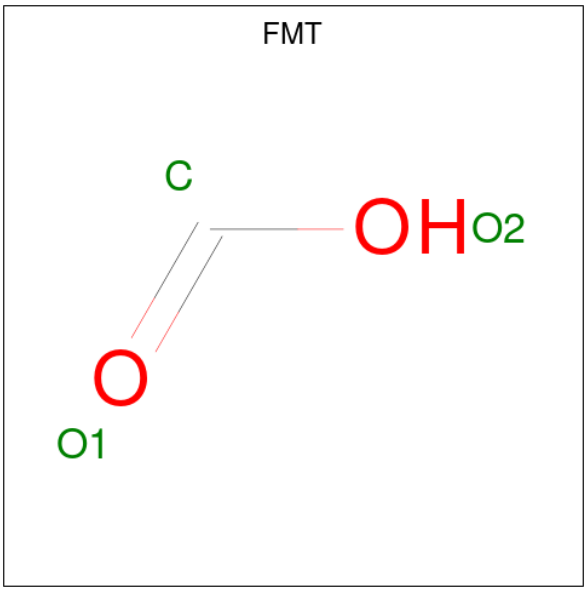
Chain	Residue	Modelled	Actual	Comment	Reference
C	1	LEU	ALA	engineered mutation	UNP Q16655
F	1	LEU	ALA	engineered mutation	UNP Q16655

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 5 is FORMIC ACID (three-letter code: FMT) (formula: CH_2O_2).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 3 1 2	0	0
5	A	1	Total C O 3 1 2	0	0
5	B	1	Total C O 3 1 2	0	0
5	D	1	Total C O 3 1 2	0	0

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total Na 1 1	0	0
6	E	1	Total Na 1 1	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	224	Total O 224 224	0	0
7	B	101	Total O 101 101	0	0
7	C	9	Total O 9 9	0	0

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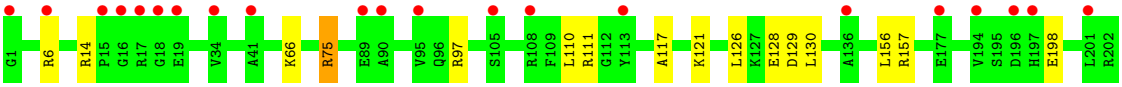
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	D	225	Total O 225 225	0	0
7	E	104	Total O 104 104	0	0
7	F	9	Total O 9 9	0	0

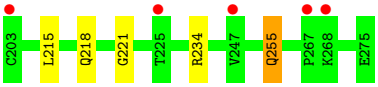
3 Residue-property plots (i)

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: HLA-A*0201 heavy chain

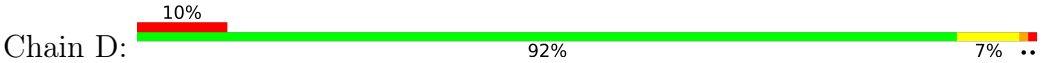
Chain A:

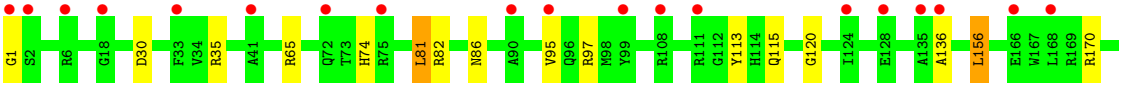


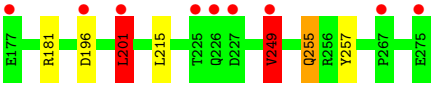


• Molecule 1: HLA-A*0201 heavy chain

Chain D:

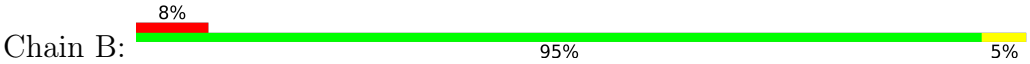


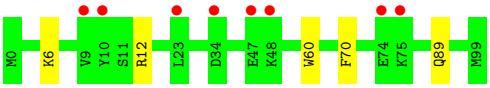




• Molecule 2: Beta-2-microglobulin

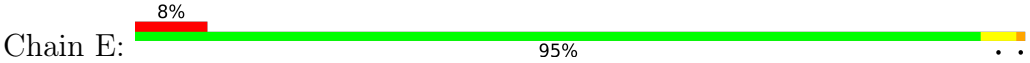
Chain B:

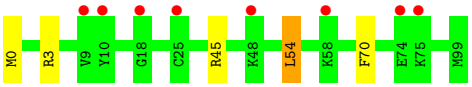




• Molecule 2: Beta-2-microglobulin

Chain E:



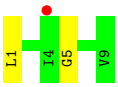


• Molecule 3: octapeptide from Melan-A/MART-1

Chain C:

• Molecule 3: octapeptide from Melan-A/MART-1

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	58.31Å 84.27Å 84.29Å 90.00° 90.11° 90.00°	Depositor
Resolution (Å)	20.00 – 1.55 19.87 – 1.55	Depositor EDS
% Data completeness (in resolution range)	93.2 (20.00-1.55) 93.2 (19.87-1.55)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.21 (at 1.55Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, R_{free}	0.181 , 0.218 0.184 , 0.220	Depositor DCC
R_{free} test set	5541 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	16.0	Xtriage
Anisotropy	0.124	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 41.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.006 for -h,l,k 0.016 for -h,-l,-k 0.119 for h,-k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	7073	wwPDB-VP
Average B, all atoms (Å^2)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.22% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, FMT, GOL

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	0.77	0/2354	0.89	4/3193 (0.1%)
1	D	0.76	0/2363	0.92	6/3207 (0.2%)
2	B	0.73	0/874	0.86	1/1180 (0.1%)
2	E	0.75	0/879	0.87	1/1186 (0.1%)
3	C	0.80	0/67	1.08	0/89
3	F	0.79	0/67	0.97	0/89
All	All	0.76	0/6604	0.90	12/8944 (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	D	0	1

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	75	ARG	NE-CZ-NH2	9.30	124.95	120.30
1	D	201	LEU	CB-CG-CD1	6.79	122.55	111.00
2	E	54	LEU	CA-CB-CG	6.26	129.70	115.30
1	D	81	LEU	CB-CG-CD1	6.15	121.46	111.00
1	A	75	ARG	NE-CZ-NH1	-6.04	117.28	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	136[B]	ALA	Peptide

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	2269	0	2122	12	0
1	D	2271	0	2117	12	0
2	B	843	0	807	1	0
2	E	846	0	811	2	0
3	C	64	0	80	1	0
3	F	64	0	80	2	0
4	A	12	0	16	0	0
4	B	6	0	8	0	0
4	D	12	0	16	1	0
5	A	6	0	2	1	0
5	B	3	0	1	0	0
5	D	3	0	1	0	0
6	B	1	0	0	0	0
6	E	1	0	0	0	0
7	A	224	0	0	4	0
7	B	101	0	0	0	0
7	C	9	0	0	0	0
7	D	225	0	0	2	0
7	E	104	0	0	1	0
7	F	9	0	0	0	0
All	All	7073	0	6061	25	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.

The worst 5 of 25 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:255:GLN:H	1:A:255:GLN:HE21	1.41	0.67
2:E:45:ARG:NH1	7:E:3096:HOH:O	2.21	0.65
1:A:234:ARG:HH12	5:A:2003:FMT:C	2.10	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:ARG:NH1	7:A:2042:HOH:O	2.33	0.62
1:D:201:LEU:HD22	1:D:249:VAL:HG21	1.86	0.58

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	278/275 (101%)	272 (98%)	6 (2%)	0	100	100
1	D	280/275 (102%)	274 (98%)	6 (2%)	0	100	100
2	B	99/100 (99%)	98 (99%)	1 (1%)	0	100	100
2	E	99/100 (99%)	98 (99%)	1 (1%)	0	100	100
3	C	8/9 (89%)	8 (100%)	0	0	100	100
3	F	8/9 (89%)	8 (100%)	0	0	100	100
All	All	772/768 (100%)	758 (98%)	14 (2%)	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	236/231 (102%)	228 (97%)	8 (3%)	37	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	D	237/231 (103%)	225 (95%)	12 (5%)	24 3
2	B	97/95 (102%)	94 (97%)	3 (3%)	40 11
2	E	97/95 (102%)	93 (96%)	4 (4%)	30 5
3	C	7/6 (117%)	7 (100%)	0	100 100
3	F	7/6 (117%)	7 (100%)	0	100 100
All	All	681/664 (103%)	654 (96%)	27 (4%)	35 6

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	86[B]	ASN
1	D	156	LEU
2	E	0[B]	MET
1	D	115	GLN
1	D	196	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	218	GLN
1	A	255	GLN
1	D	197	HIS
1	D	255	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 11 ligands modelled in this entry, 2 are monoatomic - leaving 9 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	B	1005	-	5,5,5	0.49	0	5,5,5	1.60	2 (40%)
4	GOL	A	1003	-	5,5,5	0.19	0	5,5,5	0.99	0
4	GOL	D	1002	-	5,5,5	0.32	0	5,5,5	0.91	0
4	GOL	A	1001	-	5,5,5	0.32	0	5,5,5	0.64	0
5	FMT	A	2003	-	2,2,2	0.97	0	1,1,1	0.12	0
5	FMT	D	2001	-	2,2,2	0.45	0	1,1,1	0.09	0
5	FMT	B	2002	-	2,2,2	0.62	0	1,1,1	0.12	0
4	GOL	D	1004	-	5,5,5	0.35	0	5,5,5	0.41	0
5	FMT	A	2004	-	2,2,2	0.66	0	1,1,1	0.05	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	B	1005	-	-	2/4/4/4	-
4	GOL	A	1003	-	-	1/4/4/4	-
4	GOL	D	1002	-	-	2/4/4/4	-
4	GOL	A	1001	-	-	0/4/4/4	-
4	GOL	D	1004	-	-	2/4/4/4	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	1005	GOL	O1-C1-C2	2.87	123.94	110.20
4	B	1005	GOL	O2-C2-C1	2.10	118.38	109.12

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1005	GOL	C1-C2-C3-O3
4	D	1002	GOL	C1-C2-C3-O3
4	D	1004	GOL	C1-C2-C3-O3
4	D	1002	GOL	O2-C2-C3-O3
4	D	1004	GOL	O2-C2-C3-O3

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	2003	FMT	1	0
4	D	1004	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

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^{th} 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^2)	Q<0.9
1	A	275/275 (100%)	0.78	26 (9%) 8 9	15, 20, 28, 37	0
1	D	275/275 (100%)	0.72	28 (10%) 6 7	15, 20, 28, 33	0
2	B	100/100 (100%)	0.69	8 (8%) 12 14	16, 20, 28, 34	0
2	E	100/100 (100%)	0.72	8 (8%) 12 14	15, 20, 28, 32	0
3	C	9/9 (100%)	1.00	1 (11%) 5 5	22, 24, 27, 27	0
3	F	9/9 (100%)	0.93	1 (11%) 5 5	21, 23, 24, 28	0
All	All	768/768 (100%)	0.74	72 (9%) 8 9	15, 20, 28, 37	0

The worst 5 of 72 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	GLY	8.7
2	B	48	LYS	7.0
1	A	16	GLY	6.4
1	D	136[A]	ALA	5.9
1	D	196	ASP	5.8

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no 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^{th} 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^2)	Q<0.9
5	FMT	D	2001	3/3	0.78	0.20	31,31,35,38	0
5	FMT	A	2003	3/3	0.79	0.18	26,26,27,29	0
4	GOL	D	1004	6/6	0.81	0.30	33,40,42,46	0
4	GOL	A	1003	6/6	0.82	0.18	40,41,41,43	0
5	FMT	B	2002	3/3	0.83	0.14	31,31,32,33	3
4	GOL	B	1005	6/6	0.83	0.26	25,32,33,38	0
4	GOL	D	1002	6/6	0.87	0.20	30,32,34,35	0
6	NA	E	3006	1/1	0.90	0.35	30,30,30,30	0
5	FMT	A	2004	3/3	0.92	0.14	26,26,30,33	0
4	GOL	A	1001	6/6	0.96	0.21	24,27,29,29	0
6	NA	B	3005	1/1	0.97	0.23	32,32,32,32	0

6.5 Other polymers (i)

There are no such residues in this entry.