wwPDB X-ray Structure Validation Summary Report (i)

Jun 25, 2024 – 11:29 AM EDT

PDB ID	:	6Q3S
Title	:	Engineered Human HLA_A2 MHC Class I molecule in complex with TCR and SV9 peptide
Authors	:	Meijers, R.; Anjanappa, R.; Springer, S.; Garcia-Alai, M.
Deposited on	:	2018-12-04
Resolution	:	2.50 Å(reported)

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

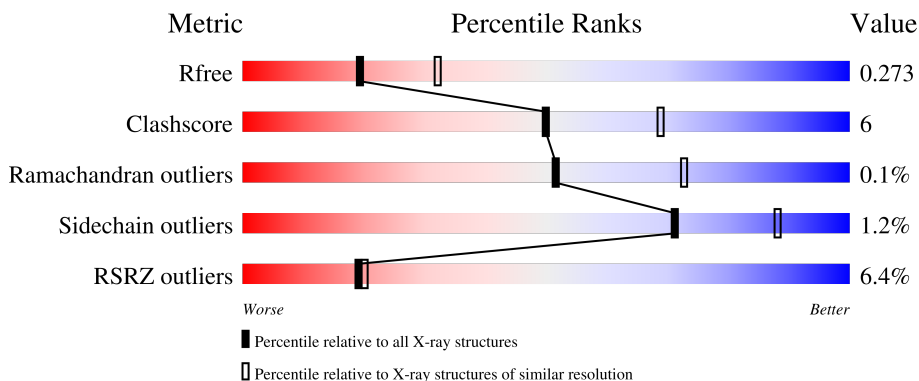|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.50 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	Percentile Ranks	Value
Rfree		0.273
Clashscore		6
Ramachandran outliers		0.1%
Sidechain outliers		1.2%
RSRZ outliers		6.4%

Worse   *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	276	5% / 87% / 12% / ·
2	B	100	6% / 84% / 16%
3	C	9	11% / 89% / 11%
4	D	207	10% / 81% / 17% / ·
5	E	241	4% / 81% / 18% / ·

2 Entry composition ⓘ

There are 8 unique types of molecules in this entry. The entry contains 6626 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 class I histocompatibility antigen, A-2 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	274	Total 2232	C 1392	N 408	O 421	S 11	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	84	CYS	TYR	conflict	UNP P01892
A	139	CYS	ALA	conflict	UNP P01892

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	100	Total 837	C 533	N 141	O 159	S 4	0	0	0

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 3 is a protein called SER-LEU-LEU-MET-TRP-ILE-THR-GLN-VAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	9	Total 76	C 51	N 11	O 13	S 1	0	0	0

- Molecule 4 is a protein called T cell receptor alpha variable 21,T-cell receptor, sp3.4 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	203	Total 1556	C 968	N 262	O 319	S 7	0	0	0

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	94	PRO	-	linker	UNP A0A0B4J279
D	95	THR	-	linker	UNP A0A0B4J279
D	96	SER	-	linker	UNP A0A0B4J279
D	97	GLY	-	linker	UNP A0A0B4J279
D	98	GLY	-	linker	UNP A0A0B4J279
D	99	SER	-	linker	UNP A0A0B4J279
D	100	TYR	-	linker	UNP A0A0B4J279
D	101	ILE	-	linker	UNP A0A0B4J279
D	102	PRO	-	linker	UNP A0A0B4J279
D	103	THR	-	linker	UNP A0A0B4J279
D	104	PHE	-	linker	UNP A0A0B4J279
D	105	GLY	-	linker	UNP A0A0B4J279
D	106	ARG	-	linker	UNP A0A0B4J279
D	107	GLY	-	linker	UNP A0A0B4J279
D	108	THR	-	linker	UNP A0A0B4J279
D	109	SER	-	linker	UNP A0A0B4J279
D	110	LEU	-	linker	UNP A0A0B4J279
D	111	ILE	-	linker	UNP A0A0B4J279
D	112	VAL	-	linker	UNP A0A0B4J279
D	113	HIS	-	linker	UNP A0A0B4J279
D	114	PRO	-	linker	UNP A0A0B4J279
D	115	TYR	-	linker	UNP A0A0B4J279

- Molecule 5 is a protein called T cell receptor beta variable 6-5,Human nkt tcr beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	E	241	1902	1196	327	370	9	0	0	0

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	95	VAL	-	linker	UNP A0A0K0K1A5
E	96	GLY	-	linker	UNP A0A0K0K1A5
E	97	ASN	-	linker	UNP A0A0K0K1A5
E	98	THR	-	linker	UNP A0A0K0K1A5
E	99	GLY	-	linker	UNP A0A0K0K1A5
E	100	GLU	-	linker	UNP A0A0K0K1A5
E	101	LEU	-	linker	UNP A0A0K0K1A5
E	102	PHE	-	linker	UNP A0A0K0K1A5
E	103	PHE	-	linker	UNP A0A0K0K1A5

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Chain	Residue	Modelled	Actual	Comment	Reference
E	104	GLY	-	linker	UNP A0A0K0K1A5
E	105	GLU	-	linker	UNP A0A0K0K1A5
E	106	GLY	-	linker	UNP A0A0K0K1A5
E	107	SER	-	linker	UNP A0A0K0K1A5
E	108	ARG	-	linker	UNP A0A0K0K1A5
E	109	LEU	-	linker	UNP A0A0K0K1A5
E	110	THR	-	linker	UNP A0A0K0K1A5
E	111	VAL	-	linker	UNP A0A0K0K1A5
E	112	LEU	-	linker	UNP A0A0K0K1A5
E	113	GLU	-	linker	UNP A0A0K0K1A5
E	114	ASP	-	linker	UNP A0A0K0K1A5
E	115	LEU	-	linker	UNP A0A0K0K1A5
E	201	ASP	ASN	conflict	UNP K7N5M4

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).
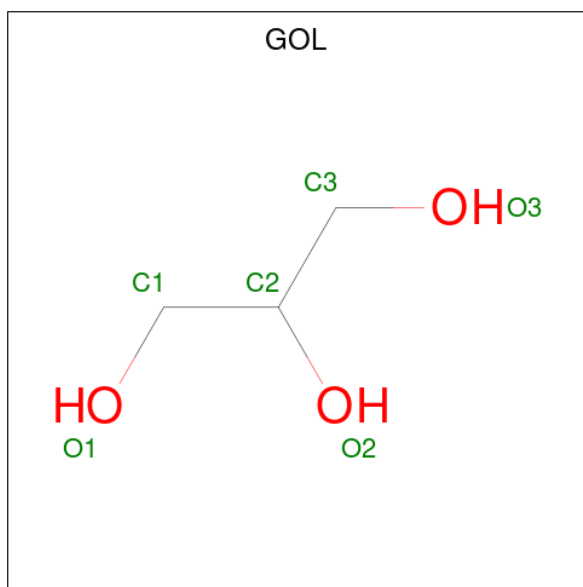
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total 6	C 3	O 3	0	0

- Molecule 7 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).

ACT

OXT

O⁻

C

CH3

O

O

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

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	5	Total 5	O 5	0	0
8	B	1	Total 1	O 1	0	0
8	D	2	Total 2	O 2	0	0
8	E	5	Total 5	O 5	0	0

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.
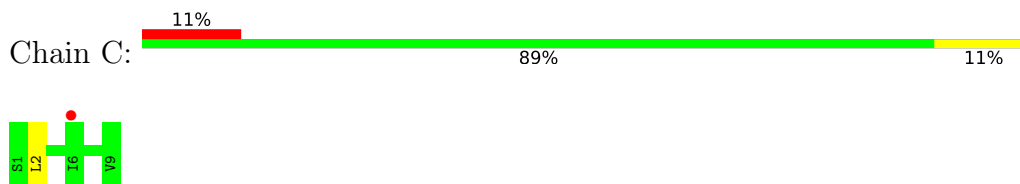
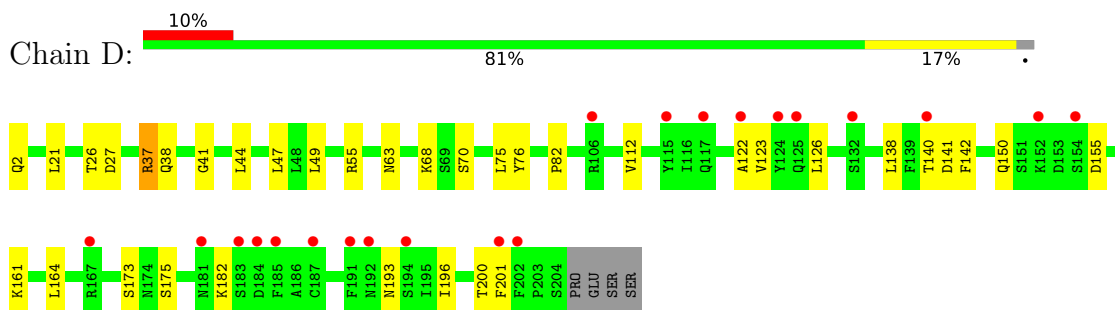• Molecule 1: HLA class I histocompatibility antigen, A-2 alpha chain
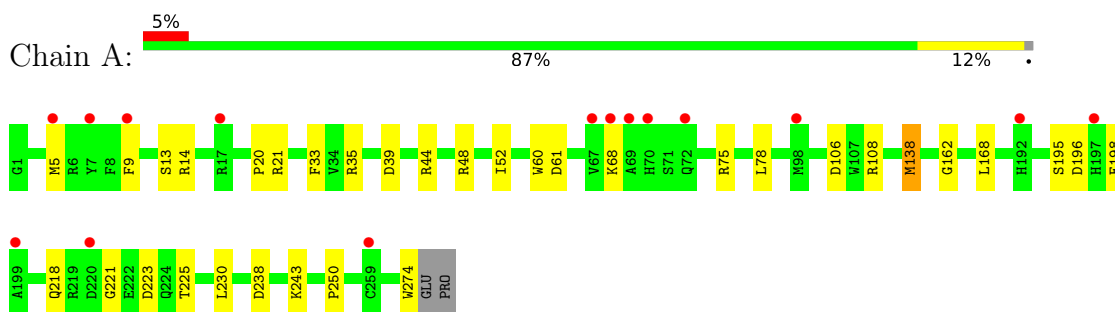
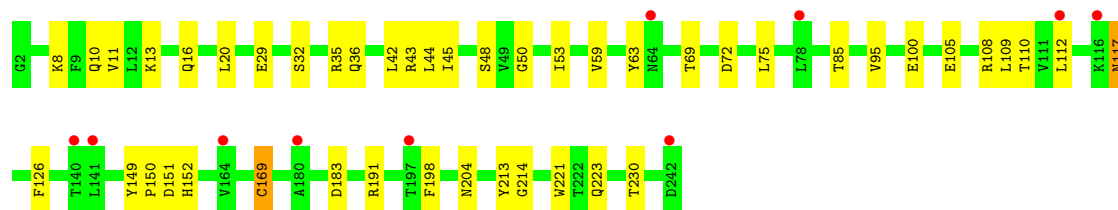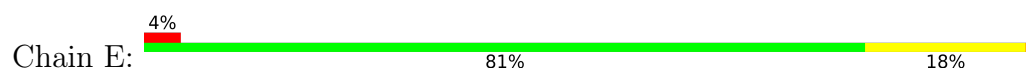• Molecule 2: Beta-2-microglobulin
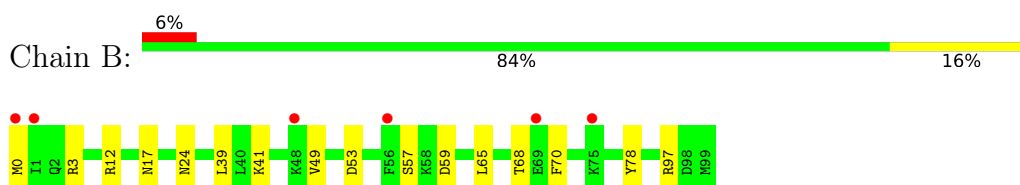
• Molecule 3: SER-LEU-LEU-MET-TRP-ILE-THR-GLN-VAL

• Molecule 4: T cell receptor alpha variable 21,T-cell receptor, sp3.4 alpha chain

• Molecule 5: T cell receptor beta variable 6-5,Human nkt tcr beta chain

Chain E:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	75.44Å 53.67Å 121.74Å 90.00° 98.02° 90.00°	Depositor
Resolution (Å)	29.94 – 2.50 29.94 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.1 (29.94-2.50) 99.1 (29.94-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.61 (at 2.51Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.229 , 0.273 0.229 , 0.273	Depositor DCC
R_{free} test set	1654 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å^2)	76.3	Xtriage
Anisotropy	0.139	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.26 , 45.2	EDS
L-test for twinning[2]	$< |L| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	6626	wwPDB-VP
Average B, all atoms (Å^2)	97.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.25% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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: GOL, ACT

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	0.23	0/2296	0.41	0/3116
2	B	0.23	0/860	0.42	0/1162
3	C	0.22	0/77	0.38	0/103
4	D	0.25	0/1588	0.44	0/2159
5	E	0.25	0/1953	0.44	0/2659
All	All	0.24	0/6774	0.43	0/9199

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 ⓘ

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	2232	0	2084	21	0
2	B	837	0	803	8	0
3	C	76	0	83	1	0
4	D	1556	0	1489	22	0
5	E	1902	0	1796	32	0
6	A	6	0	8	1	0
7	B	4	0	1	0	0
8	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	B	1	0	0	0	0
8	D	2	0	0	0	0
8	E	5	0	0	0	0
All	All	6626	0	6264	75	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 6.

The worst 5 of 75 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)
4:D:49:LEU:HD22	5:E:100:GLU:HB2	1.75	0.68
5:E:8:LYS:NZ	5:E:105:GLU:OE1	2.26	0.68
1:A:52:ILE:HD12	1:A:60:TRP:HH2	1.59	0.66
2:B:17:ASN:OD1	2:B:97:ARG:NH2	2.30	0.65
1:A:9:PHE:HZ	3:C:2:LEU:HD11	1.63	0.61

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	272/276 (99%)	258 (95%)	13 (5%)	1 (0%)	34	54
2	B	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
3	C	7/9 (78%)	7 (100%)	0	0	100	100
4	D	201/207 (97%)	184 (92%)	17 (8%)	0	100	100
5	E	239/241 (99%)	225 (94%)	14 (6%)	0	100	100
All	All	817/833 (98%)	767 (94%)	49 (6%)	1 (0%)	51	73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	162	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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	231/233 (99%)	230 (100%)	1 (0%)	91	97
2	B	95/95 (100%)	92 (97%)	3 (3%)	39	65
3	C	9/9 (100%)	9 (100%)	0	100	100
4	D	179/183 (98%)	176 (98%)	3 (2%)	60	82
5	E	208/208 (100%)	206 (99%)	2 (1%)	76	90
All	All	722/728 (99%)	713 (99%)	9 (1%)	71	88

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	117	ASN
5	E	169	CYS
2	B	70	PHE
4	D	26	THR
4	D	37	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 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	#$|Z| > 2$
7	ACT	B	101	-	3,3,3	1.27	0	3,3,3	1.52	0
6	GOL	A	301	-	5,5,5	0.90	0	5,5,5	1.02	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
6	GOL	A	301	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	301	GOL	O1-C1-C2-C3
6	A	301	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	301	GOL	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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, 95th 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	274/276 (99%)	0.21	15 (5%)	25	26	50, 80, 132, 173	0
2	B	100/100 (100%)	-0.01	6 (6%)	21	22	58, 78, 112, 144	0
3	C	9/9 (100%)	1.36	1 (11%)	5	5	62, 66, 77, 108	0
4	D	203/207 (98%)	0.54	21 (10%)	6	6	67, 112, 170, 197	0
5	E	241/241 (100%)	0.35	10 (4%)	37	40	61, 100, 148, 191	0
All	All	827/833 (99%)	0.32	53 (6%)	19	20	50, 91, 152, 197	0

The worst 5 of 53 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	E	242	ASP	7.1
4	D	183	SER	4.8
1	A	98	MET	4.7
2	B	0	MET	4.4
4	D	132	SER	4.3

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, 95th 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
6	GOL	A	301	6/6	0.75	0.15	97,107,113,116	0
7	ACT	B	101	4/4	0.93	0.33	72,82,83,86	0

6.5 Other polymers ⓘ

There are no such residues in this entry.