



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 23, 2024 – 11:48 AM EDT

PDB ID : 5M01
Title : Crystal structure of murine P14 TCR/ H-2Db complex with PA, modified gp33 peptide from LCMV
Authors : Achour, A.; Sandalova, T.; Sun, R.; Han, X.
Deposited on : 2016-10-03
Resolution : 1.95 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

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>.

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 : 2.37.1
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

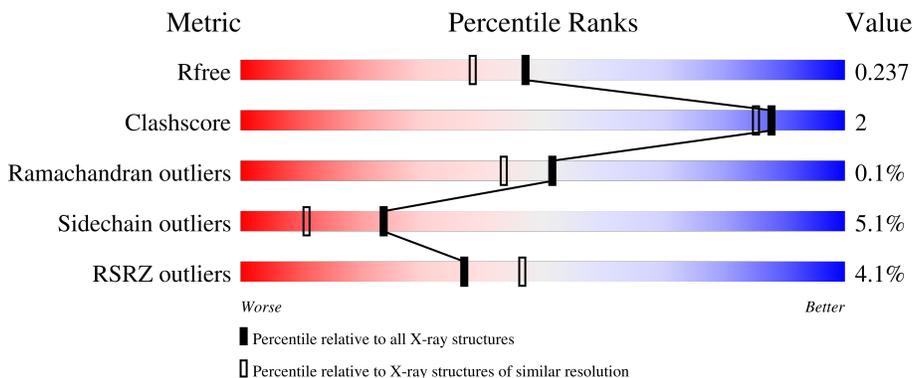
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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 $\leq 5\%$. 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	276	
2	B	119	
3	G	205	
4	H	238	
5	P	9	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6914 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 H-2 class I histocompatibility antigen, D-B alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	276	2273	1435	403	426	9	0	1	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	101	833	531	140	154	8	0	0	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	initiating methionine	UNP P01887
B	-18	ALA	-	expression tag	UNP P01887
B	-17	ARG	-	expression tag	UNP P01887
B	-16	SER	-	expression tag	UNP P01887
B	-15	VAL	-	expression tag	UNP P01887
B	-14	THR	-	expression tag	UNP P01887
B	-13	LEU	-	expression tag	UNP P01887
B	-12	VAL	-	expression tag	UNP P01887
B	-11	PHE	-	expression tag	UNP P01887
B	-10	LEU	-	expression tag	UNP P01887
B	-9	VAL	-	expression tag	UNP P01887
B	-8	LEU	-	expression tag	UNP P01887
B	-7	VAL	-	expression tag	UNP P01887
B	-6	SER	-	expression tag	UNP P01887
B	-5	LEU	-	expression tag	UNP P01887
B	-4	THR	-	expression tag	UNP P01887
B	-3	GLY	-	expression tag	UNP P01887
B	-2	LEU	-	expression tag	UNP P01887
B	-1	MET	-	cloning artifact	UNP P01887
B	0	GLY	-	cloning artifact	UNP P01887

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Chain	Residue	Modelled	Actual	Comment	Reference
B	85	ASP	ALA	variant	UNP P01887

- Molecule 3 is a protein called Protein Trav14-1,T-cell receptor alpha chain C region.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	G	188	1476	938	237	293	8	0	0	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	100	LEU	-	linker	UNP A0A0G2JF94
G	101	TYR	-	linker	UNP A0A0G2JF94
G	102	GLY	-	linker	UNP A0A0G2JF94
G	103	ASN	-	linker	UNP A0A0G2JF94
G	104	GLU	-	linker	UNP A0A0G2JF94
G	105	LYS	-	linker	UNP A0A0G2JF94
G	106	ILE	-	linker	UNP A0A0G2JF94
G	107	THR	-	linker	UNP A0A0G2JF94
G	108	PHE	-	linker	UNP A0A0G2JF94
G	109	GLY	-	linker	UNP A0A0G2JF94
G	110	ALA	-	linker	UNP A0A0G2JF94
G	111	GLY	-	linker	UNP A0A0G2JF94
G	112	THR	-	linker	UNP A0A0G2JF94
G	113	LYS	-	linker	UNP A0A0G2JF94
G	114	LEU	-	linker	UNP A0A0G2JF94
G	115	THR	-	linker	UNP A0A0G2JF94
G	116	ILE	-	linker	UNP A0A0G2JF94
G	117	LYS	-	linker	UNP A0A0G2JF94
G	118	PRO	-	linker	UNP A0A0G2JF94
G	119	ASN	-	linker	UNP A0A0G2JF94
G	166	CYS	THR	conflict	UNP P01849

- Molecule 4 is a protein called T-cell receptor beta chain V region C5,T-cell receptor beta-2 chain C region.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	H	237	1901	1192	340	363	6	0	5	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	93	ASP	-	linker	UNP P04213
H	94	ALA	-	linker	UNP P04213
H	95	GLY	-	linker	UNP P04213
H	96	GLY	-	linker	UNP P04213
H	97	ARG	-	linker	UNP P04213
H	98	ASN	-	linker	UNP P04213
H	99	THR	-	linker	UNP P04213
H	100	LEU	-	linker	UNP P04213
H	101	TYR	-	linker	UNP P04213
H	102	PHE	-	linker	UNP P04213
H	103	GLY	-	linker	UNP P04213
H	104	ALA	-	linker	UNP P04213
H	105	GLY	-	linker	UNP P04213
H	106	THR	-	linker	UNP P04213
H	107	ARG	-	linker	UNP P04213
H	108	LEU	-	linker	UNP P04213
H	109	SER	-	linker	UNP P04213
H	110	VAL	-	linker	UNP P04213
H	111	LEU	-	linker	UNP P04213
H	168	CYS	SER	conflict	UNP P01851
H	182	SER	CYS	conflict	UNP P01851

- Molecule 5 is a protein called LCMV-DERIVED GP33 ALTERED PEPTIDE LIGAND PA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	P	9	66	42	11	12	1	0	0	0

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

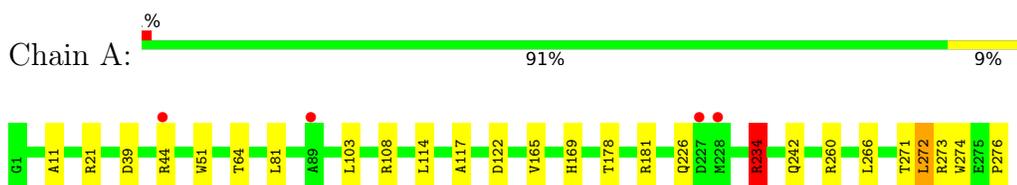
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	126	Total O 126 126	0	0
7	B	45	Total O 45 45	0	0
7	G	53	Total O 53 53	0	0
7	H	125	Total O 125 125	0	0
7	P	4	Total O 4 4	0	0

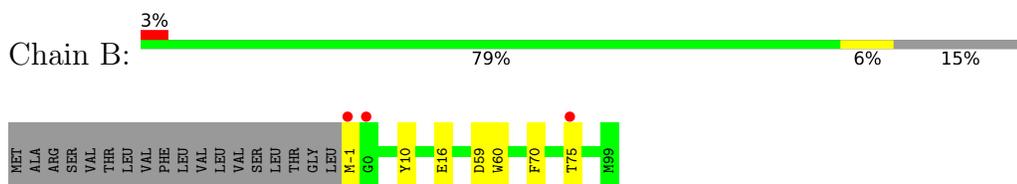
3 Residue-property plots [i](#)

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.

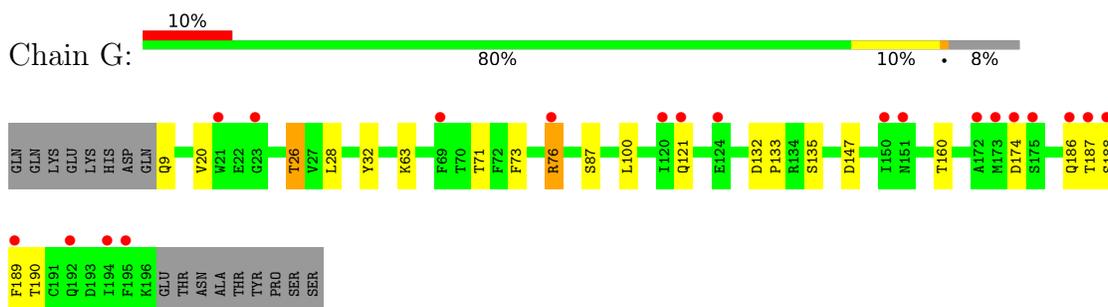
- Molecule 1: H-2 class I histocompatibility antigen, D-B alpha chain



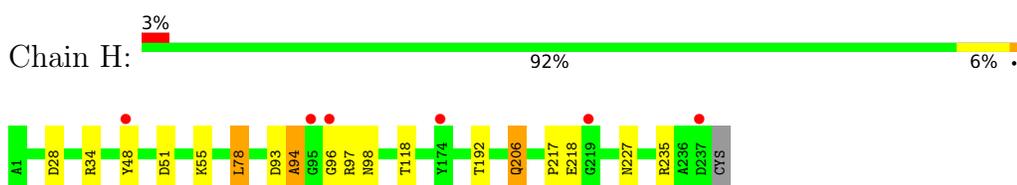
- Molecule 2: Beta-2-microglobulin



- Molecule 3: Protein Trav14-1, T-cell receptor alpha chain C region



- Molecule 4: T-cell receptor beta chain V region C5, T-cell receptor beta-2 chain C region



- Molecule 5: LCMV-DERIVED GP33 ALTERED PEPTIDE LIGAND PA



There are no outlier residues recorded for this chain.

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	255.93Å 46.54Å 89.40Å 90.00° 94.34° 90.00°	Depositor
Resolution (Å)	127.60 – 1.95 50.12 – 1.95	Depositor EDS
% Data completeness (in resolution range)	98.6 (127.60-1.95) 98.7 (50.12-1.95)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 1.95Å)	Xtrriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.196 , 0.229 0.204 , 0.237	Depositor DCC
R_{free} test set	3830 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	30.5	Xtrriage
Anisotropy	0.285	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 37.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6914	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.82% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

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	0.76	0/2343	0.97	7/3180 (0.2%)
2	B	0.70	0/859	0.84	1/1163 (0.1%)
3	G	0.70	1/1511 (0.1%)	0.81	2/2049 (0.1%)
4	H	0.74	0/1956	0.87	4/2657 (0.2%)
5	P	0.59	0/67	0.70	0/88
All	All	0.73	1/6736 (0.0%)	0.89	14/9137 (0.2%)

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
4	H	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	133	PRO	N-CD	5.22	1.55	1.47

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	234	ARG	NE-CZ-NH2	-14.23	113.19	120.30
1	A	234	ARG	NE-CZ-NH1	13.71	127.15	120.30
4	H	94[A]	ALA	N-CA-C	-6.70	92.90	111.00
4	H	94[B]	ALA	N-CA-C	-6.70	92.90	111.00
1	A	272	LEU	CA-CB-CG	6.54	130.34	115.30
1	A	39	ASP	CB-CG-OD1	5.87	123.58	118.30
2	B	59	ASP	CB-CG-OD1	5.52	123.27	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	132	ASP	C-N-CD	5.46	139.86	128.40
1	A	273	ARG	NE-CZ-NH1	5.40	123.00	120.30
3	G	76	ARG	NE-CZ-NH1	5.31	122.95	120.30
1	A	260	ARG	NE-CZ-NH1	5.25	122.92	120.30
1	A	272	LEU	CB-CG-CD1	5.19	119.82	111.00
4	H	78	LEU	CA-CB-CG	5.18	127.20	115.30
4	H	34	ARG	NE-CZ-NH2	-5.16	117.72	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	H	217	PRO	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	2273	0	2149	12	0
2	B	833	0	808	4	0
3	G	1476	0	1420	5	0
4	H	1901	0	1811	11	0
5	P	66	0	68	0	0
6	A	12	0	16	0	0
7	A	126	0	0	0	0
7	B	45	0	0	0	0
7	G	53	0	0	0	0
7	H	125	0	0	2	0
7	P	4	0	0	0	0
All	All	6914	0	6272	26	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 (26) 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:H:93[A]:ASP:O	7:H:301:HOH:O	2.09	0.71
1:A:234:ARG:HD3	2:B:10:TYR:CE2	2.29	0.67
1:A:51:TRP:HD1	1:A:178:THR:HG1	1.44	0.64
4:H:206:GLN:HG2	4:H:227:ASN:OD1	1.99	0.62
3:G:20:VAL:HG21	3:G:26:THR:HB	1.87	0.56
1:A:103:LEU:HD11	1:A:165:VAL:HG22	1.90	0.53
1:A:122:ASP:O	2:B:-1:MET:HE1	2.09	0.52
1:A:51:TRP:CD1	1:A:178:THR:OG1	2.63	0.51
1:A:234:ARG:HD3	2:B:10:TYR:CZ	2.45	0.51
4:H:192:THR:HG23	7:H:412:HOH:O	2.11	0.50
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.47	0.49
1:A:274:TRP:CZ2	1:A:276:PRO:HB3	2.47	0.49
1:A:11:ALA:HA	1:A:21:ARG:O	2.13	0.48
4:H:93[A]:ASP:OD1	4:H:93[A]:ASP:C	2.52	0.48
4:H:96[B]:GLY:O	4:H:97[B]:ARG:HB2	2.15	0.46
1:A:44[B]:ARG:HD2	1:A:64:THR:HG21	1.96	0.46
4:H:96[B]:GLY:O	4:H:97[B]:ARG:CB	2.63	0.45
1:A:234:ARG:HD2	1:A:242:GLN:HB2	1.99	0.45
4:H:235:ARG:O	4:H:235:ARG:HG2	2.16	0.45
3:G:100:LEU:HD11	4:H:97[B]:ARG:HG2	1.99	0.44
4:H:96[B]:GLY:C	4:H:97[B]:ARG:HG3	2.40	0.42
1:A:234:ARG:HD2	1:A:242:GLN:OE1	2.20	0.42
3:G:32:TYR:HH	3:G:73:PHE:HE1	1.65	0.42
4:H:94[B]:ALA:O	4:H:98:ASN:ND2	2.53	0.42
3:G:100:LEU:HD11	4:H:97[A]:ARG:HG2	2.02	0.41
3:G:26:THR:HG23	3:G:87:SER:OG	2.21	0.41

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	275/276 (100%)	270 (98%)	5 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	99/119 (83%)	97 (98%)	2 (2%)	0	100	100
3	G	186/205 (91%)	174 (94%)	11 (6%)	1 (0%)	29	17
4	H	240/238 (101%)	235 (98%)	5 (2%)	0	100	100
5	P	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
All	All	807/847 (95%)	782 (97%)	24 (3%)	1 (0%)	51	43

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	G	186	GLN

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	235/234 (100%)	225 (96%)	10 (4%)	29	16
2	B	95/111 (86%)	92 (97%)	3 (3%)	39	27
3	G	167/184 (91%)	152 (91%)	15 (9%)	9	2
4	H	205/204 (100%)	197 (96%)	8 (4%)	32	19
5	P	6/6 (100%)	6 (100%)	0	100	100
All	All	708/739 (96%)	672 (95%)	36 (5%)	24	11

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	81	LEU
1	A	108	ARG
1	A	114	LEU
1	A	169	HIS
1	A	181	ARG
1	A	226	GLN
1	A	234	ARG

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Mol	Chain	Res	Type
1	A	266	LEU
1	A	271	THR
1	A	272	LEU
2	B	16	GLU
2	B	70	PHE
2	B	75	THR
3	G	9	GLN
3	G	26	THR
3	G	28	LEU
3	G	63	LYS
3	G	71	THR
3	G	76	ARG
3	G	121	GLN
3	G	135	SER
3	G	147	ASP
3	G	160	THR
3	G	174	ASP
3	G	187	THR
3	G	188	SER
3	G	189	PHE
3	G	190	THR
4	H	28	ASP
4	H	48	TYR
4	H	51	ASP
4	H	55	LYS
4	H	78	LEU
4	H	118	THR
4	H	206	GLN
4	H	218	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
4	H	69	GLN
4	H	208	HIS

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](#)

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
6	GOL	A	301	-	5,5,5	0.40	0	5,5,5	0.32	0
6	GOL	A	302	-	5,5,5	0.41	0	5,5,5	0.27	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	-
6	GOL	A	302	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) 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

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Mol	Chain	Res	Type	Atoms
6	A	302	GOL	O2-C2-C3-O3
6	A	302	GOL	C1-C2-C3-O3

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

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, 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	276/276 (100%)	0.31	4 (1%) 75 82	19, 32, 53, 77	0
2	B	101/119 (84%)	0.24	3 (2%) 50 59	20, 39, 62, 69	0
3	G	188/205 (91%)	0.77	20 (10%) 6 10	24, 46, 86, 107	0
4	H	237/238 (99%)	0.30	6 (2%) 57 66	24, 34, 52, 67	0
5	P	9/9 (100%)	0.25	0 100 100	21, 22, 28, 29	0
All	All	811/847 (95%)	0.40	33 (4%) 37 46	19, 36, 66, 107	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	G	172	ALA	8.6
3	G	173	MET	6.6
3	G	187	THR	6.3
2	B	-1	MET	6.1
3	G	189	PHE	6.1
3	G	188	SER	5.3
3	G	174	ASP	5.2
4	H	174	TYR	4.2
3	G	21	TRP	4.0
3	G	121	GLN	4.0
2	B	75	THR	3.8
4	H	96[A]	GLY	3.7
4	H	48	TYR	3.7
3	G	175	SER	3.6
4	H	219	GLY	3.4
4	H	237	ASP	3.4
1	A	227	ASP	3.2
3	G	124	GLU	2.9
3	G	76	ARG	2.7
2	B	0	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
3	G	195	PHE	2.6
3	G	192	GLN	2.4
3	G	186	GLN	2.3
3	G	69	PHE	2.3
3	G	194	ILE	2.3
3	G	23	GLY	2.3
1	A	89	ALA	2.3
1	A	228	MET	2.2
3	G	151	ASN	2.2
1	A	44[A]	ARG	2.2
3	G	150	ILE	2.1
3	G	120	ILE	2.1
4	H	95[A]	GLY	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, 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	0.79	0.26	59,65,68,74	0
6	GOL	A	302	6/6	0.79	0.39	39,42,52,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.