wwPDB X-ray Structure Validation Summary Report (i)

Sep 4, 2023 – 10:19 PM EDT

PDB ID	:	3S5L
Title	:	Crystal structure of CD4 mutant bound to HLA-DR1
Authors	:	Li, Y.
Deposited on	:	2011-05-23
Resolution	:	2.10 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:

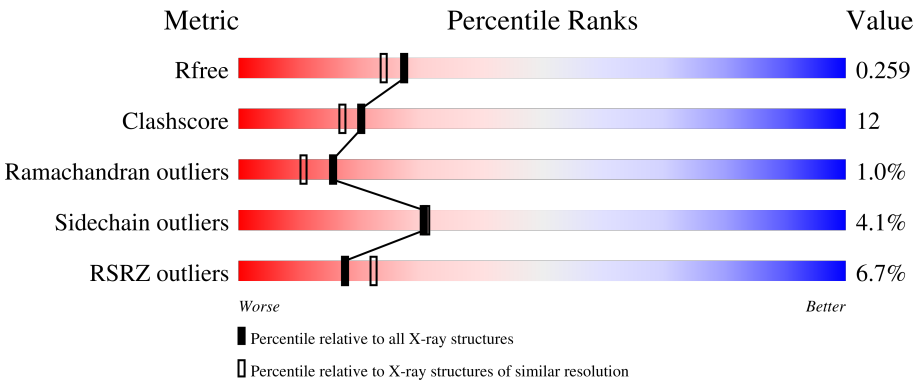
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	182	% 82% 13% • •
1	D	182	2% 79% 18% • •
2	B	193	5% 77% 20% • • •
2	E	193	7% 70% 27% • •
3	C	13	54% 38% 8%

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Mol	Chain	Length	Quality of chain
3	F	13	8% 62% 23% 15%
4	G	191	8% 60% 28% • • 8%
4	H	191	16% 61% 29% • 7%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 9272 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 II histocompatibility antigen, DR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	178	1464	949	237	273	5	0	0	0
1	D	179	1467	950	238	274	5	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	177	GLN	HIS	conflict	UNP P01903
D	177	GLN	HIS	conflict	UNP P01903

- Molecule 2 is a protein called HLA class II histocompatibility antigen DR beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	191	1533	961	275	290	7	0	0	0
2	E	191	1545	971	276	291	7	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP D7RIG0
E	0	MET	-	initiating methionine	UNP D7RIG0

- Molecule 3 is a protein called HA peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	13	106	69	18	19	0	0	0
3	F	13	106	69	18	19	0	0	0

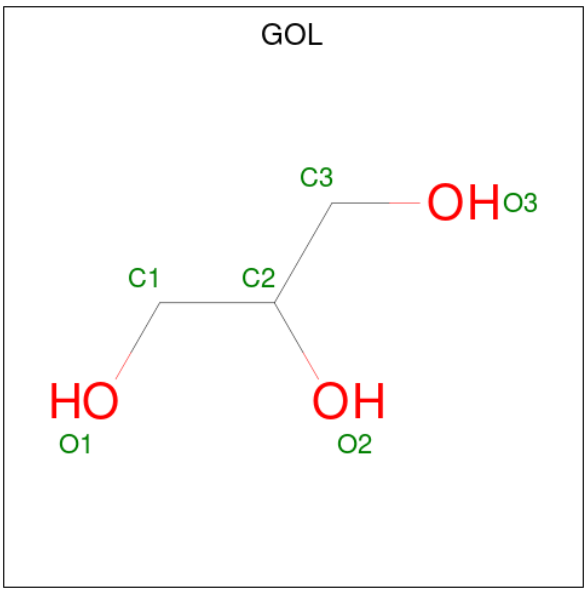
- Molecule 4 is a protein called T-cell surface glycoprotein CD4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	G	175	1369	860	244	261	4	0	0	0
			Total	C	N	O	S			
4	H	177	1354	851	241	258	4	0	0	0

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-3	ASP	-	expression tag	UNP P01730
G	-2	LEU	-	expression tag	UNP P01730
G	-1	GLY	-	expression tag	UNP P01730
G	0	SER	-	expression tag	UNP P01730
G	40	TYR	GLN	engineered mutation	UNP P01730
G	45	TRP	THR	engineered mutation	UNP P01730
G	60	ARG	SER	engineered mutation	UNP P01730
G	63	ARG	ASP	engineered mutation	UNP P01730
G	179	ALA	-	expression tag	UNP P01730
G	180	ALA	-	expression tag	UNP P01730
G	181	ALA	-	expression tag	UNP P01730
G	182	HIS	-	expression tag	UNP P01730
G	183	HIS	-	expression tag	UNP P01730
G	184	HIS	-	expression tag	UNP P01730
G	185	HIS	-	expression tag	UNP P01730
G	186	HIS	-	expression tag	UNP P01730
G	187	HIS	-	expression tag	UNP P01730
H	-3	ASP	-	expression tag	UNP P01730
H	-2	LEU	-	expression tag	UNP P01730
H	-1	GLY	-	expression tag	UNP P01730
H	0	SER	-	expression tag	UNP P01730
H	40	TYR	GLN	engineered mutation	UNP P01730
H	45	TRP	THR	engineered mutation	UNP P01730
H	60	ARG	SER	engineered mutation	UNP P01730
H	63	ARG	ASP	engineered mutation	UNP P01730
H	179	ALA	-	expression tag	UNP P01730
H	180	ALA	-	expression tag	UNP P01730
H	181	ALA	-	expression tag	UNP P01730
H	182	HIS	-	expression tag	UNP P01730
H	183	HIS	-	expression tag	UNP P01730
H	184	HIS	-	expression tag	UNP P01730
H	185	HIS	-	expression tag	UNP P01730
H	186	HIS	-	expression tag	UNP P01730
H	187	HIS	-	expression tag	UNP P01730

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	A	1	6	3	3	0	0
5	D	1	6	3	3	0	0
5	B	1	6	3	3	0	0
5	B	1	6	3	3	0	0
5	E	1	6	3	3	0	0
5	E	1	6	3	3	0	0
5	E	1	6	3	3	0	0
5	G	1	6	3	3	0	0
5	G	1	6	3	3	0	0
5	H	1	6	3	3	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	87	87	87	0	0

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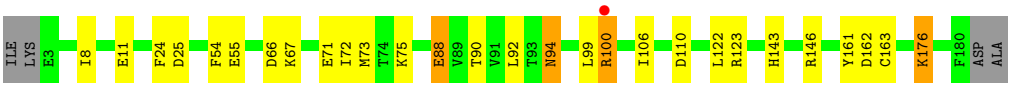
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	D	61	61	61	0	0
			Total	O		
6	B	57	57	57	0	0
			Total	O		
6	E	30	30	30	0	0
			Total	O		
6	C	5	5	5	0	0
			Total	O		
6	F	1	1	1	0	0
			Total	O		
6	G	16	16	16	0	0
			Total	O		
6	H	11	11	11	0	0

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.

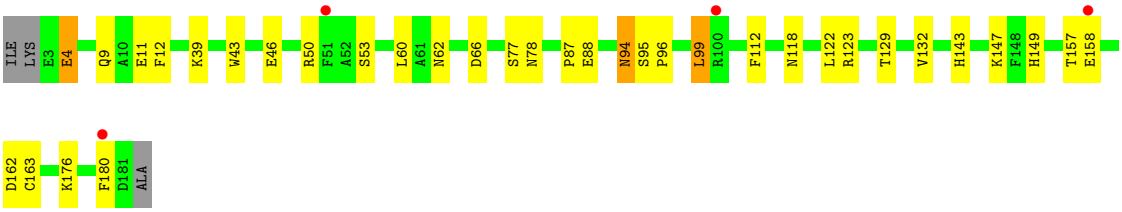
• Molecule 1: HLA class II histocompatibility antigen, DR alpha chain

Chain A:



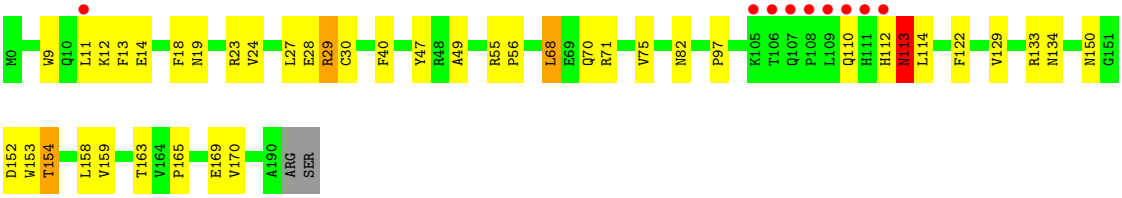
• Molecule 1: HLA class II histocompatibility antigen, DR alpha chain

Chain D:



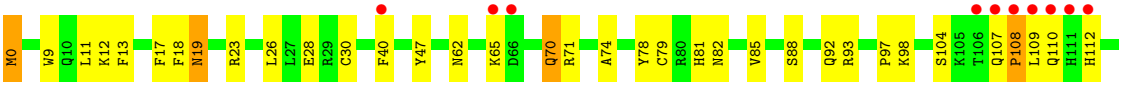
• Molecule 2: HLA class II histocompatibility antigen DR beta chain

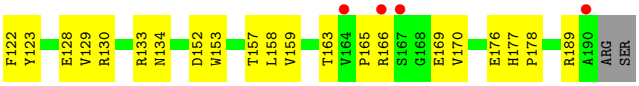
Chain B:



• Molecule 2: HLA class II histocompatibility antigen DR beta chain

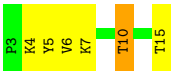
Chain E:





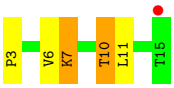
• Molecule 3: HA peptide

Chain C:



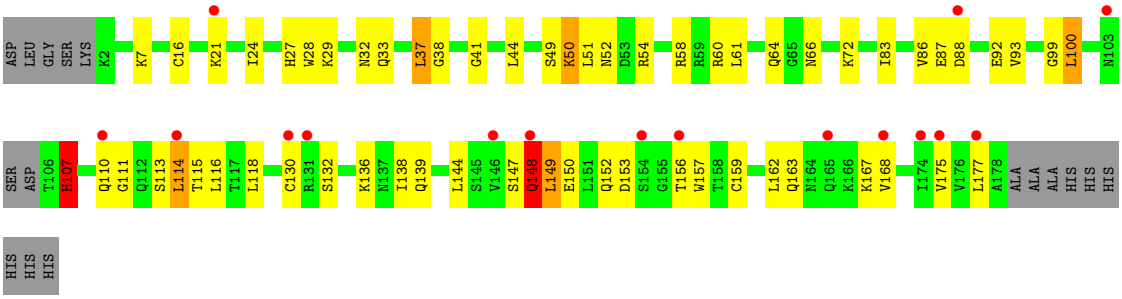
• Molecule 3: HA peptide

Chain F:



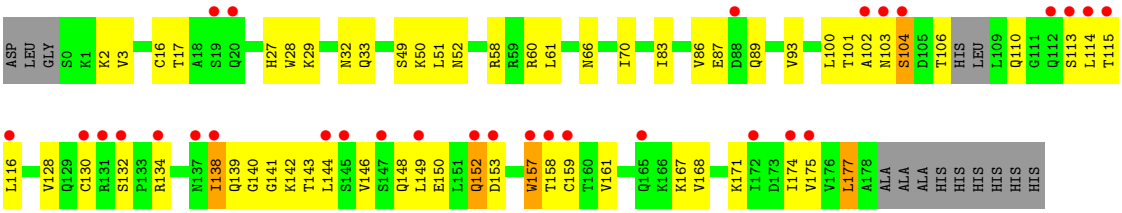
• Molecule 4: T-cell surface glycoprotein CD4

Chain G:



• Molecule 4: T-cell surface glycoprotein CD4

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	94.20Å 119.70Å 137.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.10 47.41 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-2.10) 99.8 (47.41-2.10)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.80 (at 2.10Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.234 , 0.268 0.224 , 0.259	Depositor DCC
R_{free} test set	4566 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	28.4	Xtriage
Anisotropy	0.793	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 49.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	9272	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 43.21 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.8222e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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 (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	0.56	0/1508	0.75	2/2056 (0.1%)
1	D	0.50	0/1511	0.73	1/2060 (0.0%)
2	B	0.52	0/1571	0.72	0/2130
2	E	0.46	0/1584	0.68	0/2150
3	C	0.49	0/107	0.82	0/141
3	F	0.39	0/107	0.83	0/141
4	G	0.38	0/1390	0.67	2/1873 (0.1%)
4	H	0.41	0/1374	0.68	0/1854
All	All	0.47	0/9152	0.71	5/12405 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	G	37	LEU	CA-CB-CG	5.87	128.81	115.30
4	G	41	GLY	N-CA-C	-5.64	98.99	113.10
1	D	163	CYS	N-CA-C	-5.42	96.37	111.00
1	A	88	GLU	N-CA-C	-5.22	96.90	111.00
1	A	163	CYS	N-CA-C	-5.03	97.43	111.00

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	1464	0	1404	24	0
1	D	1467	0	1403	27	0
2	B	1533	0	1442	36	0
2	E	1545	0	1466	43	0
3	C	106	0	119	12	0
3	F	106	0	119	5	0
4	G	1369	0	1385	50	0
4	H	1354	0	1339	54	0
5	A	6	0	8	0	0
5	B	12	0	16	0	0
5	D	6	0	8	0	0
5	E	18	0	24	1	0
5	G	12	0	16	3	0
5	H	6	0	8	3	0
6	A	87	0	0	1	0
6	B	57	0	0	0	0
6	C	5	0	0	0	0
6	D	61	0	0	0	0
6	E	30	0	0	1	0
6	F	1	0	0	0	0
6	G	16	0	0	0	0
6	H	11	0	0	0	0
All	All	9272	0	8757	222	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 12.

The worst 5 of 222 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:50:LYS:H	4:H:50:LYS:HD2	1.07	1.13
4:G:50:LYS:HE3	4:G:50:LYS:H	1.12	1.04
4:H:177:LEU:HD22	4:H:177:LEU:H	1.23	1.01
4:G:138:ILE:HG22	4:G:139:GLN:H	1.28	0.99
2:E:82:ASN:HD21	3:F:6:VAL:H	1.08	0.93

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	176/182 (97%)	172 (98%)	4 (2%)	0	100	100
1	D	177/182 (97%)	170 (96%)	6 (3%)	1 (1%)	25	21
2	B	189/193 (98%)	178 (94%)	9 (5%)	2 (1%)	14	9
2	E	189/193 (98%)	176 (93%)	12 (6%)	1 (0%)	29	26
3	C	11/13 (85%)	11 (100%)	0	0	100	100
3	F	11/13 (85%)	11 (100%)	0	0	100	100
4	G	171/191 (90%)	158 (92%)	10 (6%)	3 (2%)	8	4
4	H	173/191 (91%)	151 (87%)	18 (10%)	4 (2%)	6	2
All	All	1097/1158 (95%)	1027 (94%)	59 (5%)	11 (1%)	15	11

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	H	104	SER
4	G	148	GLN
4	H	113	SER
4	H	138	ILE
4	H	148	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	163/166 (98%)	159 (98%)	4 (2%)	47	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	163/166 (98%)	158 (97%)	5 (3%)	40	43
2	B	165/174 (95%)	159 (96%)	6 (4%)	35	36
2	E	168/174 (97%)	164 (98%)	4 (2%)	49	53
3	C	12/12 (100%)	10 (83%)	2 (17%)	2	1
3	F	12/12 (100%)	9 (75%)	3 (25%)	0	0
4	G	155/170 (91%)	146 (94%)	9 (6%)	20	17
4	H	146/170 (86%)	139 (95%)	7 (5%)	25	24
All	All	984/1044 (94%)	944 (96%)	40 (4%)	30	31

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	G	114	LEU
4	H	150	GLU
4	G	148	GLN
4	G	167	LYS
4	H	157	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
4	G	139	GLN
4	G	148	GLN
4	H	139	GLN
2	B	113	ASN
2	B	82	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)

10 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	$\#\|Z\| > 2$
5	GOL	B	969	-	5,5,5	0.29	0	5,5,5	0.25	0
5	GOL	B	966	-	5,5,5	0.37	0	5,5,5	0.41	0
5	GOL	E	962	-	5,5,5	0.16	0	5,5,5	0.28	0
5	GOL	A	968	-	5,5,5	0.29	0	5,5,5	0.36	0
5	GOL	E	960	-	5,5,5	0.24	0	5,5,5	0.35	0
5	GOL	G	965	-	5,5,5	0.17	0	5,5,5	0.30	0
5	GOL	E	963	-	5,5,5	0.36	0	5,5,5	0.29	0
5	GOL	D	961	-	5,5,5	0.24	0	5,5,5	0.31	0
5	GOL	H	964	-	5,5,5	0.23	0	5,5,5	0.27	0
5	GOL	G	967	-	5,5,5	0.27	0	5,5,5	0.26	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
5	GOL	B	969	-	-	0/4/4/4	-
5	GOL	B	966	-	-	0/4/4/4	-
5	GOL	E	962	-	-	0/4/4/4	-
5	GOL	A	968	-	-	0/4/4/4	-
5	GOL	E	960	-	-	0/4/4/4	-
5	GOL	G	965	-	-	0/4/4/4	-
5	GOL	E	963	-	-	0/4/4/4	-
5	GOL	D	961	-	-	0/4/4/4	-
5	GOL	H	964	-	-	0/4/4/4	-
5	GOL	G	967	-	-	0/4/4/4	-

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.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	960	GOL	1	0
5	G	965	GOL	3	0
5	H	964	GOL	3	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, 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	178/182 (97%)	0.07	1 (0%) 89 91	15, 25, 44, 61	0
1	D	179/182 (98%)	0.13	4 (2%) 62 66	16, 30, 57, 68	0
2	B	191/193 (98%)	0.02	9 (4%) 31 37	16, 29, 51, 95	0
2	E	191/193 (98%)	0.44	14 (7%) 15 19	19, 36, 63, 94	0
3	C	13/13 (100%)	0.07	0 100 100	26, 32, 39, 44	0
3	F	13/13 (100%)	0.47	1 (7%) 13 17	35, 43, 57, 58	0
4	G	175/191 (91%)	0.51	16 (9%) 9 12	25, 49, 74, 81	0
4	H	177/191 (92%)	0.60	30 (16%) 1 2	23, 45, 77, 85	0
All	All	1117/1158 (96%)	0.29	75 (6%) 17 22	15, 34, 72, 95	0

The worst 5 of 75 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	111	HIS	10.8
2	E	110	GLN	8.4
2	E	107	GLN	8.0
2	E	108	PRO	7.8
2	B	112	HIS	5.0

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
5	GOL	B	969	6/6	0.77	0.22	63,64,64,64	0
5	GOL	G	965	6/6	0.81	0.23	54,54,56,56	0
5	GOL	E	960	6/6	0.83	0.18	61,62,62,63	0
5	GOL	B	966	6/6	0.85	0.20	34,37,41,46	0
5	GOL	E	963	6/6	0.86	0.19	37,41,43,44	0
5	GOL	H	964	6/6	0.86	0.23	55,55,56,60	0
5	GOL	A	968	6/6	0.87	0.15	34,41,44,48	0
5	GOL	D	961	6/6	0.87	0.19	51,56,57,59	0
5	GOL	G	967	6/6	0.91	0.23	55,56,58,58	0
5	GOL	E	962	6/6	0.91	0.19	50,51,51,52	0

6.5 Other polymers (i)

There are no such residues in this entry.