wwPDB X-ray Structure Validation Summary Report (i)

Aug 22, 2020 – 08:06 PM BST

PDB ID	:	5XOT
Title	:	Crystal structure of pHLA-B35 in complex with TU55 T cell receptor
Authors	:	Shi, Y.; Qi, J.; Gao, G.F.
Deposited on	:	2017-05-31
Resolution	:	2.79 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 following versions of software and data (see references (1)) were used in the production of this report:

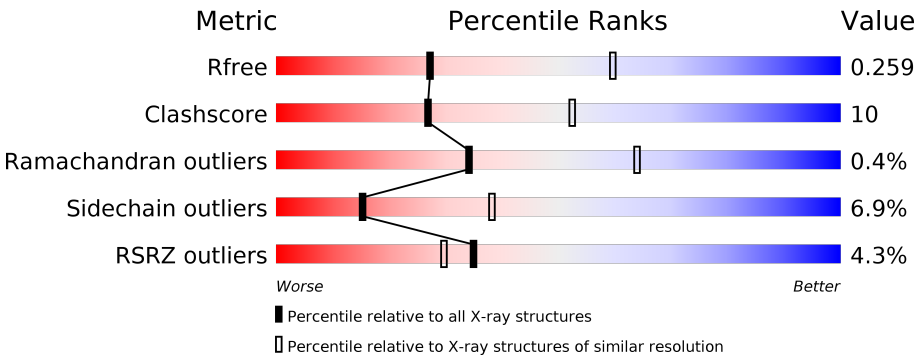
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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 2.79 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	4107 (2.80-2.76)
Clashscore	141614	4575 (2.80-2.76)
Ramachandran outliers	138981	4487 (2.80-2.76)
Sidechain outliers	138945	4489 (2.80-2.76)
RSRZ outliers	127900	4027 (2.80-2.76)

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 on 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	4%, 80%, 18%, •
2	B	99	6%, 77%, 21%, •
3	C	9	56%, 22%, 22%
4	D	204	9%, 74%, 23%, •
5	E	242	%, 74%, 20%, 6%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 6728 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, B-35 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	276	2255	1404	411	433	7	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	34	ASP	VAL	engineered mutation	UNP P30685

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	99	829	528	140	158	3	0	0	0

- Molecule 3 is a protein called An HIV reverse transcriptase epitope.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	9	71	45	9	17	0	0	0

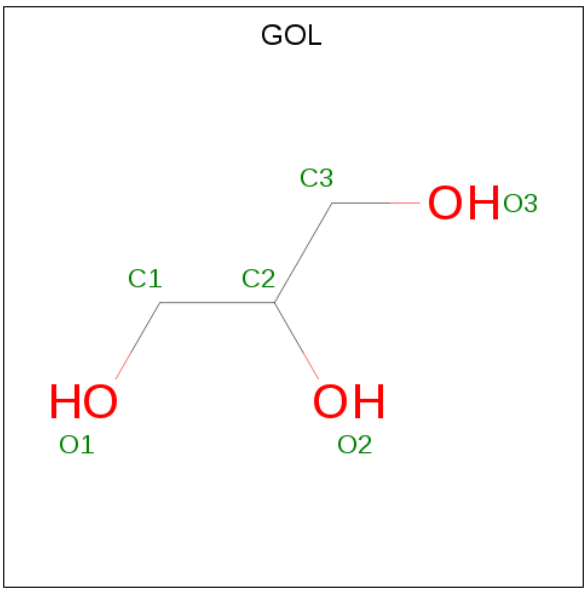
- Molecule 4 is a protein called The Delta chain of TU55 TCR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	203	1598	1010	266	313	9	0	0	0

- Molecule 5 is a protein called The beta chain of TU55 TCR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	E	242	1924	1207	339	369	9	0	0	0

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 7 is water.

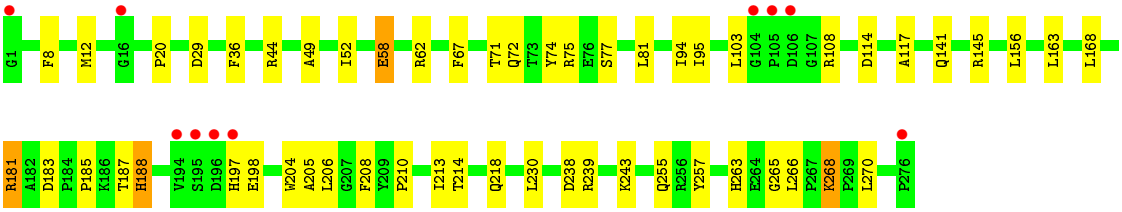
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	11	11	11	0	0
			Total	O		
7	B	1	1	1	0	0
			Total	O		
7	D	7	7	7	0	0
			Total	O		
7	E	14	14	14	0	0

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.

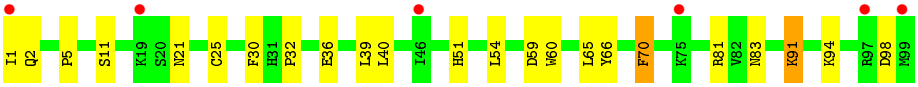
- Molecule 1: HLA class I histocompatibility antigen, B-35 alpha chain

Chain A:



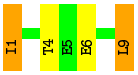
- Molecule 2: Beta-2-microglobulin

Chain B:



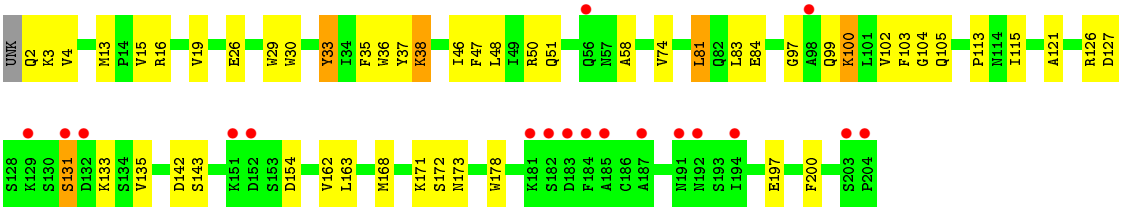
- Molecule 3: An HIV reverse transcriptase epitope

Chain C:



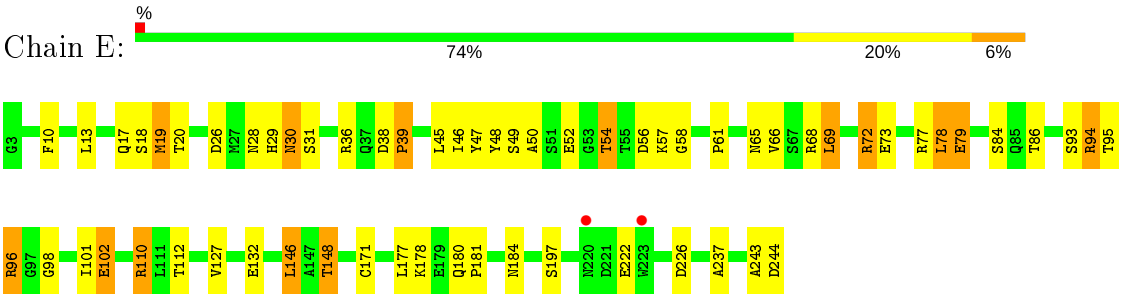
- Molecule 4: The Delta chain of TU55 TCR

Chain D:



- Molecule 5: The beta chain of TU55 TCR

Chain E:


%
74%
20%
6%
G3 F10 L13 Q17 S18 M19 T20 D26 M27 N28 H29 N30 S31 R36 Q37 D38 P39 L45 I46 Y47 Y48 S49 A50 S51 E52 G53 T54 T55 D56 K57 G58 P61 N65 V66 S67 R68 L69 R72 E73 R77 L78 E79 S84 Q85 T86 S93 R94 T95
R96 G97 G98 I101 E102 R110 L111 T112 V127 E132 L146 A147 T148 C171 L177 K178 E179 Q180 P181 N184 S197 N220 D221 E222 W223 D226 A237 A243 D244

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	195.69Å 59.60Å 92.81Å 90.00° 105.98° 90.00°	Depositor
Resolution (Å)	36.60 – 2.79 42.14 – 2.78	Depositor EDS
% Data completeness (in resolution range)	90.5 (36.60-2.79) 93.5 (42.14-2.78)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.50 (at 2.77Å)	Xtriage
Refinement program	PHENIX 1.5_2	Depositor
R, R_{free}	0.199 , 0.254 0.203 , 0.259	Depositor DCC
R_{free} test set	1259 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å^2)	45.7	Xtriage
Anisotropy	0.937	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 45.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6728	wwPDB-VP
Average B, all atoms (Å^2)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.78% 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 (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	0.22	0/2318	0.42	1/3151 (0.0%)
2	B	0.23	0/852	0.38	0/1152
3	C	0.25	0/71	0.49	0/95
4	D	0.41	0/1633	0.46	0/2210
5	E	0.31	0/1974	0.45	1/2684 (0.0%)
All	All	0.30	0/6848	0.43	2/9292 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	29	ASP	N-CA-C	-6.49	93.48	111.00
5	E	79	GLU	N-CA-C	-5.28	96.75	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	2255	0	2112	36	0
2	B	829	0	794	14	0
3	C	71	0	72	5	0
4	D	1598	0	1550	48	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	1924	0	1835	50	0
6	A	6	0	8	1	0
6	B	12	0	16	2	0
7	A	11	0	0	0	0
7	B	1	0	0	0	0
7	D	7	0	0	0	0
7	E	14	0	0	0	0
All	All	6728	0	6387	134	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 10.

The worst 5 of 134 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)
5:E:30:ASN:ND2	5:E:30:ASN:H	1.75	0.84
4:D:102:VAL:HG22	4:D:102:VAL:O	1.75	0.84
5:E:30:ASN:H	5:E:30:ASN:HD22	1.24	0.83
4:D:99:GLN:HG2	5:E:94:ARG:HH21	1.43	0.82
4:D:135:VAL:HG23	4:D:178:TRP:HB3	1.61	0.81

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	274/276 (99%)	263 (96%)	10 (4%)	1 (0%)	34 64
2	B	97/99 (98%)	94 (97%)	3 (3%)	0	100 100
3	C	7/9 (78%)	7 (100%)	0	0	100 100
4	D	201/204 (98%)	183 (91%)	17 (8%)	1 (0%)	29 58

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	E	240/242 (99%)	227 (95%)	12 (5%)	1 (0%)	34	64
All	All	819/830 (99%)	774 (94%)	42 (5%)	3 (0%)	34	64

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	131	SER
1	A	188	HIS
5	E	39	PRO

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	234/234 (100%)	225 (96%)	9 (4%)	33	64
2	B	94/94 (100%)	89 (95%)	5 (5%)	22	51
3	C	8/8 (100%)	6 (75%)	2 (25%)	0	1
4	D	180/180 (100%)	167 (93%)	13 (7%)	14	36
5	E	210/210 (100%)	189 (90%)	21 (10%)	7	20
All	All	726/726 (100%)	676 (93%)	50 (7%)	15	38

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	83	LEU
4	D	154	ASP
5	E	180	GLN
4	D	84	GLU
4	D	105	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
4	D	116	GLN
4	D	173	ASN
5	E	62	ASN
2	B	89	GLN
4	D	51	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)

3 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	B	1100	-	5,5,5	0.34	0	5,5,5	0.34	0
6	GOL	B	1101	-	5,5,5	0.36	0	5,5,5	0.24	0
6	GOL	A	301	-	5,5,5	0.34	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	B	1100	-	-	2/4/4/4	-
6	GOL	B	1101	-	-	1/4/4/4	-
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 (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	1100	GOL	O1-C1-C2-C3
6	A	301	GOL	O1-C1-C2-O2
6	A	301	GOL	O1-C1-C2-C3
6	B	1100	GOL	O1-C1-C2-O2
6	B	1101	GOL	O1-C1-C2-C3

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	1100	GOL	1	0
6	B	1101	GOL	1	0
6	A	301	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, 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%)	0.19	10 (3%) 42 37	36, 52, 82, 119	0
2	B	99/99 (100%)	0.45	6 (6%) 21 16	41, 62, 93, 123	0
3	C	9/9 (100%)	0.61	0 100 100	38, 46, 59, 63	0
4	D	203/204 (99%)	0.49	18 (8%) 9 6	36, 55, 109, 150	0
5	E	242/242 (100%)	0.12	2 (0%) 86 84	31, 51, 86, 126	0
All	All	829/830 (99%)	0.28	36 (4%) 35 30	31, 53, 95, 150	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	204	PRO	6.6
4	D	131	SER	5.4
1	A	105	PRO	4.3
4	D	182	SER	4.2
2	B	99	MET	3.9

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	0.87	0.26	65,69,70,85	0
6	GOL	B	1101	6/6	0.93	0.20	64,67,73,75	0
6	GOL	B	1100	6/6	0.96	0.15	59,64,72,72	0

6.5 Other polymers (i)

There are no such residues in this entry.