



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:43 PM GMT

PDB ID : 4FTV  
Title : The complex between the high affinity version of A6 TCR (A6c134) and human Class I MHC HLA-A2 with the bound TAX nonameric peptide  
Authors : Borbulevych, O.Y.; Baker, B.M.  
Deposited on : 2012-06-28  
Resolution : 2.74 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

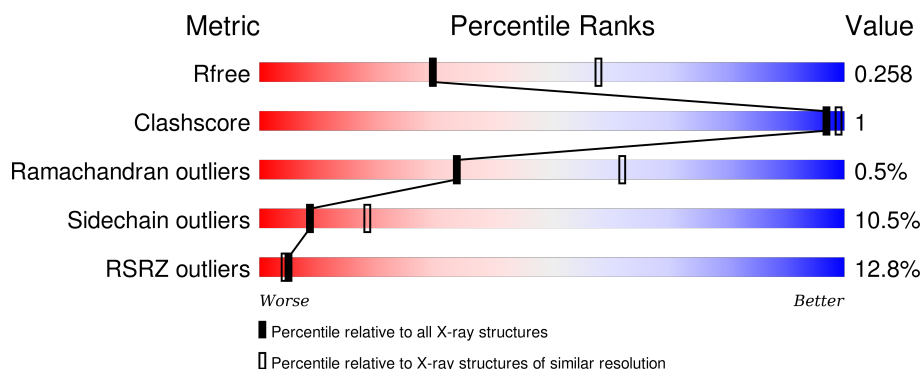
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.74 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))
$R_{free}$	91344	3050 (2.78-2.70)
Clashscore	102246	3424 (2.78-2.70)
Ramachandran outliers	100387	3367 (2.78-2.70)
Sidechain outliers	100360	3368 (2.78-2.70)
RSRZ outliers	91569	3055 (2.78-2.70)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	275	<div> <div>7%</div> <div>90%</div> <div>9%</div> <div>.</div> </div>
2	B	100	<div> <div>%</div> <div>89%</div> <div>11%</div> </div>
3	C	9	<div> <div>89%</div> <div>11%</div> </div>
4	D	200	<div> <div>29%</div> <div>86%</div> <div>13%</div> <div>.</div> </div>
5	E	245	<div> <div>11%</div> <div>86%</div> <div>13%</div> <div>.</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	GOL	A	302	-	-	-	X
6	GOL	A	306	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6740 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	275	Total	C	N	O	S	0	0	0
			2247	1403	409	426	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	1	0
			842	536	141	161	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	EXPRESSION TAG	UNP P61769

- Molecule 3 is a protein called Protein Tax-1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	0	0	0
			77	56	9	12			

- Molecule 4 is a protein called A6 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	200	Total	C	N	O	S	0	0	0
			1552	965	255	325	7			

- Molecule 5 is a protein called A6 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	245	Total	C	N	O	S	0	1	0
			1937	1215	337	376	9			

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



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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	9	Total	O	0	0
			9	9		

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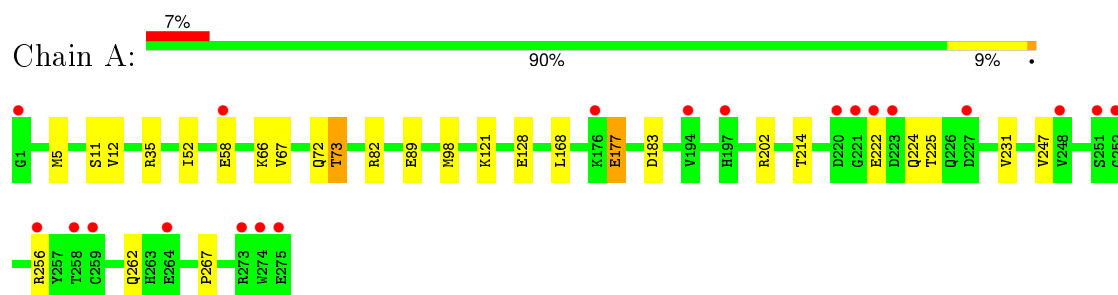
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	11	Total 11	O 11	0	0
7	D	1	Total 1	O 1	0	0
7	E	4	Total 4	O 4	0	0

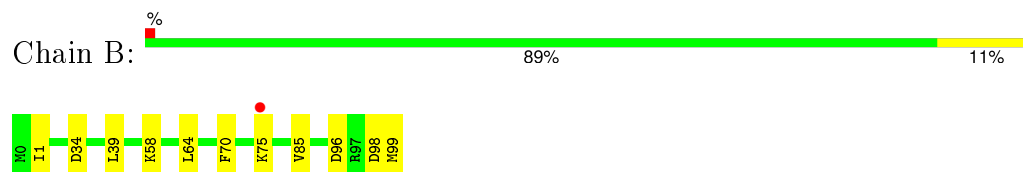
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

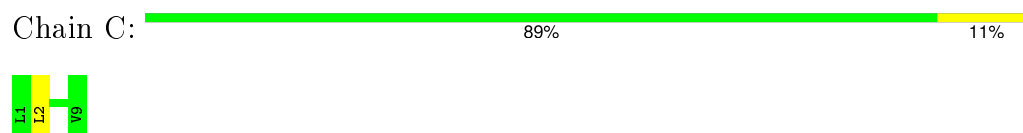
- Molecule 1: HLA class I histocompatibility antigen, A-2 alpha chain



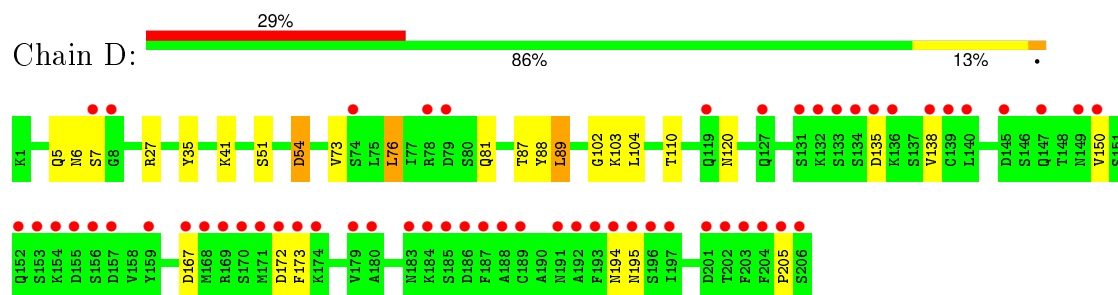
- Molecule 2: Beta-2-microglobulin



- Molecule 3: Protein Tax-1

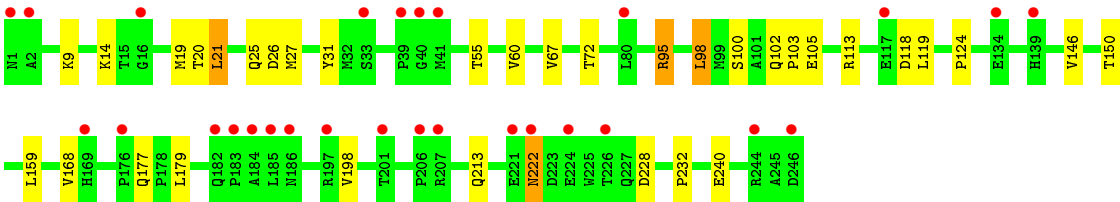


- Molecule 4: A6 alpha chain



- Molecule 5: A6 beta chain







## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	224.23Å 48.95Å 94.40Å 90.00° 89.62° 90.00°	Depositor
Resolution (Å)	20.00 – 2.74 19.32 – 2.74	Depositor EDS
% Data completeness (in resolution range)	97.6 (20.00-2.74) 97.7 (19.32-2.74)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.70 (at 2.75Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.216 , 0.260 0.214 , 0.258	Depositor DCC
$R_{free}$ test set	1370 reflections (5.40%)	DCC
Wilson B-factor (Å <sup>2</sup> )	71.4	Xtriage
Anisotropy	0.207	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 66.0	EDS
Estimated twinning fraction	0.018 for -h,-k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 26723 reflections (0.004%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6740	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.35% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.49	0/2312	0.68	0/3137
2	B	0.48	0/868	0.69	0/1173
3	C	0.58	0/80	0.83	0/108
4	D	0.43	0/1585	0.65	2/2150 (0.1%)
5	E	0.44	0/1993	0.67	1/2716 (0.0%)
All	All	0.46	0/6838	0.67	3/9284 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
5	E	21	LEU	CA-CB-CG	5.87	128.81	115.30
4	D	76	LEU	CA-CB-CG	5.48	127.90	115.30
4	D	89	LEU	CA-CB-CG	5.34	127.59	115.30

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	2247	0	2096	6	0
2	B	842	0	807	3	0
3	C	77	0	79	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	1552	0	1461	6	0
5	E	1937	0	1839	6	0
6	A	36	0	48	0	0
6	B	12	0	16	0	0
6	D	6	0	8	0	0
6	E	6	0	8	0	0
7	A	9	0	0	0	0
7	B	11	0	0	0	0
7	D	1	0	0	0	0
7	E	4	0	0	0	0
All	All	6740	0	6362	17	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 1.

All (17) 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:66:LYS:HE3	3:C:2:LEU:HB2	1.85	0.58
4:D:54:ASP:OD1	4:D:54:ASP:N	2.45	0.49
4:D:5:GLN:NE2	4:D:88:TYR:O	2.47	0.48
5:E:124:PRO:HD3	5:E:232:PRO:HB3	1.96	0.48
2:B:96:ASP:HB3	2:B:99:MET:HB2	1.95	0.48
5:E:14:LYS:HB3	5:E:119:LEU:HD13	1.95	0.48
1:A:202:ARG:NH1	2:B:99:MET:SD	2.88	0.46
1:A:177:GLU:H	1:A:177:GLU:HG2	1.55	0.45
1:A:5:MET:HB2	1:A:168:LEU:HD13	1.97	0.45
1:A:214:THR:HB	1:A:262:GLN:HB2	1.99	0.45
4:D:102:GLY:O	5:E:95:ARG:NH1	2.50	0.44
2:B:39:LEU:HD23	2:B:39:LEU:HA	1.85	0.42
4:D:138:VAL:HG11	5:E:146:VAL:HG21	2.01	0.42
5:E:102:GLN:HA	5:E:103:PRO:HD3	1.78	0.41
1:A:73:THR:HG22	5:E:98:LEU:HG	2.03	0.41
4:D:41:LYS:HE2	4:D:41:LYS:HB3	1.83	0.40
4:D:35:TYR:HB2	4:D:89:LEU:HB2	2.02	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	273/275 (99%)	257 (94%)	15 (6%)	1 (0%)	39	68
2	B	99/100 (99%)	96 (97%)	3 (3%)	0	100	100
3	C	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
4	D	198/200 (99%)	177 (89%)	19 (10%)	2 (1%)	19	43
5	E	244/245 (100%)	229 (94%)	14 (6%)	1 (0%)	39	68
All	All	821/829 (99%)	765 (93%)	52 (6%)	4 (0%)	34	62

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	172	ASP
4	D	205	PRO
5	E	222	ASN
1	A	267	PRO

### 5.3.2 Protein sidechains

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	231/231 (100%)	210 (91%)	21 (9%)	12	25
2	B	96/95 (101%)	87 (91%)	9 (9%)	11	23
3	C	8/8 (100%)	8 (100%)	0	100	100
4	D	178/178 (100%)	159 (89%)	19 (11%)	8	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	212/211 (100%)	184 (87%)	28 (13%)	5	11
All	All	725/723 (100%)	648 (89%)	77 (11%)	8	18

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	SER
1	A	12	VAL
1	A	35	ARG
1	A	52	ILE
1	A	58	GLU
1	A	67	VAL
1	A	72	GLN
1	A	73	THR
1	A	82	ARG
1	A	89	GLU
1	A	98	MET
1	A	121	LYS
1	A	128	GLU
1	A	177	GLU
1	A	183	ASP
1	A	222	GLU
1	A	224	GLN
1	A	225	THR
1	A	231	VAL
1	A	247	VAL
1	A	256	ARG
2	B	1	ILE
2	B	34[A]	ASP
2	B	34[B]	ASP
2	B	58	LYS
2	B	64	LEU
2	B	70	PHE
2	B	75	LYS
2	B	85	VAL
2	B	98	ASP
4	D	6	ASN
4	D	7	SER
4	D	27	ARG
4	D	51	SER
4	D	54	ASP
4	D	73	VAL

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Mol	Chain	Res	Type
4	D	76	LEU
4	D	81	GLN
4	D	87	THR
4	D	103	LYS
4	D	104	LEU
4	D	110	THR
4	D	120	ASN
4	D	135	ASP
4	D	150	VAL
4	D	167	ASP
4	D	173	PHE
4	D	194	ASN
4	D	195	ASN
5	E	9	LYS
5	E	19	MET
5	E	20	THR
5	E	21	LEU
5	E	25	GLN
5	E	26	ASP
5	E	27	MET
5	E	31	TYR
5	E	55	THR
5	E	60	VAL
5	E	67	VAL
5	E	72	THR
5	E	95	ARG
5	E	98	LEU
5	E	100	SER
5	E	105	GLU
5	E	113	ARG
5	E	118	ASP
5	E	150	THR
5	E	159	LEU
5	E	168	VAL
5	E	177	GLN
5	E	179	LEU
5	E	198	VAL
5	E	213	GLN
5	E	222	ASN
5	E	228	ASP
5	E	240	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such

sidechains are listed below:

Mol	Chain	Res	Type
4	D	105	GLN
5	E	22	GLN
5	E	57	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 carbohydrates 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	$\# Z  > 2$
6	GOL	A	301	-	5,5,5	0.37	0	5,5,5	0.22	0
6	GOL	A	302	-	5,5,5	0.31	0	5,5,5	0.29	0
6	GOL	A	303	-	5,5,5	0.36	0	5,5,5	0.79	0
6	GOL	A	304	-	5,5,5	0.35	0	5,5,5	0.58	0
6	GOL	A	305	-	5,5,5	0.31	0	5,5,5	0.46	0
6	GOL	A	306	-	5,5,5	0.31	0	5,5,5	0.45	0
6	GOL	B	101	-	5,5,5	0.38	0	5,5,5	0.26	0
6	GOL	B	102	-	5,5,5	0.37	0	5,5,5	0.34	0
6	GOL	D	301	-	5,5,5	0.39	0	5,5,5	0.31	0
6	GOL	E	301	-	5,5,5	0.34	0	5,5,5	0.50	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	-	-	0/4/4/4	0/0/0/0
6	GOL	A	302	-	-	0/4/4/4	0/0/0/0
6	GOL	A	303	-	-	0/4/4/4	0/0/0/0
6	GOL	A	304	-	-	0/4/4/4	0/0/0/0
6	GOL	A	305	-	-	0/4/4/4	0/0/0/0
6	GOL	A	306	-	-	0/4/4/4	0/0/0/0
6	GOL	B	101	-	-	0/4/4/4	0/0/0/0
6	GOL	B	102	-	-	0/4/4/4	0/0/0/0
6	GOL	D	301	-	-	0/4/4/4	0/0/0/0
6	GOL	E	301	-	-	0/4/4/4	0/0/0/0

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.

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	275/275 (100%)	0.29	20 (7%) 18 17	43, 67, 159, 195	0
2	B	100/100 (100%)	-0.00	1 (1%) 84 86	44, 61, 105, 118	0
3	C	9/9 (100%)	-0.19	0 100 100	51, 53, 59, 60	0
4	D	200/200 (100%)	1.51	57 (28%) 1 0	51, 108, 186, 201	0
5	E	245/245 (100%)	0.51	28 (11%) 7 6	30, 87, 143, 168	0
All	All	829/829 (100%)	0.61	106 (12%) 5 4	30, 82, 169, 201	0

All (106) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	133	SER	10.0
4	D	153	SER	9.5
4	D	167	ASP	8.4
4	D	135	ASP	7.6
4	D	186	ASP	7.4
4	D	134	SER	7.2
4	D	147	GLN	6.9
4	D	206	SER	6.7
4	D	184	LYS	6.2
4	D	205	PRO	6.1
4	D	172	ASP	5.7
4	D	197	ILE	5.6
1	A	275	GLU	5.6
4	D	203	PHE	5.6
4	D	171	MET	5.5
4	D	155	ASP	5.5
5	E	184	ALA	5.4
4	D	202	THR	5.4
4	D	185	SER	5.3
4	D	170	SER	5.2

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Mol	Chain	Res	Type	RSRZ
5	E	1	ASN	5.2
4	D	132	LYS	5.1
4	D	188	ALA	4.9
4	D	187	PHE	4.9
5	E	186	ASN	4.6
4	D	183	ASN	4.6
5	E	185	LEU	4.3
4	D	149	ASN	4.3
1	A	223	ASP	4.2
1	A	1	GLY	4.2
1	A	220	ASP	4.2
4	D	156	SER	4.2
1	A	274	TRP	4.0
4	D	191	ASN	3.9
1	A	197	HIS	3.9
4	D	169	ARG	3.9
1	A	222	GLU	3.8
5	E	226	THR	3.8
4	D	173	PHE	3.8
4	D	154	LYS	3.7
4	D	192	ALA	3.6
4	D	157	ASP	3.6
1	A	273	ARG	3.5
4	D	195	ASN	3.5
5	E	246	ASP	3.4
5	E	176	PRO	3.4
1	A	256	ARG	3.4
5	E	41	MET	3.4
4	D	131	SER	3.4
4	D	150	VAL	3.4
4	D	127	GLN	3.3
4	D	194	ASN	3.3
5	E	221	GLU	3.2
5	E	222	ASN	3.2
4	D	193	PHE	3.2
4	D	8	GLY	3.1
4	D	145	ASP	3.1
5	E	169	HIS	3.1
4	D	7	SER	3.0
4	D	152	GLN	2.9
5	E	2	ALA	2.9
4	D	179	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
4	D	136	LYS	2.9
4	D	174	LYS	2.9
4	D	189	CYS	2.9
1	A	194	VAL	2.9
5	E	224	GLU	2.9
4	D	119	GLN	2.8
4	D	139	CYS	2.8
5	E	206	PRO	2.8
4	D	159	TYR	2.7
1	A	252	GLY	2.7
4	D	79	ASP	2.7
5	E	182	GLN	2.6
5	E	197	ARG	2.6
4	D	180	ALA	2.6
4	D	138	VAL	2.6
4	D	204	PHE	2.5
1	A	248	VAL	2.5
5	E	33	SER	2.5
5	E	80	LEU	2.4
2	B	75	LYS	2.4
1	A	258	THR	2.4
4	D	74	SER	2.3
4	D	201	ASP	2.3
1	A	221	GLY	2.3
1	A	259	CYS	2.3
4	D	168	MET	2.3
5	E	16	GLY	2.3
5	E	40	GLY	2.3
1	A	176	LYS	2.3
1	A	227	ASP	2.3
1	A	58	GLU	2.3
1	A	264	GLU	2.3
5	E	139	HIS	2.3
5	E	39	PRO	2.2
1	A	251	SER	2.2
4	D	140	LEU	2.2
5	E	201	THR	2.2
5	E	134	GLU	2.2
5	E	244	ARG	2.2
4	D	196	SER	2.2
4	D	78	ARG	2.2
5	E	207	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
5	E	183	PRO	2.1
5	E	117	GLU	2.1

## 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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
6	GOL	A	306	6/6	0.83	0.25	5.93	89,90,91,91	0
6	GOL	A	302	6/6	0.64	0.44	3.58	60,61,62,62	6
6	GOL	A	304	6/6	0.86	0.25	1.39	82,83,84,84	0
6	GOL	E	301	6/6	0.93	0.23	1.34	86,86,87,87	0
6	GOL	A	305	6/6	0.78	0.23	1.17	89,90,91,92	0
6	GOL	B	101	6/6	0.92	0.15	-0.20	82,83,83,84	0
6	GOL	A	303	6/6	0.93	0.13	-0.39	59,61,61,64	0
6	GOL	A	301	6/6	0.95	0.13	-0.71	71,73,73,73	0
6	GOL	D	301	6/6	0.86	0.15	-1.84	96,98,98,98	0
6	GOL	B	102	6/6	0.74	0.33	-	62,62,64,65	6

## 6.5 Other polymers [i](#)

There are no such residues in this entry.