



# Full wwPDB X-ray Structure Validation Report

Sep 12, 2014 – 12:50 AM EDT

PDB ID : 4UQ2  
Title : Crystal structure of HLA-A1101 in complex with an azobenzene- containing peptide  
Authors : Thong, S.Y.; Yap, J.W.; Lim, P.Y.; Verhelst, S.H.; Lescar, J.; Meijers, R.; Grotenbreg, G.M.  
Deposited on : 2014-06-19  
Resolution : 2.43 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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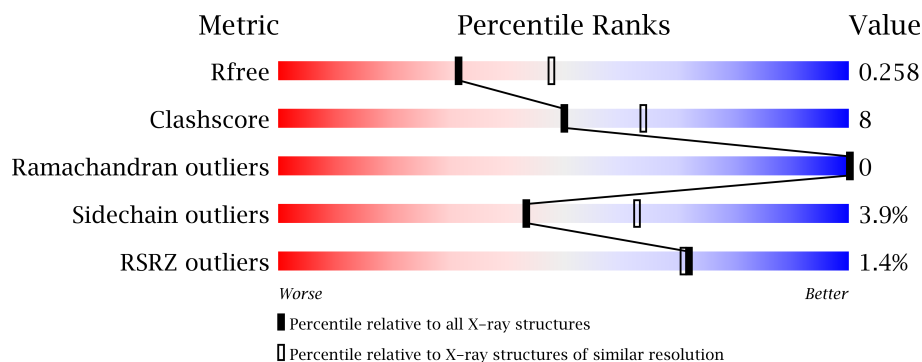
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.16 November 2013  
Xtriage (Phenix) : dev-1439  
EDS : stable23489  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable23489

# 1 Overall quality at a glance

The reported resolution of this entry is 2.43 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))
$R_{free}$	66092	2989 (2.48-2.40)
Clashscore	79885	3698 (2.48-2.40)
Ramachandran outliers	78287	3639 (2.48-2.40)
Sidechain outliers	78261	3640 (2.48-2.40)
RSRZ outliers	66119	2993 (2.48-2.40)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	275	
1	C	275	
2	B	99	
2	D	99	
3	E	7	
3	G	7	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6761 atoms, of which 0 are hydrogen and 0 are deuterium.

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-11 ALPHA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	275	Total	C	N	O	S	0	5	0
			2283	1417	416	440	10			
1	C	275	Total	C	N	O	S	0	5	0
			2282	1416	415	441	10			

- Molecule 2 is a protein called BETA-2-MICROGLOBULIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	99	Total	C	N	O	S	0	0	0
			829	528	140	158	3			
2	D	99	Total	C	N	O	S	0	1	0
			838	534	142	159	3			

- Molecule 3 is a protein called AZOBENZENE-CONTAININGPEPTIDE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	7	Total	C	N	O	S	0	7	0
			140	98	20	20	2			
3	G	7	Total	C	N	O	S	0	7	0
			140	98	20	20	2			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	74	Total	O	0	0
			74	74		
4	B	39	Total	O	0	0
			39	39		
4	C	92	Total	O	0	0
			92	92		
4	D	36	Total	O	0	0
			36	36		

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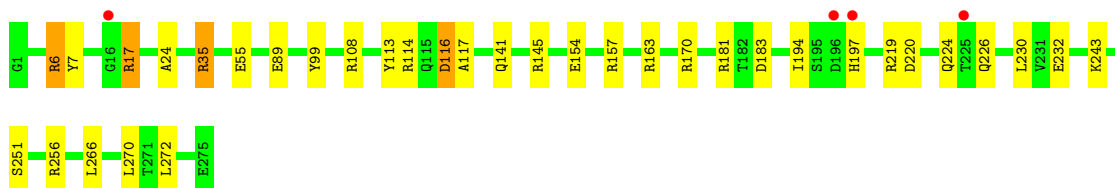
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	6	Total	O	0	0
			6	6		
4	G	2	Total	O	0	0
			2	2		

### 3 Residue-property plots

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.

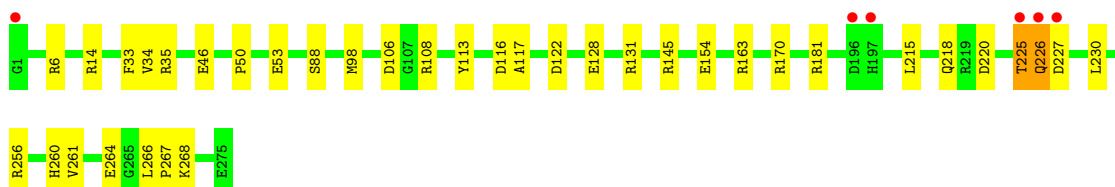
- Molecule 1: HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-11 ALPHA CHAIN

Chain A: 



- Molecule 1: HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-11 ALPHA CHAIN

Chain C: 



- Molecule 2: BETA-2-MICROGLOBULIN

Chain B: 

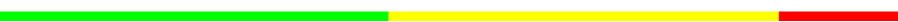


- Molecule 2: BETA-2-MICROGLOBULIN

Chain D: 



- Molecule 3: AZOBENZENE-CONTAININGPEPTIDE

Chain E: 



- Molecule 3: AZOBENZENE-CONTAININGPEPTIDE

Chain G: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.14Å 71.46Å 75.43Å 106.74° 96.74° 105.28°	Depositor
Resolution (Å)	29.93 – 2.43 29.93 – 2.43	Depositor EDS
% Data completeness (in resolution range)	94.6 (29.93-2.43) 94.7 (29.93-2.43)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	7.38 (at 2.42Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.187 , 0.251 0.193 , 0.258	Depositor DCC
$R_{free}$ test set	1740 reflections (5.23%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.3	Xtriage
Anisotropy	0.064	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 16.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 35018 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6761	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.85% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: XY1

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	0.73	0/2350	0.84	4/3187 (0.1%)
1	C	0.73	0/2349	0.86	2/3186 (0.1%)
2	B	0.79	0/852	0.86	1/1152 (0.1%)
2	D	0.76	0/861	0.80	0/1163
3	E	1.90	6/100 (6.0%)	1.63	2/126 (1.6%)
3	G	1.96	6/100 (6.0%)	2.05	6/126 (4.8%)
All	All	0.80	12/6612 (0.2%)	0.89	15/8940 (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
3	E	0	2
3	G	0	3
All	All	0	5

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	5[A]	TYR	C-O	9.20	1.40	1.23
3	G	5[B]	TYR	C-O	9.20	1.40	1.23
3	E	5[A]	TYR	C-O	8.81	1.40	1.23
3	E	5[B]	TYR	C-O	8.81	1.40	1.23
3	G	5[A]	TYR	C-N	6.06	1.45	1.34
3	G	5[B]	TYR	C-N	6.06	1.45	1.34
3	E	5[A]	TYR	C-N	5.86	1.45	1.34
3	E	5[B]	TYR	C-N	5.86	1.45	1.34
3	G	7[A]	LYS	C-O	5.64	1.34	1.23
3	G	7[B]	LYS	C-O	5.64	1.34	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	7[A]	LYS	C-O	5.63	1.34	1.23
3	E	7[B]	LYS	C-O	5.63	1.34	1.23

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	6	ARG	NE-CZ-NH1	7.08	123.84	120.30
3	G	5[A]	TYR	CB-CG-CD1	-7.06	116.76	121.00
3	G	5[B]	TYR	CB-CG-CD1	-7.06	116.76	121.00
3	E	5[A]	TYR	O-C-N	-6.93	107.93	121.10
3	E	5[B]	TYR	O-C-N	-6.93	107.93	121.10
3	G	5[A]	TYR	O-C-N	-6.32	109.09	121.10
3	G	5[B]	TYR	O-C-N	-6.32	109.09	121.10
3	G	3[A]	MET	CG-SD-CE	5.46	108.94	100.20
3	G	3[B]	MET	CG-SD-CE	5.46	108.94	100.20
1	C	145	ARG	NE-CZ-NH2	-5.46	117.57	120.30
2	B	34	ASP	CB-CG-OD1	-5.36	113.47	118.30
1	A	6	ARG	NE-CZ-NH2	-5.35	117.62	120.30
1	A	35	ARG	NE-CZ-NH2	-5.29	117.65	120.30
1	C	122	ASP	CB-CG-OD1	5.09	122.88	118.30
1	A	116	ASP	CB-CG-OD1	5.02	122.82	118.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	E	5[A]	TYR	Mainchain
3	E	5[B]	TYR	Mainchain
3	G	5[A]	TYR	Mainchain
3	G	5[B]	TYR	Mainchain
3	G	6[B]	PRO	Peptide

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2283	0	2133	24	0
1	C	2282	0	2131	23	0
2	B	829	0	794	6	0
2	D	838	0	806	10	0
3	E	140	0	129	32	0
3	G	140	0	130	35	0
4	A	74	0	0	5	1
4	B	39	0	0	0	0
4	C	92	0	0	9	1
4	D	36	0	0	2	0
4	E	6	0	0	1	0
4	G	2	0	0	0	0
All	All	6761	0	6123	95	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 8.

All (95) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:E:6[B]:PRO:HD3	3:G:4[B]:XY1:O30	1.03	1.19
3:E:4[B]:XY1:C26	3:G:4[B]:XY1:C26	2.20	1.19
3:E:4[A]:XY1:O30	4:E:2004:HOH:O	1.62	1.16
3:E:6[B]:PRO:CD	3:G:4[B]:XY1:O30	1.95	1.15
1:A:17[A]:ARG:CD	1:A:17[A]:ARG:O	2.04	1.04
1:C:227[A]:ASP:O	1:C:227[A]:ASP:OD1	1.76	1.01
3:E:5[B]:TYR:O	3:G:4[B]:XY1:H27	1.62	0.98
3:E:4[B]:XY1:C29	3:G:4[B]:XY1:C26	2.26	0.97
1:A:17[A]:ARG:HD3	1:A:17[A]:ARG:O	1.65	0.95
3:E:4[B]:XY1:C25	3:G:4[B]:XY1:C27	2.44	0.94
3:E:4[B]:XY1:C26	3:G:4[B]:XY1:C25	2.55	0.84
3:E:4[B]:XY1:C27	3:G:4[B]:XY1:C25	2.57	0.81
1:A:17[A]:ARG:HD2	1:A:17[A]:ARG:O	1.81	0.79
3:E:4[B]:XY1:C25	3:G:4[B]:XY1:C28	2.62	0.78
3:E:4[B]:XY1:H27	3:G:5[B]:TYR:O	1.83	0.77
3:E:4[B]:XY1:C25	3:G:4[B]:XY1:C26	2.62	0.77
3:E:4[B]:XY1:H25	3:G:4[B]:XY1:C27	2.21	0.71
3:E:5[B]:TYR:N	3:G:4[B]:XY1:C27	2.54	0.70
1:A:17[A]:ARG:HH11	1:A:17[A]:ARG:HG3	1.58	0.68
1:C:220:ASP:OD2	1:C:256:ARG:NH1	2.26	0.67
1:A:163:ARG:NH1	4:A:2049:HOH:O	2.27	0.67
1:A:6:ARG:NH2	1:A:113:TYR:CE1	2.61	0.67
3:E:4[B]:XY1:C24	3:G:4[B]:XY1:C23	2.73	0.67
3:E:5[B]:TYR:N	3:G:4[B]:XY1:H27	2.10	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:131:ARG:NH2	4:C:2054:HOH:O	2.25	0.64
3:E:4[B]:XY1:C26	3:G:4[B]:XY1:C27	2.72	0.64
1:A:17[A]:ARG:NH1	1:A:17[A]:ARG:HG3	2.12	0.64
3:E:4[B]:XY1:C29	3:G:4[B]:XY1:C27	2.76	0.64
3:E:5[B]:TYR:CA	3:G:4[B]:XY1:O30	2.45	0.63
4:C:2049:HOH:O	2:D:1:ILE:HA	1.97	0.63
3:G:4[B]:XY1:C29	3:G:5[B]:TYR:CD1	2.86	0.59
1:A:219:ARG:HD3	4:A:2062:HOH:O	2.04	0.57
1:C:218:GLN:HG3	1:C:260:HIS:CD2	2.40	0.57
1:C:131:ARG:NE	4:C:2054:HOH:O	2.31	0.57
1:A:7:TYR:CE1	3:G:2[B]:ILE:HG22	2.39	0.56
1:C:6:ARG:NH2	1:C:113:TYR:CE1	2.73	0.56
3:E:5[B]:TYR:N	3:G:4[B]:XY1:O30	2.39	0.55
1:A:89:GLU:HG2	4:A:2031:HOH:O	2.06	0.55
1:C:35[B]:ARG:CZ	1:C:46:GLU:OE2	2.55	0.54
1:C:181:ARG:NH2	4:C:2015:HOH:O	2.40	0.54
1:C:215:LEU:HD22	1:C:261:VAL:HG22	1.89	0.54
1:A:220:ASP:OD2	1:A:256:ARG:NH1	2.40	0.54
1:C:266:LEU:O	1:C:267:PRO:C	2.44	0.53
3:E:5[B]:TYR:N	3:G:4[B]:XY1:C26	2.72	0.53
3:E:5[B]:TYR:HA	3:G:4[B]:XY1:O30	2.07	0.53
1:C:225[B]:THR:OG1	1:C:226[B]:GLN:HG3	2.09	0.52
3:E:4[B]:XY1:H25	3:G:4[B]:XY1:C28	2.39	0.52
1:C:128:GLU:HG2	4:C:2042:HOH:O	2.09	0.51
2:D:96:ASP:O	2:D:97:ARG:C	2.48	0.50
2:D:16:GLU:O	2:D:19[A]:LYS:HB2	2.11	0.50
3:E:4[B]:XY1:C24	3:G:4[B]:XY1:C24	2.90	0.50
2:D:89:GLN:HB3	4:D:2035:HOH:O	2.11	0.50
1:A:224:GLN:HG3	1:A:224:GLN:O	2.12	0.48
2:D:49:VAL:HG21	4:D:2019:HOH:O	2.13	0.48
1:C:117:ALA:HB2	2:D:60:TRP:CE2	2.49	0.47
1:A:17[A]:ARG:HH11	1:A:17[A]:ARG:CG	2.24	0.47
1:A:197:HIS:HA	1:A:251:SER:HB3	1.97	0.47
3:E:4[B]:XY1:C23	3:G:4[B]:XY1:C24	2.93	0.47
2:B:98:ASP:O	2:B:99:MET:HG2	2.15	0.47
2:D:98:ASP:O	2:D:99:MET:HG2	2.16	0.46
1:A:55:GLU:OE2	1:A:170:ARG:NH2	2.48	0.46
1:C:154:GLU:HG2	4:C:2063:HOH:O	2.16	0.46
3:E:4[B]:XY1:C25	3:G:4[B]:XY1:C23	2.93	0.46
1:A:99:TYR:CE2	3:G:3[B]:MET:HE3	2.50	0.46
2:B:1:ILE:O	2:B:1:ILE:HG23	2.15	0.46
1:A:219:ARG:CD	4:A:2062:HOH:O	2.61	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:19[A]:LYS:O	2:D:72:PRO:HD2	2.16	0.46
3:E:4[B]:XY1:C27	3:G:5[B]:TYR:N	2.79	0.46
4:A:2021:HOH:O	1:C:163:ARG:NH1	2.49	0.45
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.50	0.45
2:D:19[B]:LYS:O	2:D:72:PRO:HD2	2.16	0.45
1:C:170:ARG:HD3	4:C:2072:HOH:O	2.16	0.44
1:C:50:PRO:HA	1:C:53:GLU:OE1	2.17	0.44
3:E:4[B]:XY1:C25	3:G:4[B]:XY1:C25	2.92	0.44
1:A:141:GLN:HG3	1:A:145:ARG:HH11	1.83	0.44
1:C:225[B]:THR:OG1	1:C:226[B]:GLN:CG	2.66	0.43
3:G:5[B]:TYR:N	3:G:5[B]:TYR:CD1	2.79	0.43
3:E:4[B]:XY1:H27	3:G:5[B]:TYR:N	2.33	0.43
1:C:14:ARG:NE	4:C:2011:HOH:O	2.51	0.43
2:B:1:ILE:HD12	2:B:1:ILE:HA	1.90	0.42
1:C:106:ASP:OD1	1:C:108:ARG:HG2	2.20	0.42
1:A:154:GLU:HG3	1:A:157:ARG:HH22	1.84	0.42
1:A:181:ARG:NH1	1:A:183:ASP:OD2	2.46	0.42
3:E:4[B]:XY1:C24	3:G:4[B]:XY1:C28	2.98	0.42
2:B:24:ASN:HB3	2:B:65:LEU:HD11	2.01	0.42
1:A:230:LEU:HD11	1:A:243:LYS:HE3	2.02	0.41
1:C:33:PHE:CD2	1:C:34:VAL:HG13	2.55	0.41
1:C:14:ARG:CZ	4:C:2011:HOH:O	2.68	0.41
2:B:51:HIS:HA	2:B:65:LEU:O	2.20	0.41
3:E:4[B]:XY1:C28	3:G:4[B]:XY1:C25	2.99	0.41
1:A:266:LEU:HD13	1:A:270:LEU:HG	2.03	0.41
1:A:24:ALA:O	1:A:35:ARG:HA	2.21	0.41
3:E:4[B]:XY1:O30	3:G:6[B]:PRO:HD3	2.21	0.41
2:D:51:HIS:HB3	2:D:66:TYR:CD2	2.56	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:A:2018:HOH:O	4:C:2038:HOH:O[1_454]	2.13	0.07

## 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	278/275 (101%)	266 (96%)	12 (4%)	0	100	100
1	C	278/275 (101%)	269 (97%)	9 (3%)	0	100	100
2	B	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
2	D	98/99 (99%)	95 (97%)	3 (3%)	0	100	100
3	E	4/7 (57%)	2 (50%)	2 (50%)	0	100	100
3	G	4/7 (57%)	2 (50%)	2 (50%)	0	100	100
All	All	759/762 (100%)	728 (96%)	31 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	237/232 (102%)	227 (96%)	10 (4%)	40	59
1	C	237/232 (102%)	228 (96%)	9 (4%)	44	64
2	B	94/94 (100%)	89 (95%)	5 (5%)	32	47
2	D	95/94 (101%)	88 (93%)	7 (7%)	20	29
3	E	10/5 (200%)	10 (100%)	0	100	100
3	G	10/5 (200%)	10 (100%)	0	100	100
All	All	683/662 (103%)	652 (96%)	31 (4%)	43	56

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17[A]	ARG
1	A	17[B]	ARG
1	A	108	ARG
1	A	114	ARG
1	A	116	ASP
1	A	194	ILE

*Continued on next page...*

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Mol	Chain	Res	Type
1	A	226[A]	GLN
1	A	226[B]	GLN
1	A	232	GLU
1	A	272	LEU
2	B	4	THR
2	B	19	LYS
2	B	34	ASP
2	B	70	PHE
2	B	74	GLU
1	C	88	SER
1	C	116	ASP
1	C	225[A]	THR
1	C	225[B]	THR
1	C	226[A]	GLN
1	C	226[B]	GLN
1	C	230	LEU
1	C	264	GLU
1	C	268	LYS
2	D	1	ILE
2	D	19[A]	LYS
2	D	19[B]	LYS
2	D	20	SER
2	D	70	PHE
2	D	91	LYS
2	D	99	MET

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

Mol	Chain	Res	Type
1	A	62	GLN
1	A	156	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 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 ⓘ

### 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%)	-0.25	4 (1%) 70 69	15, 27, 55, 87	0
1	C	275/275 (100%)	-0.28	6 (2%) 59 56	13, 28, 53, 88	0
2	B	99/99 (100%)	-0.47	0 100 100	14, 25, 46, 62	0
2	D	99/99 (100%)	-0.37	1 (1%) 79 79	16, 29, 50, 61	0
3	E	6/7 (85%)	0.39	0 100 100	17, 19, 21, 28	0
3	G	6/7 (85%)	0.17	0 100 100	18, 19, 22, 30	0
All	All	760/762 (99%)	-0.30	11 (1%) 72 71	13, 27, 53, 88	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	196	ASP	4.9
1	A	196	ASP	4.3
1	C	197	HIS	4.2
1	C	1	GLY	3.5
1	C	226[A]	GLN	3.3
1	A	197	HIS	3.3
2	D	99	MET	2.8
1	C	227[A]	ASP	2.7
1	A	16	GLY	2.1
1	C	225[A]	THR	2.1
1	A	225	THR	2.1

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.



### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

There are no ligands in this entry.

### 6.5 Other polymers ⓘ

There are no such residues in this entry.