wwPDB X-ray Structure Validation Summary Report (i)

Oct 7, 2026 – 04:05 pm BST

PDB ID	:	31VO / pdb_000031vo
Title	:	Crystal structure of amyloid beta 1-15 fragment bound to HLA-DR1
Authors	:	Lopez-Sagaseta, J.; Erausquin, E.; Dichiara-Rodriguez, M.G.; Oyon-Olea, L.
Deposited on	:	2026-06-24
Resolution	:	2.00 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:

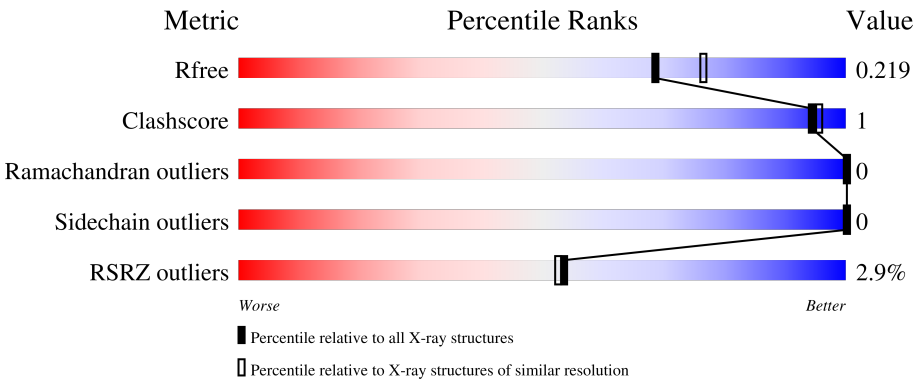
MolProbity	:	4-5-2 with Phenix2.2
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

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 2.00 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	B	227	3% 86% • 11%
1	D	227	4% 87% • 12%
2	A	198	3% 83% 6% 11%
2	C	198	2% 87% • 11%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 6200 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 Amyloid-beta protein 40,HLA class II histocompatibility antigen, DRB1 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	203	1613	1019	288	300	6	0	0	0
1	D	199	1581	1000	281	294	6	0	0	0

There are 70 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-16B	GLY	-	linker	UNP P05067
B	-16C	GLY	-	linker	UNP P05067
B	-16D	GLY	-	linker	UNP P05067
B	-16E	GLY	-	linker	UNP P05067
B	-16F	GLY	-	linker	UNP P05067
B	-16G	SER	-	linker	UNP P05067
B	-16H	GLY	-	linker	UNP P05067
B	-16I	GLY	-	linker	UNP P05067
B	-16J	GLY	-	linker	UNP P05067
B	-16K	SER	-	linker	UNP P05067
B	-16L	GLY	-	linker	UNP P05067
B	-16M	GLY	-	linker	UNP P05067
B	-16N	SER	-	linker	UNP P05067
B	-16O	GLY	-	linker	UNP P05067
B	-16P	GLY	-	linker	UNP P05067
B	10	LEU	PRO	conflict	UNP P01911
B	12	PHE	ARG	conflict	UNP P01911
B	25	LEU	PHE	conflict	UNP P01911
B	27	GLU	ASP	conflict	UNP P01911
B	29	CYS	TYR	conflict	UNP P01911
B	30	ILE	PHE	conflict	UNP P01911
B	46	TYR	PHE	conflict	UNP P01911
B	66	LEU	ILE	conflict	UNP P01911
B	70	ARG	ALA	conflict	UNP P01911

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Chain	Residue	Modelled	Actual	Comment	Reference
B	85	GLY	VAL	conflict	UNP P01911
B	95	GLU	GLN	conflict	UNP P01911
B	132	ARG	LEU	conflict	UNP P01911
B	141	VAL	MET	conflict	UNP P01911
B	190	SER	-	expression tag	UNP P01911
B	191	LEU	-	expression tag	UNP P01911
B	192	GLU	-	expression tag	UNP P01911
B	193	VAL	-	expression tag	UNP P01911
B	194	LEU	-	expression tag	UNP P01911
B	195	PHE	-	expression tag	UNP P01911
B	196	GLN	-	expression tag	UNP P01911
D	-16B	GLY	-	linker	UNP P05067
D	-16C	GLY	-	linker	UNP P05067
D	-16D	GLY	-	linker	UNP P05067
D	-16E	GLY	-	linker	UNP P05067
D	-16F	GLY	-	linker	UNP P05067
D	-16G	SER	-	linker	UNP P05067
D	-16H	GLY	-	linker	UNP P05067
D	-16I	GLY	-	linker	UNP P05067
D	-16J	GLY	-	linker	UNP P05067
D	-16K	SER	-	linker	UNP P05067
D	-16L	GLY	-	linker	UNP P05067
D	-16M	GLY	-	linker	UNP P05067
D	-16N	SER	-	linker	UNP P05067
D	-16O	GLY	-	linker	UNP P05067
D	-16P	GLY	-	linker	UNP P05067
D	10	LEU	PRO	conflict	UNP P01911
D	12	PHE	ARG	conflict	UNP P01911
D	25	LEU	PHE	conflict	UNP P01911
D	27	GLU	ASP	conflict	UNP P01911
D	29	CYS	TYR	conflict	UNP P01911
D	30	ILE	PHE	conflict	UNP P01911
D	46	TYR	PHE	conflict	UNP P01911
D	66	LEU	ILE	conflict	UNP P01911
D	70	ARG	ALA	conflict	UNP P01911
D	85	GLY	VAL	conflict	UNP P01911
D	95	GLU	GLN	conflict	UNP P01911
D	132	ARG	LEU	conflict	UNP P01911
D	141	VAL	MET	conflict	UNP P01911
D	190	SER	-	expression tag	UNP P01911
D	191	LEU	-	expression tag	UNP P01911
D	192	GLU	-	expression tag	UNP P01911

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Chain	Residue	Modelled	Actual	Comment	Reference
D	193	VAL	-	expression tag	UNP P01911
D	194	LEU	-	expression tag	UNP P01911
D	195	PHE	-	expression tag	UNP P01911
D	196	GLN	-	expression tag	UNP P01911

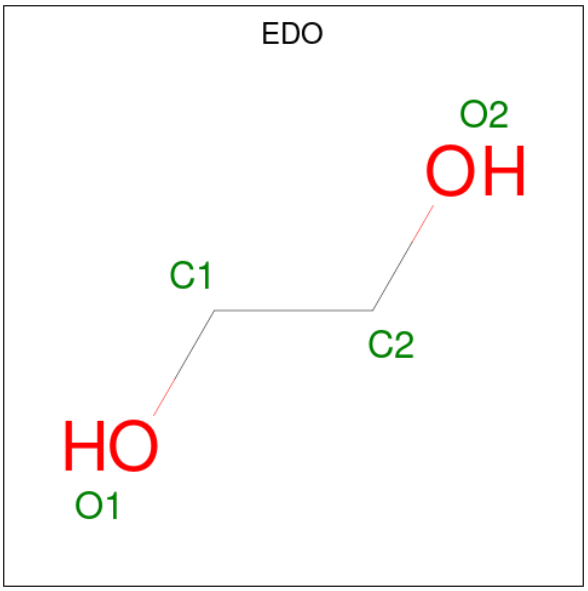
- Molecule 2 is a protein called HLA class II histocompatibility antigen, DR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	A	176	1400	908	229	258	5	0	0	0
			Total	C	N	O	S			
2	C	177	1400	909	228	258	5	0	0	0

There are 14 discrepancies between the modelled and reference sequences:

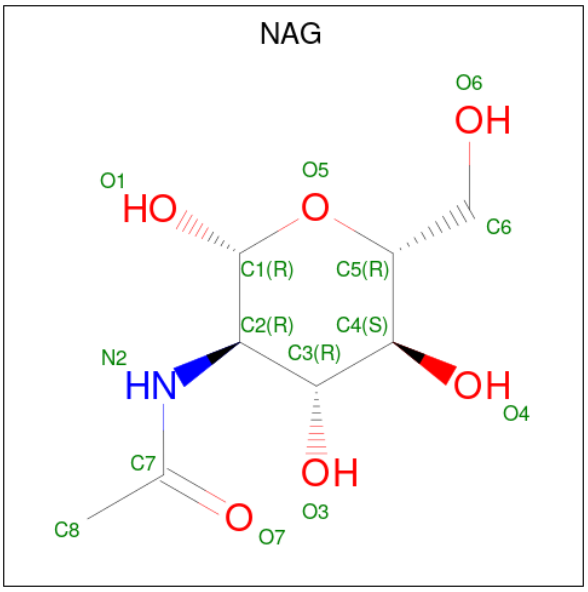
Chain	Residue	Modelled	Actual	Comment	Reference
A	192	SER	-	expression tag	UNP P01903
A	193	LEU	-	expression tag	UNP P01903
A	194	GLU	-	expression tag	UNP P01903
A	195	VAL	-	expression tag	UNP P01903
A	196	LEU	-	expression tag	UNP P01903
A	197	PHE	-	expression tag	UNP P01903
A	198	GLN	-	expression tag	UNP P01903
C	192	SER	-	expression tag	UNP P01903
C	193	LEU	-	expression tag	UNP P01903
C	194	GLU	-	expression tag	UNP P01903
C	195	VAL	-	expression tag	UNP P01903
C	196	LEU	-	expression tag	UNP P01903
C	197	PHE	-	expression tag	UNP P01903
C	198	GLN	-	expression tag	UNP P01903

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	4	2	2	0	0
			Total	C	O		
3	A	1	4	2	2	0	0
			Total	C	O		
3	C	1	4	2	2	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	14	8	1	5	0	0

- Molecule 5 is water.

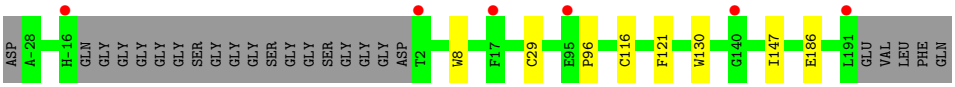
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	B	54	54	54	0	0
			Total	O		
5	A	44	44	44	0	0
			Total	O		
5	D	51	51	51	0	0
			Total	O		
5	C	31	31	31	0	0

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.

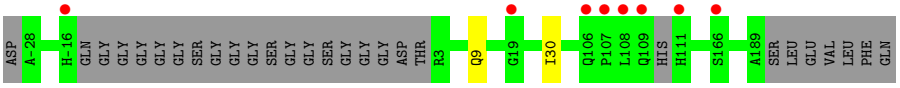
• Molecule 1: Amyloid-beta protein 40,HLA class II histocompatibility antigen, DRB1 beta chain

Chain B:



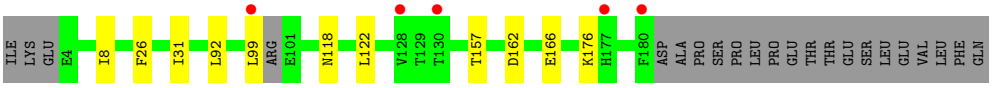
• Molecule 1: Amyloid-beta protein 40,HLA class II histocompatibility antigen, DRB1 beta chain

Chain D:



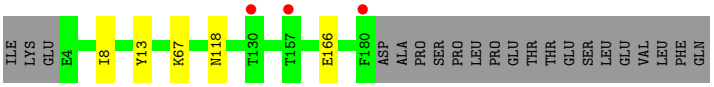
• Molecule 2: HLA class II histocompatibility antigen, DR alpha chain

Chain A:



• Molecule 2: HLA class II histocompatibility antigen, DR alpha chain

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	57.31Å 118.51Å 67.13Å 90.00° 109.15° 90.00°	Depositor
Resolution (Å)	31.71 – 2.00 31.71 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.1 (31.71-2.00) 99.2 (31.71-2.00)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.94 (at 2.00Å)	Xtriage
Refinement program	PHENIX 2.2.1_6174	Depositor
R, R_{free}	0.191 , 0.219 0.191 , 0.219	Depositor DCC
R_{free} test set	2903 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å^2)	34.7	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 42.1	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	0.95	EDS
Total number of atoms	6200	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.36% 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: NAG, EDO

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	B	0.29	0/1656	0.45	0/2256
1	D	0.25	0/1622	0.43	0/2207
2	A	0.27	0/1442	0.46	0/1972
2	C	0.26	0/1444	0.47	0/1981
All	All	0.27	0/6164	0.45	0/8416

There are no bond length outliers.

There are no bond angle outliers.

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	B	1613	0	1489	5	0
1	D	1581	0	1465	1	0
2	A	1400	0	1317	7	0
2	C	1400	0	1298	3	0
3	A	8	0	12	1	0
3	C	4	0	6	1	0
4	A	14	0	13	0	0
5	A	44	0	0	0	0
5	B	54	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	31	0	0	0	0
5	D	51	0	0	0	0
All	All	6200	0	5600	15	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.

The worst 5 of 15 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)
2:C:13:TYR:CE2	2:C:67:LYS:HG3	2.39	0.58
1:B:186:GLU:CD	1:B:186:GLU:H	2.13	0.57
2:A:99:LEU:HD21	2:A:157:THR:HG23	1.89	0.55
2:A:118:ASN:HB2	2:A:166:GLU:HB2	1.93	0.49
2:C:118:ASN:HB2	2:C:166:GLU:HB2	1.95	0.47

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	B	199/227 (88%)	197 (99%)	2 (1%)	0	100	100
1	D	193/227 (85%)	191 (99%)	2 (1%)	0	100	100
2	A	172/198 (87%)	171 (99%)	1 (1%)	0	100	100
2	C	175/198 (88%)	174 (99%)	1 (1%)	0	100	100
All	All	739/850 (87%)	733 (99%)	6 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	B	169/194 (87%)	169 (100%)	0	100	100
1	D	166/194 (86%)	166 (100%)	0	100	100
2	A	151/182 (83%)	151 (100%)	0	100	100
2	C	149/182 (82%)	149 (100%)	0	100	100
All	All	635/752 (84%)	635 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	111	HIS
1	D	111	HIS
1	D	173	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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

4 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	$\#\|Z\| > 2$
3	EDO	A	201	-	3,3,3	0.27	0	2,2,2	0.35	0
4	NAG	A	203	2	14,14,15	0.68	0	17,19,21	0.92	0
3	EDO	A	202	-	3,3,3	0.35	0	2,2,2	0.46	0
3	EDO	C	201	-	3,3,3	0.31	0	2,2,2	0.51	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
3	EDO	A	201	-	-	0/1/1/1	-
4	NAG	A	203	2	-	0/6/23/26	0/1/1/1
3	EDO	A	202	-	-	0/1/1/1	-
3	EDO	C	201	-	-	0/1/1/1	-

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.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	202	EDO	1	0
3	C	201	EDO	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	B	203/227 (89%)	0.02	6 (2%)	52	51	25, 35, 50, 61	0
1	D	199/227 (87%)	0.19	8 (4%)	42	41	28, 37, 54, 68	0
2	A	176/198 (88%)	0.21	5 (2%)	55	54	24, 37, 55, 66	0
2	C	177/198 (89%)	0.33	3 (1%)	69	68	27, 43, 63, 77	0
All	All	755/850 (88%)	0.18	22 (2%)	53	52	24, 38, 58, 77	0

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	109	GLN	3.8
2	A	177	HIS	3.7
2	A	180	PHE	3.6
2	C	130	THR	3.4
2	C	180	PHE	3.4

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 oligosaccharides 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
4	NAG	A	203	14/15	0.75	0.12	50,63,69,69	0
3	EDO	C	201	4/4	0.93	0.10	36,38,39,41	0
3	EDO	A	202	4/4	0.94	0.09	36,36,41,42	0
3	EDO	A	201	4/4	0.97	0.07	36,41,42,42	0

6.5 Other polymers (i)

There are no such residues in this entry.