wwPDB X-ray Structure Validation Summary Report (i)

Nov 2, 2023 – 01:52 PM EDT

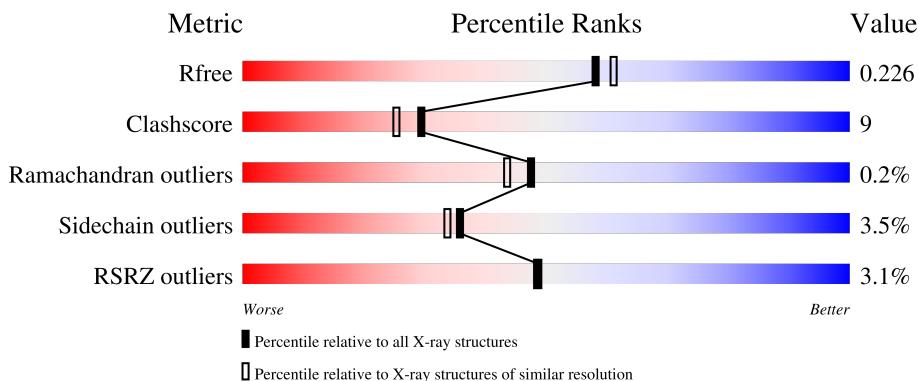|		
PDB ID	:	3VNK
Title	:	Crystal structures of D-Psicose 3-epimerase with D-fructose from Clostridium cellulolyticum H10
Authors	:	Chan, H.C.; Zhu, Y.; Hu, Y.; Ko, T.P.; Huang, C.H.; Ren, F.; Chen, C.C.; Guo, R.T.; Sun, Y.
Deposited on	:	2012-01-16
Resolution	:	2.02 Å(reported)

1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.02 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	Percentile Ranks	Value
Rfree		0.226
Clashscore		9
Ramachandran outliers		0.2%
Sidechain outliers		3.5%
RSRZ outliers		3.1%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	10434 (2.04-2.00)
Clashscore	141614	11643 (2.04-2.00)
Ramachandran outliers	138981	11493 (2.04-2.00)
Sidechain outliers	138945	11492 (2.04-2.00)
RSRZ outliers	127900	10220 (2.04-2.00)

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	A	293	2% / 81% / 15% / ··
1	B	293	3% / 84% / 12% / ··
1	C	293	4% / 77% / 19% / ··
1	D	293	4% / 76% / 21% / ··

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 10179 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 Xylose isomerase domain protein TIM barrel.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	290	Total	C	N	O	S	0	0	0
			2303	1465	391	436	11			
1	B	288	Total	C	N	O	S	0	0	0
			2287	1456	387	434	10			
1	C	289	Total	C	N	O	S	0	0	0
			2292	1459	388	435	10			
1	D	288	Total	C	N	O	S	0	0	0
			2287	1456	387	434	10			

- Molecule 2 is D-fructose (three-letter code: FUD) (formula: $C_6H_{12}O_6$).
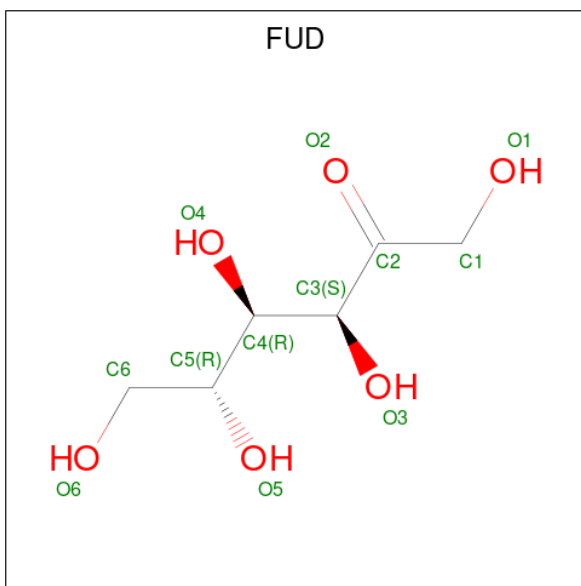
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			12	6	6		
2	B	1	Total	C	O	0	0
			12	6	6		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total 12	C 6	O 6	0	0
2	D	1	Total 12	C 6	O 6	0	0

• Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total 2	Mn 2	0	0
3	B	2	Total 2	Mn 2	0	0
3	C	2	Total 2	Mn 2	0	0
3	D	2	Total 2	Mn 2	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	263	Total 263	O 263	0	0
4	B	255	Total 255	O 255	0	0
4	C	205	Total 205	O 205	0	0
4	D	231	Total 231	O 231	0	0

3 Residue-property plots ⓘ

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.

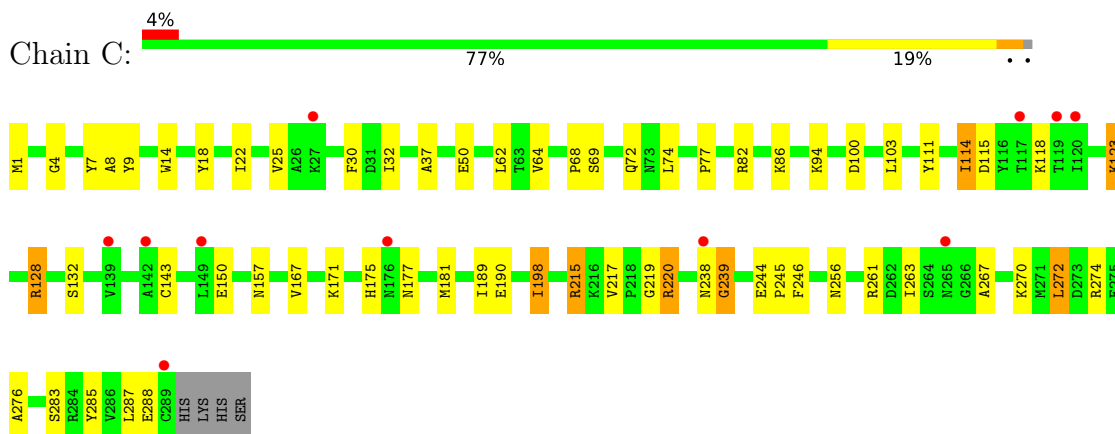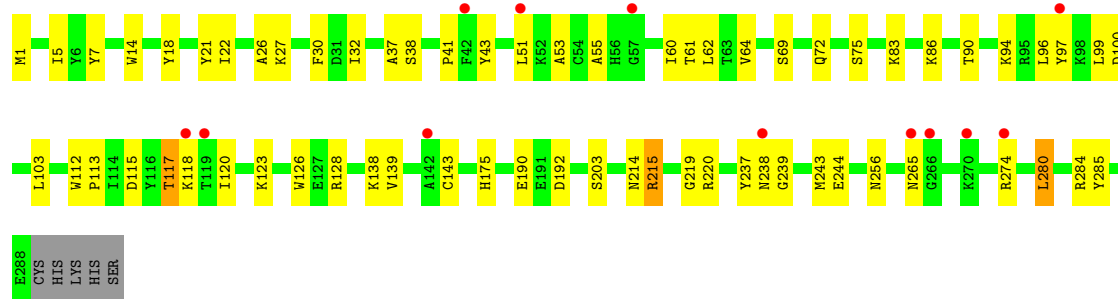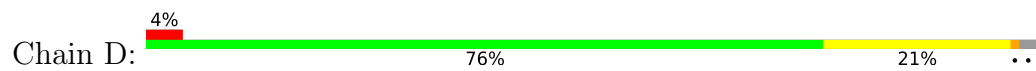- Molecule 1: Xylose isomerase domain protein TIM barrel
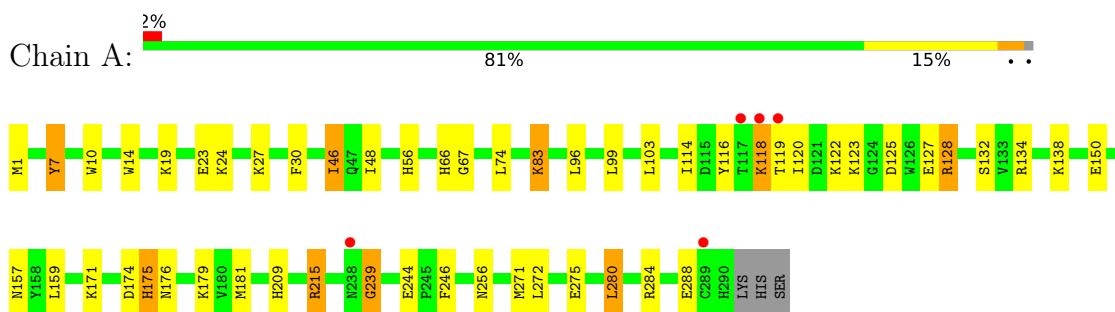
Chain A:

- Molecule 1: Xylose isomerase domain protein TIM barrel

Chain B:

- Molecule 1: Xylose isomerase domain protein TIM barrel

Chain C:

- Molecule 1: Xylose isomerase domain protein TIM barrel

Chain D:
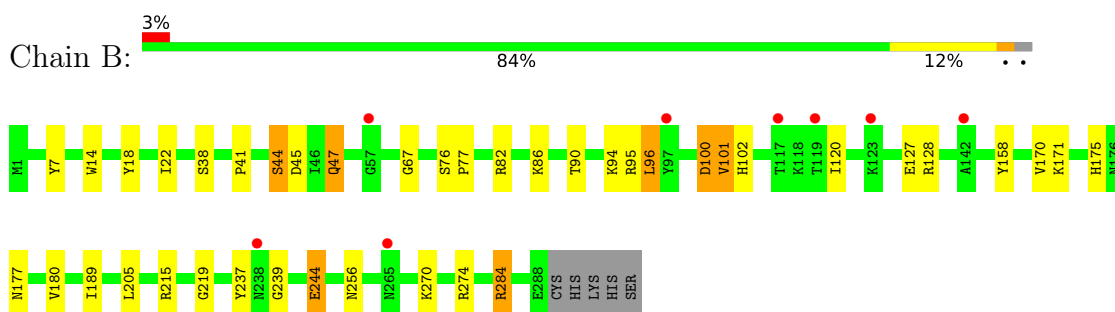
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	80.04Å 115.21Å 91.38Å 90.00° 105.08° 90.00°	Depositor
Resolution (Å)	25.00 – 2.02 24.78 – 2.02	Depositor EDS
% Data completeness (in resolution range)	(Not available) (25.00-2.02) 95.8 (24.78-2.02)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	3.76 (at 2.03Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.186 , 0.227 0.185 , 0.226	Depositor DCC
R_{free} test set	5062 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	29.3	Xtriage
Anisotropy	0.265	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.41 , 62.3	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	0.96	EDS
Total number of atoms	10179	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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: FUD, MN

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	0.80	0/2357	0.88	4/3192 (0.1%)
1	B	0.75	0/2340	0.86	6/3169 (0.2%)
1	C	0.69	0/2345	0.85	6/3176 (0.2%)
1	D	0.71	0/2340	0.83	5/3169 (0.2%)
All	All	0.74	0/9382	0.86	21/12706 (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
1	A	0	1
1	B	0	1
1	D	0	2
All	All	0	4

There are no bond length outliers.

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	215	ARG	NE-CZ-NH2	-11.24	114.68	120.30
1	C	215	ARG	NE-CZ-NH2	-8.99	115.80	120.30
1	B	215	ARG	NE-CZ-NH2	-8.88	115.86	120.30
1	B	215	ARG	NE-CZ-NH1	6.82	123.71	120.30
1	B	284	ARG	NE-CZ-NH1	-6.82	116.89	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	7	TYR	Sidechain
1	B	7	TYR	Sidechain
1	D	21	TYR	Sidechain
1	D	7	TYR	Sidechain

5.2   Too-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 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	2303	0	2235	43	0
1	B	2287	0	2223	45	0
1	C	2292	0	2225	54	0
1	D	2287	0	2223	35	0
2	A	12	0	12	4	0
2	B	12	0	11	1	0
2	C	12	0	12	1	0
2	D	12	0	12	1	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
4	A	263	0	0	9	0
4	B	255	0	0	5	1
4	C	205	0	0	6	0
4	D	231	0	0	5	1
All	All	10179	0	8953	172	1

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 9.

The worst 5 of 172 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:C:114:ILE:HD13	1:C:157:ASN:HA	1.45	0.99
1:B:86:LYS:O	1:B:90:THR:HG23	1.68	0.94
1:A:125:ASP:HA	1:A:128:ARG:HH12	1.36	0.91
1:B:189:ILE:HG12	1:C:189:ILE:CD1	2.03	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:115:ASP:OD2	1:D:117:THR:HB	1.74	0.86

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	Interatomic distance (Å)	Clash overlap (Å)
4:B:1534:HOH:O	4:D:407:HOH:O[1_556]	2.15	0.05

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	288/293 (98%)	279 (97%)	8 (3%)	1 (0%)	41	36
1	B	286/293 (98%)	278 (97%)	8 (3%)	0	100	100
1	C	287/293 (98%)	277 (96%)	9 (3%)	1 (0%)	41	36
1	D	286/293 (98%)	270 (94%)	16 (6%)	0	100	100
All	All	1147/1172 (98%)	1104 (96%)	41 (4%)	2 (0%)	47	43

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	239	GLY
1	A	239	GLY

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	242/245 (99%)	233 (96%)	9 (4%)	34	31
1	B	240/245 (98%)	233 (97%)	7 (3%)	42	41
1	C	240/245 (98%)	233 (97%)	7 (3%)	42	41
1	D	240/245 (98%)	229 (95%)	11 (5%)	27	22
All	All	962/980 (98%)	928 (96%)	34 (4%)	36	34

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	117	THR
1	D	118	LYS
1	D	265	ASN
1	B	101	VAL
1	B	96	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	175	HIS
1	D	256	ASN
1	C	177	ASN
1	D	265	ASN
1	D	12	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 monosaccharides in this entry.

5.6   Ligand geometry   ⓘ

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 for Mogul analysis.

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	$\#\|Z\| > 2$
2	FUD	D	301	3	10,11,11	0.53	0	9,14,14	1.15	0
2	FUD	C	301	3	10,11,11	0.48	0	9,14,14	0.73	0
2	FUD	A	301	3	10,11,11	0.53	0	9,14,14	1.00	0
2	FUD	B	1301	3	10,11,11	0.53	0	9,14,14	1.00	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
2	FUD	D	301	3	-	8/16/16/16	-
2	FUD	C	301	3	-	8/16/16/16	-
2	FUD	A	301	3	-	3/16/16/16	-
2	FUD	B	1301	3	-	7/16/16/16	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	FUD	C1-C2-C3-C4
2	A	301	FUD	O2-C2-C3-C4
2	A	301	FUD	O2-C2-C3-O3
2	B	1301	FUD	C1-C2-C3-C4
2	B	1301	FUD	O2-C2-C3-C4

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	301	FUD	1	0
2	C	301	FUD	1	0
2	A	301	FUD	4	0
2	B	1301	FUD	1	0

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, 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	290/293 (98%)	-0.34	5 (1%)	70	69	21, 30, 46, 64	0
1	B	288/293 (98%)	-0.21	8 (2%)	53	52	21, 33, 50, 64	0
1	C	289/293 (98%)	0.02	11 (3%)	40	40	25, 39, 54, 66	0
1	D	288/293 (98%)	-0.02	12 (4%)	36	35	23, 38, 54, 66	0
All	All	1155/1172 (98%)	-0.14	36 (3%)	49	48	21, 35, 52, 66	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	119	THR	6.4
1	A	119	THR	5.3
1	D	238	ASN	5.2
1	A	289	CYS	5.2
1	D	119	THR	4.8

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 monosaccharides in this entry.

6.4 Ligands ⓘ

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
2	FUD	A	301	12/12	0.88	0.21	37,43,45,46	0
2	FUD	C	301	12/12	0.91	0.19	35,42,48,49	0
3	MN	C	303	1/1	0.92	0.09	61,61,61,61	0
2	FUD	D	301	12/12	0.93	0.17	30,40,41,43	0
2	FUD	B	1301	12/12	0.94	0.14	27,36,41,42	0
3	MN	B	1303	1/1	0.97	0.03	48,48,48,48	0
3	MN	A	303	1/1	0.98	0.06	62,62,62,62	0
3	MN	D	303	1/1	0.98	0.02	48,48,48,48	0
3	MN	C	302	1/1	0.99	0.09	29,29,29,29	0
3	MN	A	302	1/1	1.00	0.10	25,25,25,25	0
3	MN	D	302	1/1	1.00	0.09	29,29,29,29	0
3	MN	B	1302	1/1	1.00	0.08	24,24,24,24	0

6.5 Other polymers ⓘ

There are no such residues in this entry.