wwPDB X-ray Structure Validation Summary Report (i)

Oct 26, 2024 – 01:57 PM EDT

PDB ID	:	2HK1
Title	:	Crystal structure of D-psicose 3-epimerase (DPEase) in the presence of D-fructose
Authors	:	Kim, K.; Kim, H.J.; Oh, D.K.; Cha, S.S.; Rhee, S.
Deposited on	:	2006-07-03
Resolution	:	2.30 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:

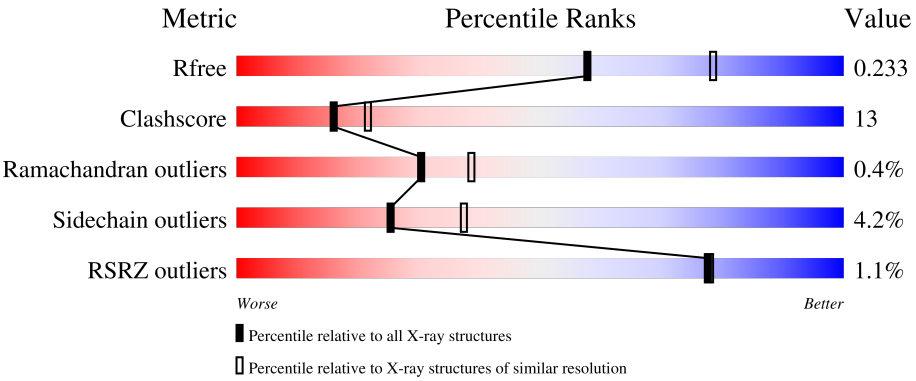
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

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 2.30 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}	164625	5963 (2.30-2.30)
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (2.30-2.30)

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	309	% 69% 22% • 6%
1	B	309	% 71% 22% • 6%
1	C	309	% 69% 23% • 6%
1	D	309	% 71% 21% • 6%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9344 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 D-PSICOSE 3-EPIMERASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	289	Total	C	N	O	S	Se	0	0	0
			2229	1413	390	419	1	6			
1	B	289	Total	C	N	O	S	Se	0	0	0
			2229	1413	390	419	1	6			
1	C	289	Total	C	N	O	S	Se	0	0	0
			2229	1413	390	419	1	6			
1	D	289	Total	C	N	O	S	Se	0	0	0
			2229	1413	390	419	1	6			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MSE	-	expression tag	UNP A9CH28
A	-18	GLY	-	expression tag	UNP A9CH28
A	-17	SER	-	expression tag	UNP A9CH28
A	-16	SER	-	expression tag	UNP A9CH28
A	-15	HIS	-	expression tag	UNP A9CH28
A	-14	HIS	-	expression tag	UNP A9CH28
A	-13	HIS	-	expression tag	UNP A9CH28
A	-12	HIS	-	expression tag	UNP A9CH28
A	-11	HIS	-	expression tag	UNP A9CH28
A	-10	SER	-	expression tag	UNP A9CH28
A	-9	SER	-	expression tag	UNP A9CH28
A	-8	GLY	-	expression tag	UNP A9CH28
A	-7	GLU	-	expression tag	UNP A9CH28
A	-6	ASN	-	expression tag	UNP A9CH28
A	-5	LEU	-	expression tag	UNP A9CH28
A	-4	TYR	-	expression tag	UNP A9CH28
A	-3	PHE	-	expression tag	UNP A9CH28
A	-2	GLN	-	expression tag	UNP A9CH28
A	-1	GLY	-	expression tag	UNP A9CH28
A	0	HIS	-	expression tag	UNP A9CH28
B	-19	MSE	-	expression tag	UNP A9CH28

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	expression tag	UNP A9CH28
B	-17	SER	-	expression tag	UNP A9CH28
B	-16	SER	-	expression tag	UNP A9CH28
B	-15	HIS	-	expression tag	UNP A9CH28
B	-14	HIS	-	expression tag	UNP A9CH28
B	-13	HIS	-	expression tag	UNP A9CH28
B	-12	HIS	-	expression tag	UNP A9CH28
B	-11	HIS	-	expression tag	UNP A9CH28
B	-10	SER	-	expression tag	UNP A9CH28
B	-9	SER	-	expression tag	UNP A9CH28
B	-8	GLY	-	expression tag	UNP A9CH28
B	-7	GLU	-	expression tag	UNP A9CH28
B	-6	ASN	-	expression tag	UNP A9CH28
B	-5	LEU	-	expression tag	UNP A9CH28
B	-4	TYR	-	expression tag	UNP A9CH28
B	-3	PHE	-	expression tag	UNP A9CH28
B	-2	GLN	-	expression tag	UNP A9CH28
B	-1	GLY	-	expression tag	UNP A9CH28
B	0	HIS	-	expression tag	UNP A9CH28
C	-19	MSE	-	expression tag	UNP A9CH28
C	-18	GLY	-	expression tag	UNP A9CH28
C	-17	SER	-	expression tag	UNP A9CH28
C	-16	SER	-	expression tag	UNP A9CH28
C	-15	HIS	-	expression tag	UNP A9CH28
C	-14	HIS	-	expression tag	UNP A9CH28
C	-13	HIS	-	expression tag	UNP A9CH28
C	-12	HIS	-	expression tag	UNP A9CH28
C	-11	HIS	-	expression tag	UNP A9CH28
C	-10	SER	-	expression tag	UNP A9CH28
C	-9	SER	-	expression tag	UNP A9CH28
C	-8	GLY	-	expression tag	UNP A9CH28
C	-7	GLU	-	expression tag	UNP A9CH28
C	-6	ASN	-	expression tag	UNP A9CH28
C	-5	LEU	-	expression tag	UNP A9CH28
C	-4	TYR	-	expression tag	UNP A9CH28
C	-3	PHE	-	expression tag	UNP A9CH28
C	-2	GLN	-	expression tag	UNP A9CH28
C	-1	GLY	-	expression tag	UNP A9CH28
C	0	HIS	-	expression tag	UNP A9CH28
D	-19	MSE	-	expression tag	UNP A9CH28
D	-18	GLY	-	expression tag	UNP A9CH28
D	-17	SER	-	expression tag	UNP A9CH28

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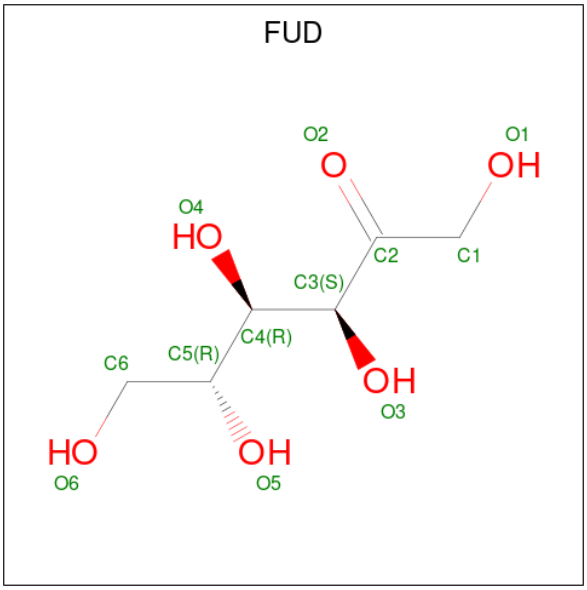
Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	expression tag	UNP A9CH28
D	-15	HIS	-	expression tag	UNP A9CH28
D	-14	HIS	-	expression tag	UNP A9CH28
D	-13	HIS	-	expression tag	UNP A9CH28
D	-12	HIS	-	expression tag	UNP A9CH28
D	-11	HIS	-	expression tag	UNP A9CH28
D	-10	SER	-	expression tag	UNP A9CH28
D	-9	SER	-	expression tag	UNP A9CH28
D	-8	GLY	-	expression tag	UNP A9CH28
D	-7	GLU	-	expression tag	UNP A9CH28
D	-6	ASN	-	expression tag	UNP A9CH28
D	-5	LEU	-	expression tag	UNP A9CH28
D	-4	TYR	-	expression tag	UNP A9CH28
D	-3	PHE	-	expression tag	UNP A9CH28
D	-2	GLN	-	expression tag	UNP A9CH28
D	-1	GLY	-	expression tag	UNP A9CH28
D	0	HIS	-	expression tag	UNP A9CH28

- 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 12 6 6	0	0
2	B	1	Total C O 12 6 6	0	0
2	C	1	Total C O 12 6 6	0	0

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

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mn 1 1	0	0
3	B	1	Total Mn 1 1	0	0
3	C	1	Total Mn 1 1	0	0
3	D	1	Total Mn 1 1	0	0

- Molecule 4 is water.

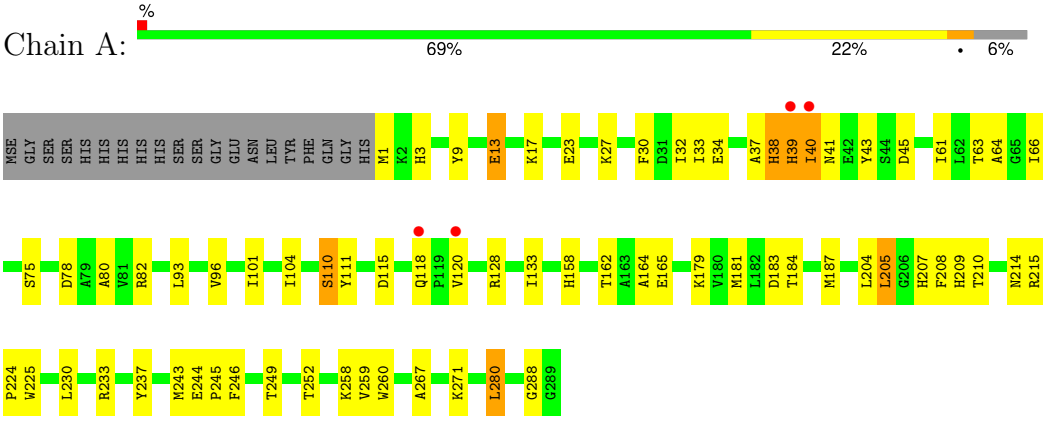
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	88	Total O 88 88	0	0
4	B	100	Total O 100 100	0	0
4	C	79	Total O 79 79	0	0
4	D	109	Total O 109 109	0	0

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.

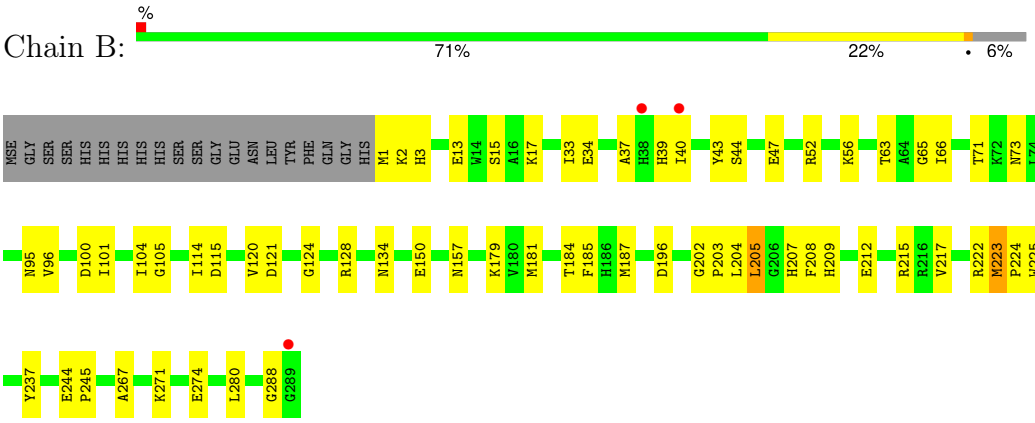
• Molecule 1: D-PSICOSE 3-EPIMERASE

Chain A:



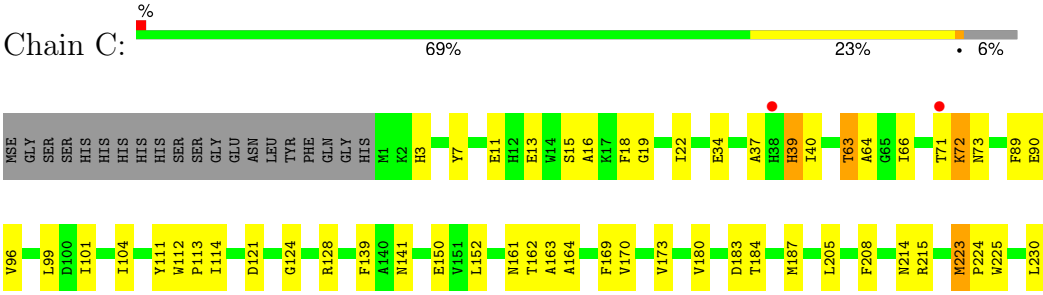
• Molecule 1: D-PSICOSE 3-EPIMERASE

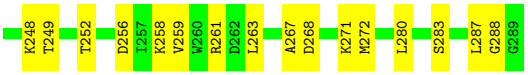
Chain B:



• Molecule 1: D-PSICOSE 3-EPIMERASE

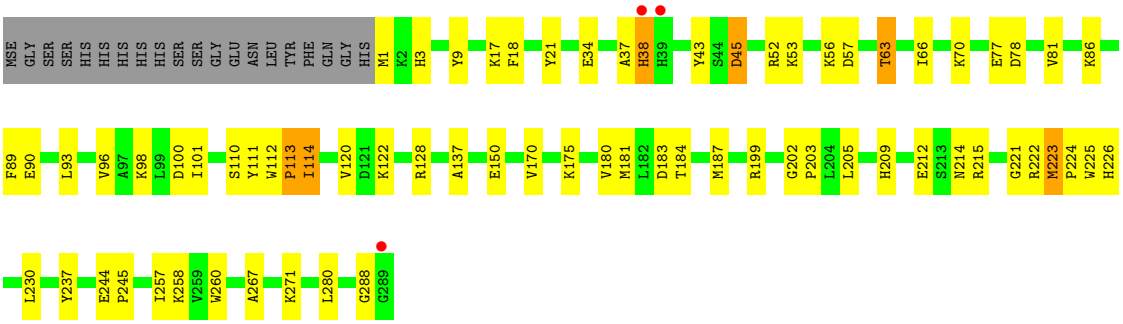
Chain C:





• Molecule 1: D-PSICOSE 3-EPIMERASE

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	103.90Å 113.50Å 133.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.50 – 2.30 33.50 – 2.31	Depositor EDS
% Data completeness (in resolution range)	92.0 (33.50-2.30) 93.2 (33.50-2.31)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.93 (at 2.31Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.192 , 0.239 0.186 , 0.233	Depositor DCC
R_{free} test set	7027 reflections (10.12%)	wwPDB-VP
Wilson B-factor (Å^2)	39.5	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 33.1	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	9344	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.30% 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

5.1 Standard geometry

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	0.49	0/2274	0.68	0/3065
1	B	0.49	0/2274	0.67	0/3065
1	C	0.50	0/2274	0.67	0/3065
1	D	0.48	0/2274	0.66	0/3065
All	All	0.49	0/9096	0.67	0/12260

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

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	2229	0	2179	64	0
1	B	2229	0	2179	58	0
1	C	2229	0	2179	60	0
1	D	2229	0	2179	51	0
2	A	12	0	12	2	0
2	B	12	0	11	2	0
2	C	12	0	11	2	0
2	D	12	0	11	2	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	88	0	0	1	0
4	B	100	0	0	2	0
4	C	79	0	0	3	0
4	D	109	0	0	4	0
All	All	9344	0	8761	231	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 13.

The worst 5 of 231 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:B:184:THR:HA	1:B:187:MSE:HE3	1.54	0.88
1:D:78:ASP:OD2	1:D:81:VAL:HG23	1.77	0.83
1:C:162:THR:HG22	1:C:164:ALA:N	1.99	0.77
1:A:96:VAL:HG13	1:A:101:ILE:HB	1.67	0.77
1:C:162:THR:HG22	1:C:164:ALA:H	1.49	0.77

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	287/309 (93%)	277 (96%)	7 (2%)	3 (1%)	13 15
1	B	287/309 (93%)	282 (98%)	5 (2%)	0	100 100
1	C	287/309 (93%)	281 (98%)	6 (2%)	0	100 100
1	D	287/309 (93%)	274 (96%)	11 (4%)	2 (1%)	19 23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1148/1236 (93%)	1114 (97%)	29 (2%)	5 (0%)	30 39

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	40	ILE
1	D	113	PRO
1	D	114	ILE
1	A	39	HIS
1	A	38	HIS

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	227/237 (96%)	216 (95%)	11 (5%)	21 32
1	B	227/237 (96%)	220 (97%)	7 (3%)	35 51
1	C	227/237 (96%)	216 (95%)	11 (5%)	21 32
1	D	227/237 (96%)	218 (96%)	9 (4%)	27 40
All	All	908/948 (96%)	870 (96%)	38 (4%)	25 37

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	280	LEU
1	D	205	LEU
1	D	38	HIS
1	D	70	LYS
1	D	280	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	3	HIS
1	C	73	ASN
1	D	73	ASN
1	C	146	ASN
1	D	3	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 8 ligands modelled in this entry, 4 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	B	1301	3	11,11,11	1.60	3 (27%)	10,14,14	0.67	0
2	FUD	A	1300	3	11,11,11	1.67	3 (27%)	10,14,14	0.65	0
2	FUD	D	1303	3	11,11,11	1.85	3 (27%)	10,14,14	0.54	0
2	FUD	C	1302	3	11,11,11	1.97	3 (27%)	10,14,14	0.64	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	B	1301	3	-	1/16/16/16	-
2	FUD	A	1300	3	-	2/16/16/16	-
2	FUD	D	1303	3	-	2/16/16/16	-
2	FUD	C	1302	3	-	2/16/16/16	-

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1302	FUD	C4-C3	3.96	1.62	1.53
2	D	1303	FUD	C4-C3	3.27	1.60	1.53
2	D	1303	FUD	C5-C4	3.27	1.59	1.53
2	C	1302	FUD	C5-C4	3.24	1.59	1.53
2	B	1301	FUD	C5-C4	3.09	1.58	1.53

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1300	FUD	O1-C1-C2-C3
2	A	1300	FUD	O1-C1-C2-O2
2	C	1302	FUD	O1-C1-C2-C3
2	C	1302	FUD	O1-C1-C2-O2
2	B	1301	FUD	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1301	FUD	2	0
2	A	1300	FUD	2	0
2	D	1303	FUD	2	0
2	C	1302	FUD	2	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

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^{th} 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	283/309 (91%)	-0.27	4 (1%)	73	74	26, 39, 63, 86	0
1	B	283/309 (91%)	-0.31	3 (1%)	77	78	25, 39, 60, 75	0
1	C	283/309 (91%)	-0.26	2 (0%)	84	84	26, 41, 57, 79	0
1	D	283/309 (91%)	-0.22	3 (1%)	77	78	24, 40, 65, 81	0
All	All	1132/1236 (91%)	-0.27	12 (1%)	77	78	24, 40, 63, 86	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	40	ILE	3.3
1	B	289	GLY	3.2
1	C	38	HIS	2.8
1	A	39	HIS	2.7
1	D	38	HIS	2.5

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, 95^{th} 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	1300	12/12	0.83	0.17	53,62,68,71	0
2	FUD	B	1301	12/12	0.85	0.16	60,66,72,74	0
2	FUD	C	1302	12/12	0.87	0.14	42,53,63,66	0
2	FUD	D	1303	12/12	0.90	0.14	53,62,69,71	0
3	MN	B	1002	1/1	0.99	0.02	36,36,36,36	0
3	MN	D	1001	1/1	0.99	0.02	38,38,38,38	0
3	MN	C	1003	1/1	1.00	0.01	34,34,34,34	0
3	MN	A	1004	1/1	1.00	0.02	32,32,32,32	0

6.5 Other polymers (i)

There are no such residues in this entry.