



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 18, 2026 – 05:44 PM UTC

PDB ID : 4PFH / pdb_00004pfh
Title : Crystal structure of engineered D-tagatose 3-epimerase PcDTE-IDF8
Authors : Hee, C.S.; Bosshart, A.; Schirmer, T.
Deposited on : 2014-04-29
Resolution : 1.90 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

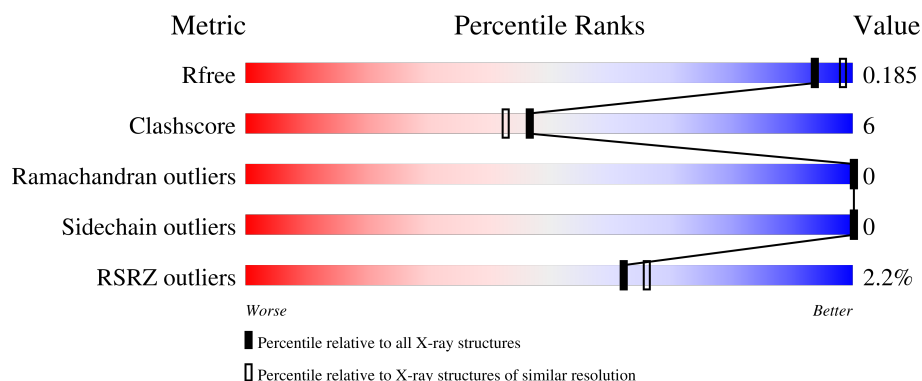
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

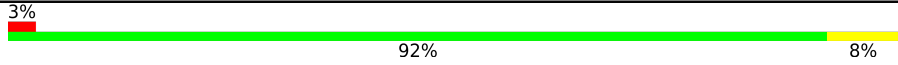
The reported resolution of this entry is 1.90 Å.

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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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 $\leq 5\%$. 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	298	
1	B	298	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5285 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-tagatose 3-epimerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	298	Total	C	N	O	S	0	9	0
			2447	1548	426	450	23			
1	B	291	Total	C	N	O	S	0	8	0
			2367	1501	407	438	21			

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	37	ASN	SER	engineered mutation	UNP O50580
A	39	GLU	GLY	engineered mutation	UNP O50580
A	109	ASN	THR	engineered mutation	UNP O50580
A	116	HIS	SER	engineered mutation	UNP O50580
A	122	VAL	LYS	engineered mutation	UNP O50580
A	157	TYR	PHE	engineered mutation	UNP O50580
A	194	ASN	THR	engineered mutation	UNP O50580
A	209	VAL	HIS	engineered mutation	UNP O50580
A	212	ILE	LEU	engineered mutation	UNP O50580
A	215	GLN	ALA	engineered mutation	UNP O50580
A	251	THR	LYS	engineered mutation	UNP O50580
A	256	GLY	SER	engineered mutation	UNP O50580
A	258	ASP	ALA	engineered mutation	UNP O50580
A	260	CYS	GLY	engineered mutation	UNP O50580
A	265	LEU	MET	engineered mutation	UNP O50580
A	291	LEU	-	expression tag	UNP O50580
A	292	GLU	-	expression tag	UNP O50580
A	293	HIS	-	expression tag	UNP O50580
A	294	HIS	-	expression tag	UNP O50580
A	295	HIS	-	expression tag	UNP O50580
A	296	HIS	-	expression tag	UNP O50580
A	297	HIS	-	expression tag	UNP O50580
A	298	HIS	-	expression tag	UNP O50580
B	37	ASN	SER	engineered mutation	UNP O50580
B	39	GLU	GLY	engineered mutation	UNP O50580

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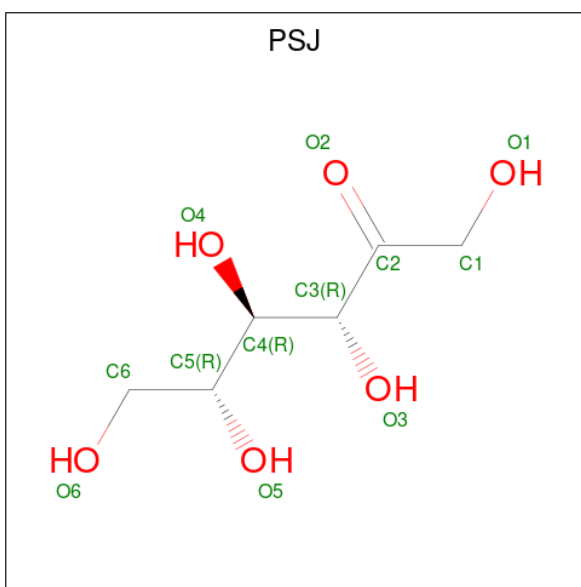
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Chain	Residue	Modelled	Actual	Comment	Reference
B	109	ASN	THR	engineered mutation	UNP O50580
B	116	HIS	SER	engineered mutation	UNP O50580
B	122	VAL	LYS	engineered mutation	UNP O50580
B	157	TYR	PHE	engineered mutation	UNP O50580
B	194	ASN	THR	engineered mutation	UNP O50580
B	209	VAL	HIS	engineered mutation	UNP O50580
B	212	ILE	LEU	engineered mutation	UNP O50580
B	215	GLN	ALA	engineered mutation	UNP O50580
B	251	THR	LYS	engineered mutation	UNP O50580
B	256	GLY	SER	engineered mutation	UNP O50580
B	258	ASP	ALA	engineered mutation	UNP O50580
B	260	CYS	GLY	engineered mutation	UNP O50580
B	265	LEU	MET	engineered mutation	UNP O50580
B	291	LEU	-	expression tag	UNP O50580
B	292	GLU	-	expression tag	UNP O50580
B	293	HIS	-	expression tag	UNP O50580
B	294	HIS	-	expression tag	UNP O50580
B	295	HIS	-	expression tag	UNP O50580
B	296	HIS	-	expression tag	UNP O50580
B	297	HIS	-	expression tag	UNP O50580
B	298	HIS	-	expression tag	UNP O50580

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

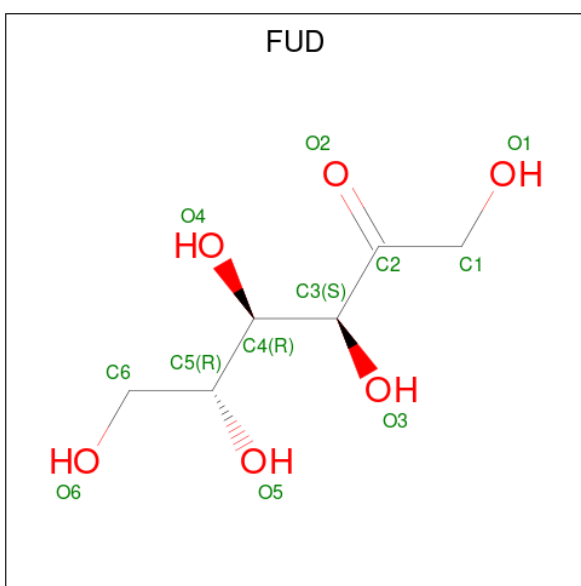
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Mn 2 2	0	0
2	B	1	Total Mn 1 1	0	0

- Molecule 3 is D-psicose (CCD ID: PSJ) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	1
			12	6	6		
3	B	1	Total	C	O	0	1
			12	6	6		

- Molecule 4 is D-fructose (CCD ID: FUD) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	1
			12	6	6		
4	B	1	Total	C	O	0	1
			12	6	6		

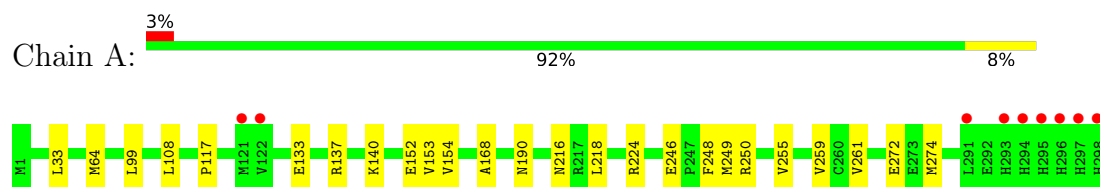
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	236	Total 241	O 241	0	5
5	B	175	Total 179	O 179	0	4

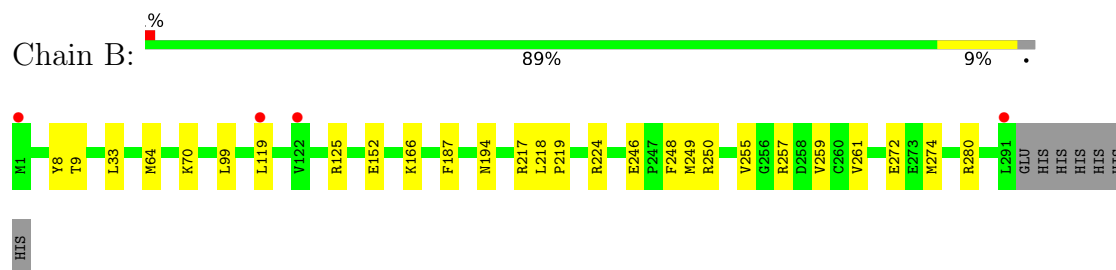
3 Residue-property plots [i](#)

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-tagatose 3-epimerase



- Molecule 1: D-tagatose 3-epimerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	57.46Å 86.74Å 61.82Å 90.00° 99.10° 90.00°	Depositor
Resolution (Å)	56.74 – 1.90 56.74 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.6 (56.74-1.90) 98.6 (56.74-1.90)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.11 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.144 , 0.177 0.156 , 0.185	Depositor DCC
R_{free} test set	2357 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	14.1	Xtriage
Anisotropy	0.417	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 45.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5285	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: PSJ, 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	0.87	0/2513	0.87	0/3393
1	B	0.83	1/2430 (0.0%)	0.87	0/3281
All	All	0.85	1/4943 (0.0%)	0.87	0/6674

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	219	PRO	CA-C	7.45	1.55	1.51

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	A	2447	0	2379	26	0
1	B	2367	0	2328	27	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0
3	A	12	0	11	2	0
3	B	12	0	11	5	0
4	A	12	0	11	1	0
4	B	12	0	12	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	241	0	0	4	0
5	B	179	0	0	6	0
All	All	5285	0	4752	55	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 6.

All (55) 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:280:ARG:HD2	5:B:604:HOH:O	1.40	1.19
1:A:33:LEU:HD11	1:A:64[B]:MET:HE3	1.39	1.03
1:B:152:GLU:OE1	3:B:502[B]:PSJ:H3	1.57	1.02
3:B:502[B]:PSJ:O4	3:B:502[B]:PSJ:H1	1.68	0.90
1:A:137:ARG:HG2	1:A:137:ARG:HH21	1.57	0.69
1:B:166:LYS:HE3	5:B:736:HOH:O	1.97	0.64
1:A:216:ASN:ND2	1:B:194[A]:ASN:OD1	2.32	0.63
1:A:152:GLU:OE1	3:A:503[B]:PSJ:H3	2.00	0.62
1:B:272:GLU:HG2	5:B:717:HOH:O	1.99	0.62
1:B:249[A]:MET:CE	1:B:274[A]:MET:SD	2.89	0.60
3:B:502[B]:PSJ:O4	3:B:502[B]:PSJ:C1	2.44	0.60
1:A:133[B]:GLU:HG2	5:A:666:HOH:O	2.00	0.59
1:A:259[B]:VAL:HG23	1:A:261:VAL:HG23	1.85	0.57
1:B:259:VAL:HG23	1:B:261:VAL:HG23	1.87	0.56
1:B:224[B]:ARG:NH2	5:B:731:HOH:O	2.41	0.53
1:B:70[B]:LYS:HE3	5:B:727:HOH:O	2.08	0.53
1:A:250:ARG:CZ	1:A:274[B]:MET:SD	2.98	0.51
1:B:119:LEU:HD12	1:B:119:LEU:C	2.36	0.51
1:B:218:LEU:HD23	1:B:249[A]:MET:HG2	1.93	0.49
1:B:246:GLU:OE2	4:B:503[A]:FUD:C3	2.61	0.49
1:A:33:LEU:CD1	1:A:64[B]:MET:HE3	2.26	0.49
1:B:152:GLU:CD	3:B:502[B]:PSJ:H3	2.36	0.48
1:A:246:GLU:HG2	1:A:248:PHE:CE2	2.50	0.47
1:B:255:VAL:O	1:B:259:VAL:HG22	2.14	0.47
1:B:152:GLU:OE1	4:B:503[A]:FUD:O4	2.31	0.47
1:B:125:ARG:HD3	1:B:125:ARG:O	2.14	0.46
1:A:153:VAL:HG22	1:A:168:ALA:HB2	1.97	0.46
3:A:503[B]:PSJ:O4	3:A:503[B]:PSJ:H1A	2.14	0.46
1:A:140:LYS:HE2	5:A:814:HOH:O	2.15	0.46
1:A:190:ASN:OD1	1:B:224[B]:ARG:NH1	2.47	0.46
1:A:249[A]:MET:HE1	1:A:274[A]:MET:SD	2.56	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:108:LEU:HD21	1:A:154:VAL:HG11	1.98	0.46
1:A:117:PRO:O	1:B:257[B]:ARG:NH2	2.49	0.45
1:B:70[B]:LYS:HA	1:B:70[B]:LYS:HD2	1.74	0.45
1:A:249[A]:MET:CE	1:A:274[A]:MET:SD	3.05	0.45
1:B:8:TYR:CE1	1:B:9:THR:HG23	2.52	0.44
1:A:137:ARG:HG2	1:A:137:ARG:NH2	2.29	0.44
1:B:246:GLU:HG2	1:B:248:PHE:CE2	2.52	0.44
3:B:502[B]:PSJ:H1	3:B:502[B]:PSJ:HO4	1.78	0.44
1:A:255:VAL:O	1:A:259[B]:VAL:HG22	2.18	0.44
4:A:504[A]:FUD:H4	4:A:504[A]:FUD:H12	1.59	0.43
1:B:250:ARG:CZ	1:B:274[B]:MET:SD	3.06	0.43
1:A:33:LEU:HD21	1:A:64[A]:MET:HG2	2.00	0.42
1:A:140:LYS:HG2	5:A:711:HOH:O	2.18	0.42
1:A:140:LYS:CE	5:A:814:HOH:O	2.68	0.41
1:A:99:LEU:C	1:A:99:LEU:HD23	2.45	0.41
1:A:272:GLU:N	1:A:272:GLU:CD	2.79	0.41
1:B:272:GLU:HA	1:B:272:GLU:OE1	2.21	0.41
1:B:249[A]:MET:HE2	1:B:274[A]:MET:SD	2.59	0.41
1:A:64[B]:MET:HE2	1:A:64[B]:MET:HB3	1.64	0.40
1:A:224[B]:ARG:NH2	5:B:733[B]:HOH:O	2.50	0.40
1:B:33:LEU:HD21	1:B:64:MET:HG2	2.02	0.40
1:B:99:LEU:C	1:B:99:LEU:HD23	2.47	0.40
1:A:218:LEU:HD23	1:A:249[A]:MET:HG2	2.03	0.40
1:B:187:PHE:CD1	1:B:217:ARG:HG2	2.57	0.40

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	305/298 (102%)	299 (98%)	6 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	297/298 (100%)	294 (99%)	3 (1%)	0	100	100
All	All	602/596 (101%)	593 (98%)	9 (2%)	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	260/251 (104%)	260 (100%)	0	100	100
1	B	252/251 (100%)	252 (100%)	0	100	100
All	All	512/502 (102%)	512 (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 (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2	ASN
1	A	194	ASN
1	A	283	GLN
1	A	296	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 3 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
4	FUD	A	504[A]	2	11,11,11	1.06	1 (9%)	10,14,14	2.09	2 (20%)
3	PSJ	B	502[B]	2	11,11,11	0.55	0	10,14,14	0.79	0
4	FUD	B	503[A]	2	11,11,11	0.83	0	10,14,14	1.37	1 (10%)
3	PSJ	A	503[B]	2	11,11,11	0.69	0	10,14,14	1.11	1 (10%)

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
4	FUD	A	504[A]	2	-	6/16/16/16	-
3	PSJ	B	502[B]	2	-	8/16/16/16	-
4	FUD	B	503[A]	2	-	4/16/16/16	-
3	PSJ	A	503[B]	2	-	12/16/16/16	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	504[A]	FUD	O3-C3	2.13	1.46	1.42

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	504[A]	FUD	C5-C4-C3	4.59	119.58	112.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	504[A]	FUD	O3-C3-C4	2.81	116.47	110.38
4	B	503[A]	FUD	C5-C4-C3	2.73	116.53	112.05
3	A	503[B]	PSJ	C6-C5-C4	-2.11	107.87	112.17

There are no chirality outliers.

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	503[B]	PSJ	O1-C1-C2-O2
3	A	503[B]	PSJ	C1-C2-C3-C4
3	A	503[B]	PSJ	O2-C2-C3-C4
3	A	503[B]	PSJ	C3-C4-C5-O5
3	A	503[B]	PSJ	O4-C4-C5-O5
3	A	503[B]	PSJ	O5-C5-C6-O6
3	B	502[B]	PSJ	C1-C2-C3-C4
3	B	502[B]	PSJ	O2-C2-C3-C4
3	B	502[B]	PSJ	C3-C4-C5-O5
3	B	502[B]	PSJ	O4-C4-C5-O5
4	A	504[A]	FUD	O1-C1-C2-O2
4	A	504[A]	FUD	C1-C2-C3-C4
4	A	504[A]	FUD	O2-C2-C3-C4
3	A	503[B]	PSJ	C4-C5-C6-O6
3	A	503[B]	PSJ	O4-C4-C5-C6
3	B	502[B]	PSJ	O4-C4-C5-C6
3	A	503[B]	PSJ	C3-C4-C5-C6
3	B	502[B]	PSJ	C3-C4-C5-C6
4	B	503[A]	FUD	C3-C4-C5-C6
4	A	504[A]	FUD	C3-C4-C5-C6
3	A	503[B]	PSJ	C1-C2-C3-O3
4	A	504[A]	FUD	C3-C4-C5-O5
4	B	503[A]	FUD	C3-C4-C5-O5
4	B	503[A]	FUD	O1-C1-C2-O2
3	A	503[B]	PSJ	O2-C2-C3-O3
3	B	502[B]	PSJ	C4-C5-C6-O6
3	B	502[B]	PSJ	O1-C1-C2-O2
3	A	503[B]	PSJ	O1-C1-C2-C3
4	A	504[A]	FUD	O1-C1-C2-C3
4	B	503[A]	FUD	O1-C1-C2-C3

There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	504[A]	FUD	1	0
3	B	502[B]	PSJ	5	0
4	B	503[A]	FUD	2	0
3	A	503[B]	PSJ	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 [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	A	298/298 (100%)	-0.23	9 (3%)	52	56	5, 12, 31, 71	9 (3%)
1	B	291/298 (97%)	-0.08	4 (1%)	73	76	5, 16, 35, 53	8 (2%)
All	All	589/596 (98%)	-0.16	13 (2%)	62	66	5, 14, 34, 71	17 (2%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	291	LEU	4.4
1	A	295	HIS	4.4
1	B	119	LEU	3.9
1	A	293	HIS	3.9
1	B	1	MET	3.9
1	B	291	LEU	3.4
1	A	297	HIS	3.3
1	A	298	HIS	3.3
1	A	296	HIS	2.8
1	A	294	HIS	2.8
1	A	122	VAL	2.7
1	A	121	MET	2.1
1	B	122	VAL	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 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
3	PSJ	A	503[B]	12/12	0.67	0.15	19,22,24,24	12
4	FUD	B	503[A]	12/12	0.80	0.17	25,35,44,46	12
4	FUD	A	504[A]	12/12	0.81	0.18	18,34,51,54	12
3	PSJ	B	502[B]	12/12	0.93	0.12	8,10,12,13	12
2	MN	A	502	1/1	0.99	0.04	15,15,15,15	0
2	MN	B	501	1/1	0.99	0.08	16,16,16,16	0
2	MN	A	501	1/1	0.99	0.04	14,14,14,14	0

6.5 Other polymers [i](#)

There are no such residues in this entry.