



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 7, 2026 – 01:33 AM UTC

PDB ID : 8OZT / pdb_00008ozt
Title : Crystal Structure of Fucosidase B
Authors : Gallego del Sol, F.; Marina, A.
Deposited on : 2023-05-09
Resolution : 2.51 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 ⓘ 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

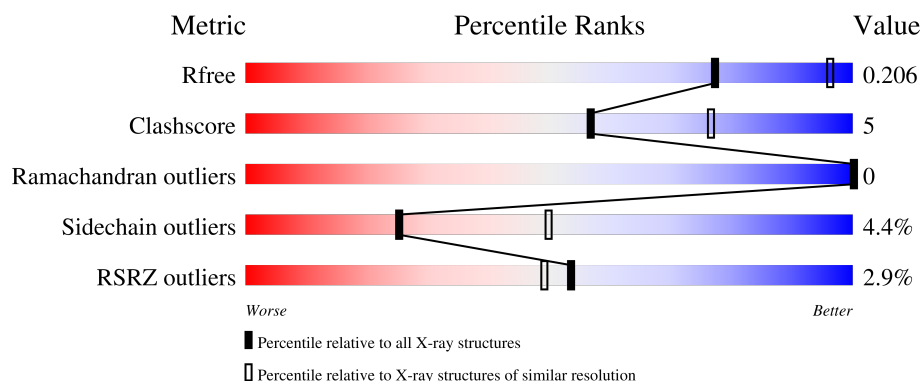
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.51 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	414	2% 87% 9% ...
1	B	414	3% 87% 9% ..
1	C	414	2% 85% 10% ..
1	D	414	3% 87% 10% ..
1	E	414	3% 87% 9% ...

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Mol	Chain	Length	Quality of chain
1	F	414	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MPD	A	503	X	-	-	-
2	MPD	A	504	X	-	-	-
2	MPD	A	505	X	-	-	-
2	MPD	B	501	X	-	-	-
2	MPD	B	503	X	-	-	-
2	MPD	C	504	X	-	-	-
2	MPD	C	506	-	-	X	-
2	MPD	C	507	X	-	-	-
2	MPD	E	502	X	-	-	-
2	MPD	F	501	X	-	-	-
2	MPD	F	502	X	-	-	-
2	MPD	F	504	X	-	-	-
2	MPD	F	505	X	-	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 20556 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.

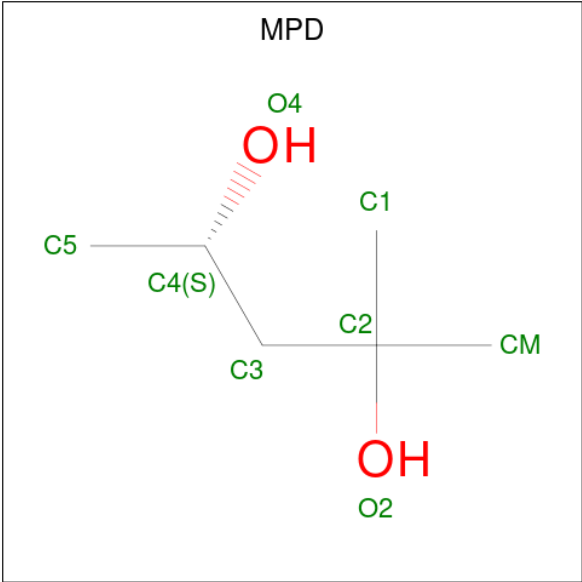
- Molecule 1 is a protein called Alpha-L-fucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	407	Total	C	N	O	S	0	0	0
			3258	2096	555	598	9			
1	B	407	Total	C	N	O	S	0	0	0
			3258	2096	555	598	9			
1	C	406	Total	C	N	O	S	0	0	0
			3254	2094	554	597	9			
1	D	406	Total	C	N	O	S	0	0	0
			3254	2094	554	597	9			
1	E	403	Total	C	N	O	S	0	0	0
			3223	2077	544	593	9			
1	F	406	Total	C	N	O	S	0	1	0
			3261	2099	556	597	9			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	217	GLN	GLU	conflict	UNP A0A806E3N7
B	217	GLN	GLU	conflict	UNP A0A806E3N7
C	217	GLN	GLU	conflict	UNP A0A806E3N7
D	217	GLN	GLU	conflict	UNP A0A806E3N7
E	217	GLN	GLU	conflict	UNP A0A806E3N7
F	217	GLN	GLU	conflict	UNP A0A806E3N7

- Molecule 2 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			8	6	2		
2	A	1	Total	C	O		
			8	6	2		
2	A	1	Total	C	O		
			8	6	2	0	0
2	A	1	Total	C	O		
			8	6	2		
2	A	1	Total	C	O		
			8	6	2		
2	A	1	Total	C	O	0	0
			8	6	2		
2	B	1	Total	C	O		
			8	6	2		
2	B	1	Total	C	O		
			8	6	2	0	0
2	B	1	Total	C	O		
			8	6	2		
2	C	1	Total	C	O		
			8	6	2		
2	C	1	Total	C	O	0	0
			8	6	2		
2	C	1	Total	C	O		
			8	6	2		
2	C	1	Total	C	O		
			8	6	2	0	0
2	C	1	Total	C	O		
			8	6	2		
2	C	1	Total	C	O		
			8	6	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	1	Total C O 8 6 2	0	0
2	C	1	Total C O 8 6 2	0	0
2	D	1	Total C O 8 6 2	0	0
2	D	1	Total C O 8 6 2	0	0
2	E	1	Total C O 8 6 2	0	0
2	E	1	Total C O 8 6 2	0	0
2	E	1	Total C O 8 6 2	0	0
2	F	1	Total C O 8 6 2	0	0
2	F	1	Total C O 8 6 2	0	0
2	F	1	Total C O 8 6 2	0	0
2	F	1	Total C O 8 6 2	0	0
2	F	1	Total C O 8 6 2	0	0

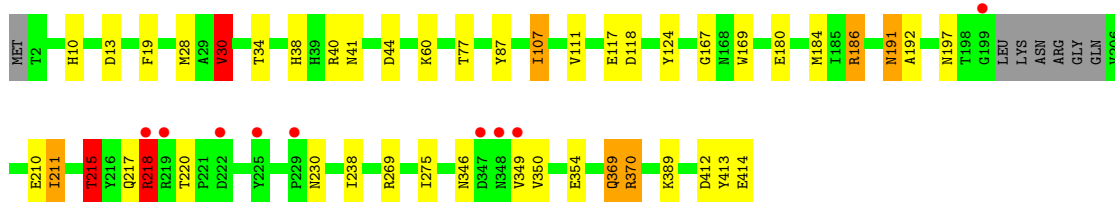
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	158	Total O 158 158	0	0
3	B	161	Total O 161 161	0	0
3	C	167	Total O 167 167	0	0
3	D	139	Total O 139 139	0	0
3	E	123	Total O 123 123	0	0
3	F	92	Total O 92 92	0	0

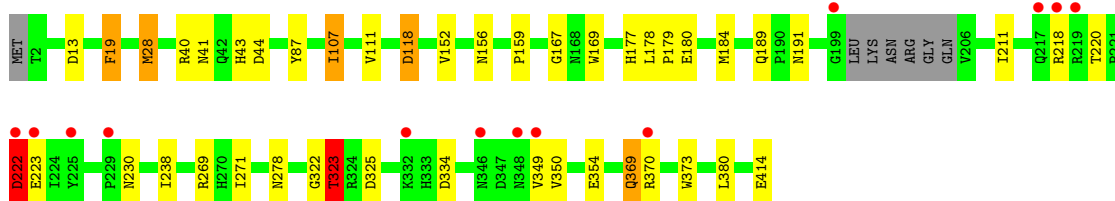
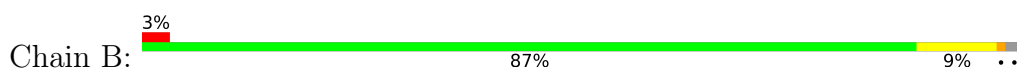
3 Residue-property plots [i](#)

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.

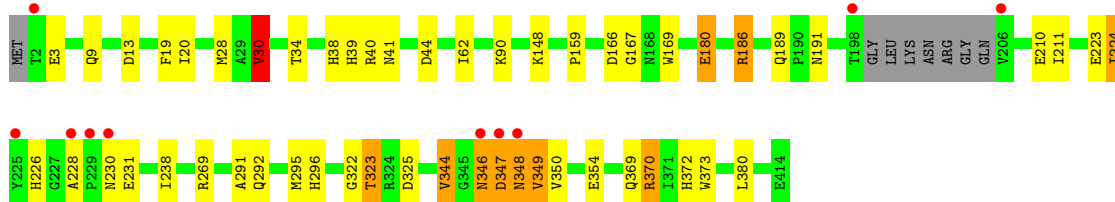
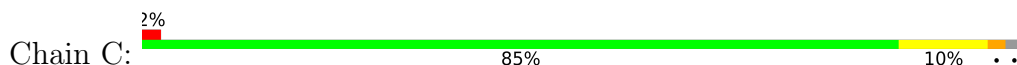
- Molecule 1: Alpha-L-fucosidase



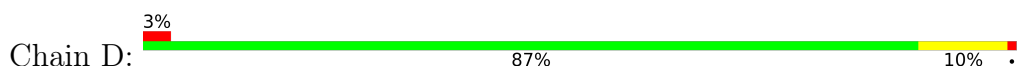
- Molecule 1: Alpha-L-fucosidase

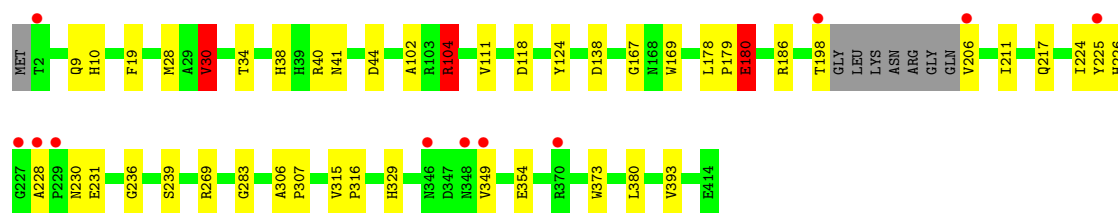


- Molecule 1: Alpha-L-fucosidase

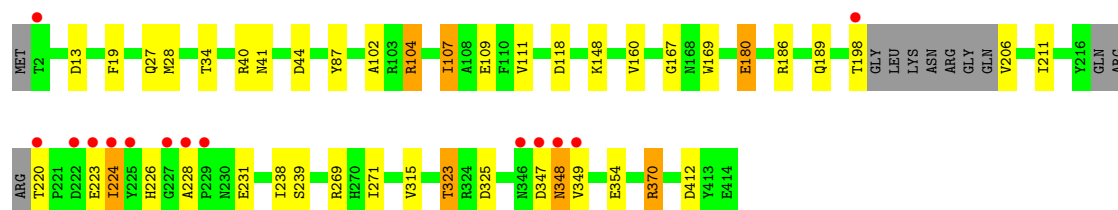
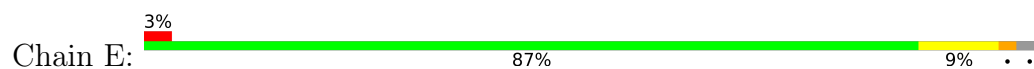


- Molecule 1: Alpha-L-fucosidase

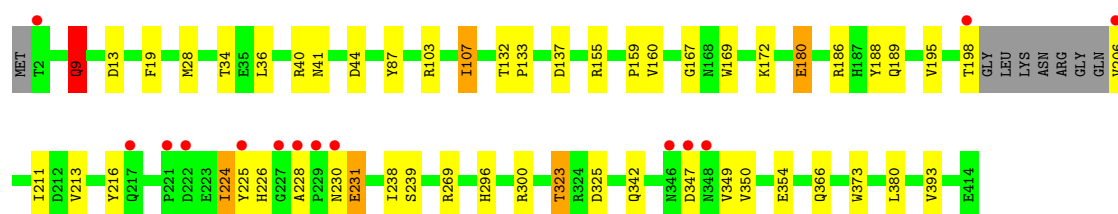
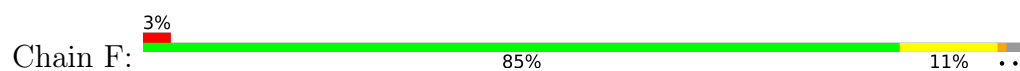




● Molecule 1: Alpha-L-fucosidase



● Molecule 1: Alpha-L-fucosidase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	167.46Å 306.65Å 169.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	153.32 – 2.51 153.32 – 2.51	Depositor EDS
% Data completeness (in resolution range)	100.0 (153.32-2.51) 100.0 (153.32-2.51)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.24 (at 2.52Å)	Xtriage
Refinement program	REFMAC 5.8.0411	Depositor
R, R_{free}	0.169 , 0.200 0.178 , 0.206	Depositor DCC
R_{free} test set	7571 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	33.4	Xtriage
Anisotropy	0.482	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 38.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.012 for 1/2*h+1/2*k,3/2*h-1/2*k,-l 0.009 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	20556	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 2.50% 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: MPD

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	0.74	0/3355	1.09	12/4578 (0.3%)
1	B	0.78	1/3355 (0.0%)	1.08	9/4578 (0.2%)
1	C	0.76	1/3351 (0.0%)	1.10	15/4573 (0.3%)
1	D	0.73	1/3351 (0.0%)	1.06	9/4573 (0.2%)
1	E	0.73	0/3319	1.09	12/4530 (0.3%)
1	F	0.70	0/3362	1.06	9/4588 (0.2%)
All	All	0.74	3/20093 (0.0%)	1.08	66/27420 (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	3
1	B	0	3
1	C	0	2
1	D	0	1
1	E	0	4
1	F	0	2
All	All	0	15

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	177	HIS	CG-CD2	-6.06	1.29	1.35
1	C	372	HIS	CE1-NE2	6.01	1.38	1.32
1	D	138	ASP	CG-OD1	5.16	1.35	1.25

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	198	THR	CA-CB-OG1	-15.14	86.88	109.60
1	D	198	THR	CA-CB-OG1	-12.34	91.09	109.60
1	F	198	THR	CA-CB-OG1	-12.20	91.30	109.60
1	A	186	ARG	NE-CZ-NH2	-10.98	109.32	119.20
1	C	186	ARG	NE-CZ-NH2	-10.53	109.72	119.20

There are no chirality outliers.

5 of 15 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	218	ARG	Sidechain
1	A	269	ARG	Sidechain
1	A	370	ARG	Sidechain
1	B	218	ARG	Sidechain
1	B	269	ARG	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	3258	0	3127	26	0
1	B	3258	0	3127	23	0
1	C	3254	0	3124	32	0
1	D	3254	0	3124	22	0
1	E	3223	0	3089	22	0
1	F	3261	0	3131	29	0
2	A	48	0	81	6	0
2	B	24	0	40	7	0
2	C	56	0	96	18	0
2	D	16	0	28	1	0
2	E	24	0	41	3	0
2	F	40	0	66	4	0
3	A	158	0	0	8	0
3	B	161	0	0	2	0
3	C	167	0	0	4	0
3	D	139	0	0	5	0
3	E	123	0	0	2	0
3	F	92	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	20556	0	19074	178	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 5.

The worst 5 of 178 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:B:502:MPD:H51	2:B:503:MPD:H12	1.38	1.02
1:A:186:ARG:HD2	1:A:210:GLU:OE1	1.64	0.96
2:A:506:MPD:H4	3:A:676:HOH:O	1.74	0.88
2:C:506:MPD:H12	2:C:506:MPD:H53	1.55	0.87
1:F:296[B]:HIS:CE1	1:F:300:ARG:HH21	1.94	0.86

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	403/414 (97%)	391 (97%)	12 (3%)	0	100	100
1	B	403/414 (97%)	388 (96%)	15 (4%)	0	100	100
1	C	402/414 (97%)	390 (97%)	12 (3%)	0	100	100
1	D	402/414 (97%)	388 (96%)	14 (4%)	0	100	100
1	E	397/414 (96%)	386 (97%)	11 (3%)	0	100	100
1	F	403/414 (97%)	387 (96%)	16 (4%)	0	100	100
All	All	2410/2484 (97%)	2330 (97%)	80 (3%)	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	A	340/346 (98%)	324 (95%)	16 (5%)	23	47
1	B	340/346 (98%)	326 (96%)	14 (4%)	27	53
1	C	340/346 (98%)	321 (94%)	19 (6%)	19	39
1	D	340/346 (98%)	327 (96%)	13 (4%)	29	56
1	E	337/346 (97%)	325 (96%)	12 (4%)	31	58
1	F	341/346 (99%)	325 (95%)	16 (5%)	23	47
All	All	2038/2076 (98%)	1948 (96%)	90 (4%)	25	50

5 of 90 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	230	ASN
1	E	348	ASN
1	D	349	VAL
1	E	180	GLU
1	F	107	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	410	GLN
1	F	189	GLN
1	D	168	ASN
1	F	168	ASN
1	F	410	GLN

5.3.3 RNA [i](#)

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 ⓘ

26 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	$\# Z > 2$
2	MPD	B	502	-	7,7,7	0.21	0	9,10,10	0.88	1 (11%)
2	MPD	C	506	-	7,7,7	0.32	0	9,10,10	0.93	1 (11%)
2	MPD	A	503	-	7,7,7	0.47	0	9,10,10	1.52	3 (33%)
2	MPD	A	501	-	7,7,7	0.34	0	9,10,10	0.83	0
2	MPD	C	502	-	7,7,7	0.64	0	9,10,10	1.16	1 (11%)
2	MPD	E	501	-	7,7,7	0.37	0	9,10,10	0.75	0
2	MPD	D	502	-	7,7,7	0.37	0	9,10,10	1.35	2 (22%)
2	MPD	F	501	-	7,7,7	0.43	0	9,10,10	1.38	2 (22%)
2	MPD	C	507	-	7,7,7	0.40	0	9,10,10	1.46	1 (11%)
2	MPD	F	502	-	7,7,7	0.47	0	9,10,10	1.60	2 (22%)
2	MPD	A	506	-	7,7,7	0.62	0	9,10,10	1.08	0
2	MPD	A	502	-	7,7,7	0.33	0	9,10,10	0.78	0
2	MPD	B	503	-	7,7,7	0.45	0	9,10,10	1.62	2 (22%)
2	MPD	F	504	-	7,7,7	0.32	0	9,10,10	1.45	2 (22%)
2	MPD	E	502	-	7,7,7	0.38	0	9,10,10	1.50	2 (22%)
2	MPD	B	501	-	7,7,7	0.57	0	9,10,10	1.93	2 (22%)
2	MPD	C	505	-	7,7,7	0.40	0	9,10,10	0.73	0
2	MPD	C	504	-	7,7,7	0.31	0	9,10,10	1.56	1 (11%)
2	MPD	C	503	-	7,7,7	0.52	0	9,10,10	1.16	1 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MPD	C	501	-	7,7,7	0.30	0	9,10,10	1.56	2 (22%)
2	MPD	F	503	-	7,7,7	0.29	0	9,10,10	1.01	0
2	MPD	A	505	-	7,7,7	0.27	0	9,10,10	1.77	2 (22%)
2	MPD	E	503	-	7,7,7	0.18	0	9,10,10	0.93	1 (11%)
2	MPD	D	501	-	7,7,7	0.63	0	9,10,10	1.30	1 (11%)
2	MPD	A	504	-	7,7,7	0.68	0	9,10,10	1.68	1 (11%)
2	MPD	F	505	-	7,7,7	0.71	0	9,10,10	1.60	3 (33%)

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	MPD	B	502	-	-	5/5/5/5	-
2	MPD	C	506	-	-	2/5/5/5	-
2	MPD	A	503	-	1/1/2/2	4/5/5/5	-
2	MPD	A	501	-	-	2/5/5/5	-
2	MPD	C	502	-	-	0/5/5/5	-
2	MPD	E	501	-	-	5/5/5/5	-
2	MPD	D	502	-	-	4/5/5/5	-
2	MPD	F	501	-	1/1/2/2	5/5/5/5	-
2	MPD	C	507	-	1/1/2/2	2/5/5/5	-
2	MPD	F	502	-	1/1/2/2	1/5/5/5	-
2	MPD	A	506	-	-	1/5/5/5	-
2	MPD	A	502	-	-	5/5/5/5	-
2	MPD	B	503	-	1/1/2/2	1/5/5/5	-
2	MPD	F	504	-	1/1/2/2	2/5/5/5	-
2	MPD	E	502	-	1/1/2/2	4/5/5/5	-
2	MPD	B	501	-	1/1/2/2	3/5/5/5	-
2	MPD	C	505	-	-	5/5/5/5	-
2	MPD	C	504	-	1/1/2/2	1/5/5/5	-
2	MPD	C	503	-	-	2/5/5/5	-
2	MPD	C	501	-	-	4/5/5/5	-
2	MPD	F	503	-	-	1/5/5/5	-
2	MPD	A	505	-	1/1/2/2	2/5/5/5	-
2	MPD	E	503	-	-	2/5/5/5	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MPD	D	501	-	-	2/5/5/5	-
2	MPD	A	504	-	1/1/2/2	1/5/5/5	-
2	MPD	F	505	-	1/1/2/2	1/5/5/5	-

There are no bond length outliers.

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	MPD	C5-C4-C3	4.70	133.49	111.67
2	C	504	MPD	C5-C4-C3	4.13	130.84	111.67
2	A	505	MPD	C5-C4-C3	3.96	130.08	111.67
2	A	504	MPD	C5-C4-C3	3.77	129.19	111.67
2	F	502	MPD	C5-C4-C3	3.47	127.77	111.67

5 of 12 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	503	MPD	C4
2	A	504	MPD	C4
2	A	505	MPD	C4
2	B	501	MPD	C4
2	B	503	MPD	C4

5 of 67 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	502	MPD	C2-C3-C4-O4
2	A	502	MPD	C2-C3-C4-C5
2	B	501	MPD	C1-C2-C3-C4
2	C	501	MPD	C2-C3-C4-O4
2	C	501	MPD	C2-C3-C4-C5

There are no ring outliers.

18 monomers are involved in 39 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	502	MPD	4	0
2	C	506	MPD	7	0
2	D	502	MPD	1	0
2	C	507	MPD	4	0
2	F	502	MPD	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	506	MPD	2	0
2	A	502	MPD	1	0
2	B	503	MPD	5	0
2	E	502	MPD	3	0
2	B	501	MPD	1	0
2	C	505	MPD	3	0
2	C	504	MPD	1	0
2	C	503	MPD	2	0
2	C	501	MPD	3	0
2	F	503	MPD	1	0
2	A	505	MPD	2	0
2	A	504	MPD	2	0
2	F	505	MPD	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	407/414 (98%)	-0.43	9 (2%) 62 58	21, 32, 63, 118	0
1	B	407/414 (98%)	-0.44	13 (3%) 50 46	22, 30, 60, 135	0
1	C	406/414 (98%)	-0.44	10 (2%) 58 54	22, 31, 65, 118	0
1	D	406/414 (98%)	-0.34	11 (2%) 56 51	21, 35, 66, 123	0
1	E	403/414 (97%)	-0.31	14 (3%) 47 42	23, 35, 68, 123	0
1	F	406/414 (98%)	-0.22	14 (3%) 48 43	19, 37, 72, 128	1 (0%)
All	All	2435/2484 (98%)	-0.36	71 (2%) 53 49	19, 33, 67, 135	1 (0%)

The worst 5 of 71 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	225	TYR	6.8
1	E	2	THR	6.2
1	B	218	ARG	6.2
1	F	225	TYR	5.8
1	A	218	ARG	5.8

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 ⓘ

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	MPD	F	505	8/8	0.73	0.30	61,75,86,93	0
2	MPD	A	506	8/8	0.75	0.31	63,87,99,105	0
2	MPD	B	501	8/8	0.82	0.29	67,77,93,117	0
2	MPD	D	501	8/8	0.83	0.28	57,69,89,91	0
2	MPD	C	502	8/8	0.83	0.26	60,76,86,86	0
2	MPD	C	503	8/8	0.84	0.24	59,70,73,78	0
2	MPD	E	502	8/8	0.85	0.26	63,74,82,95	0
2	MPD	F	502	8/8	0.85	0.24	65,76,82,83	0
2	MPD	D	502	8/8	0.85	0.26	58,73,81,81	0
2	MPD	F	501	8/8	0.87	0.27	64,81,92,98	0
2	MPD	F	503	8/8	0.89	0.26	61,82,93,100	0
2	MPD	C	506	8/8	0.89	0.24	58,71,84,88	0
2	MPD	C	505	8/8	0.90	0.22	62,71,79,83	0
2	MPD	A	502	8/8	0.90	0.20	59,69,76,78	0
2	MPD	C	504	8/8	0.90	0.22	65,78,90,90	0
2	MPD	E	501	8/8	0.91	0.18	51,68,82,82	0
2	MPD	A	505	8/8	0.91	0.19	48,69,82,83	0
2	MPD	A	503	8/8	0.92	0.18	60,72,80,83	0
2	MPD	E	503	8/8	0.92	0.20	64,72,89,95	0
2	MPD	C	507	8/8	0.92	0.24	70,86,103,111	0
2	MPD	A	501	8/8	0.92	0.18	58,67,85,85	0
2	MPD	B	502	8/8	0.92	0.20	65,80,89,95	0
2	MPD	F	504	8/8	0.92	0.18	60,63,67,69	0
2	MPD	B	503	8/8	0.92	0.22	73,85,106,110	0
2	MPD	C	501	8/8	0.93	0.16	46,62,68,72	0
2	MPD	A	504	8/8	0.95	0.16	46,51,61,66	0

6.5 Other polymers ⓘ

There are no such residues in this entry.