wwPDB X-ray Structure Validation Summary Report (i)

Nov 15, 2023 – 06:40 PM JST

PDB ID	:	6JOW
Title	:	Exo-beta-D-glucosaminidase from Pyrococcus furiosus
Authors	:	Mine, S.; Watanabe, M.
Deposited on	:	2019-03-24
Resolution	:	1.75 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 (1)) were used in the production of this report:

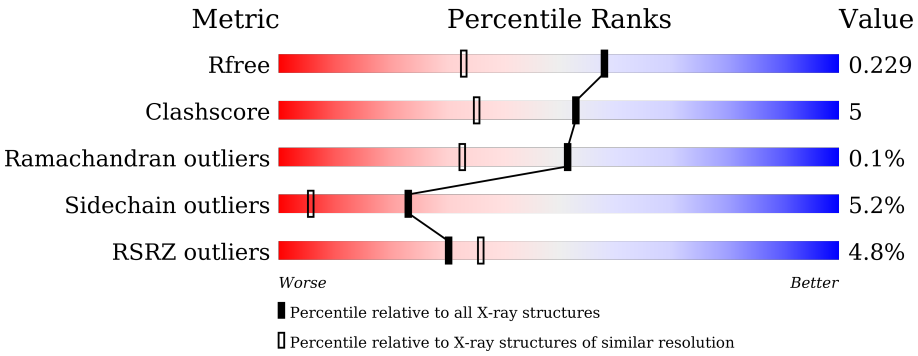
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.75 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}	130704	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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	762	6% 84% 14% ·
1	B	762	6% 86% 13% ·
1	C	762	3% 85% 14% ·
1	D	762	5% 85% 13% ·

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 27343 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.

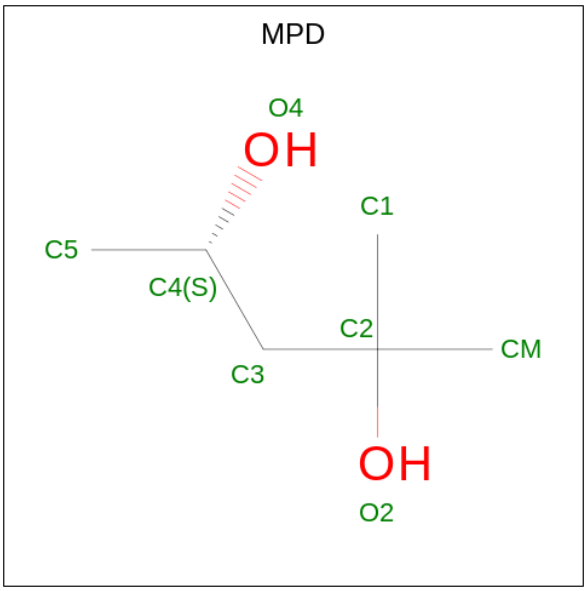
- Molecule 1 is a protein called Beta-galactosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	762	Total	C	N	O	S	0	2	0
			6326	4124	1040	1146	16			
1	B	762	Total	C	N	O	S	0	1	0
			6321	4121	1041	1144	15			
1	C	762	Total	C	N	O	S	0	3	0
			6344	4137	1042	1149	16			
1	D	762	Total	C	N	O	S	0	2	0
			6330	4130	1039	1146	15			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		
2	C	1	Total	Ca	0	0
			1	1		

- Molecule 3 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



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

- Molecule 4 is water.

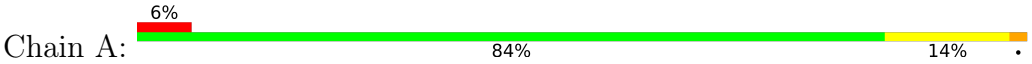
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	432	Total O 432 432	0	0
4	B	488	Total O 488 488	0	0
4	C	532	Total O 532 532	0	0
4	D	504	Total O 504 504	0	0

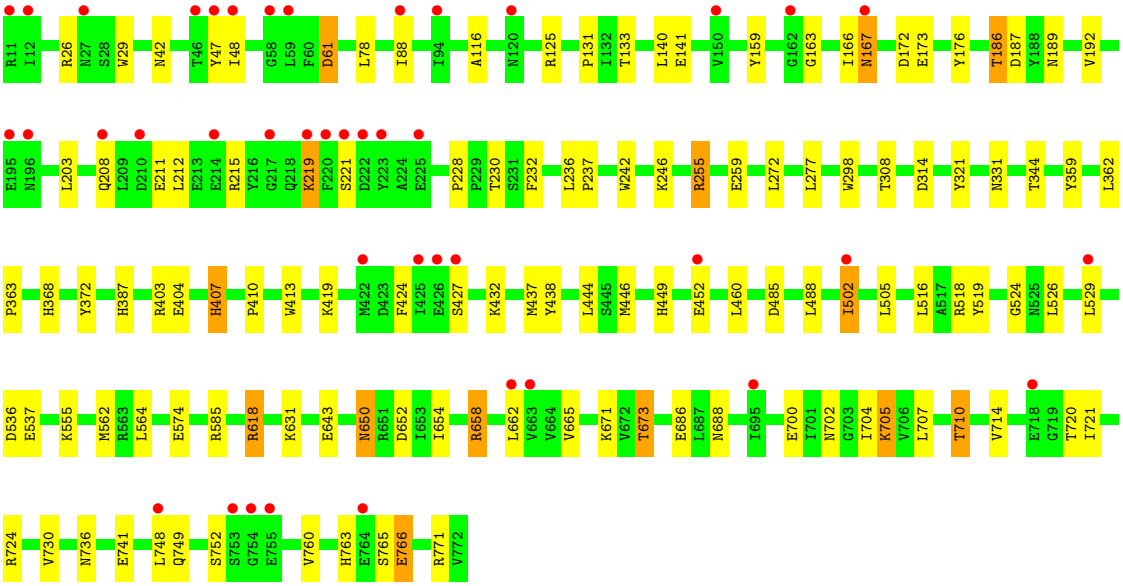
3 Residue-property plots (i)

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: Beta-galactosidase

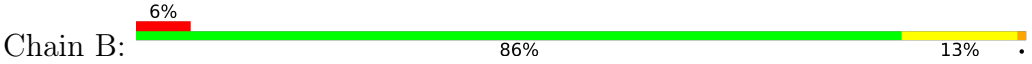
Chain A:

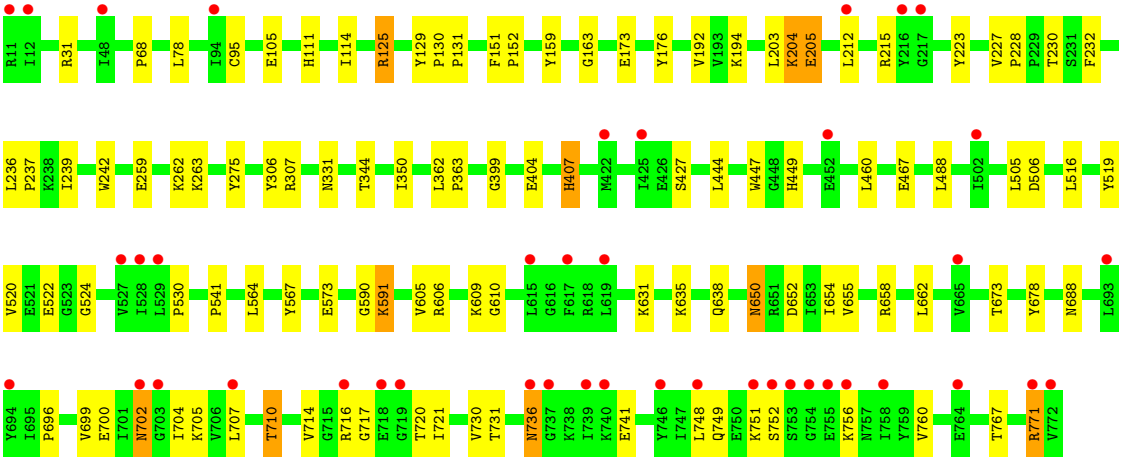




• Molecule 1: Beta-galactosidase

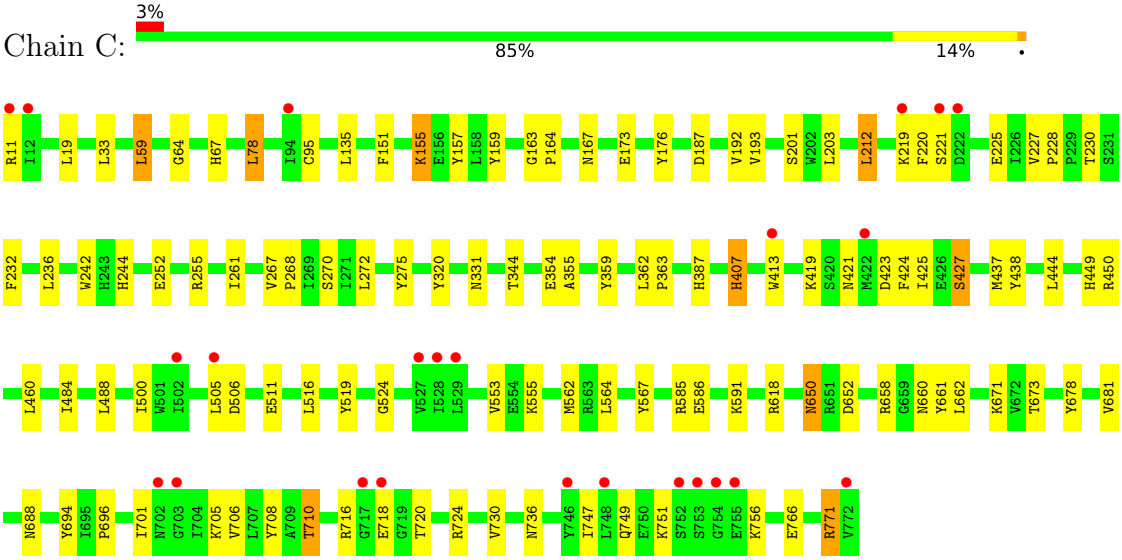
Chain B:





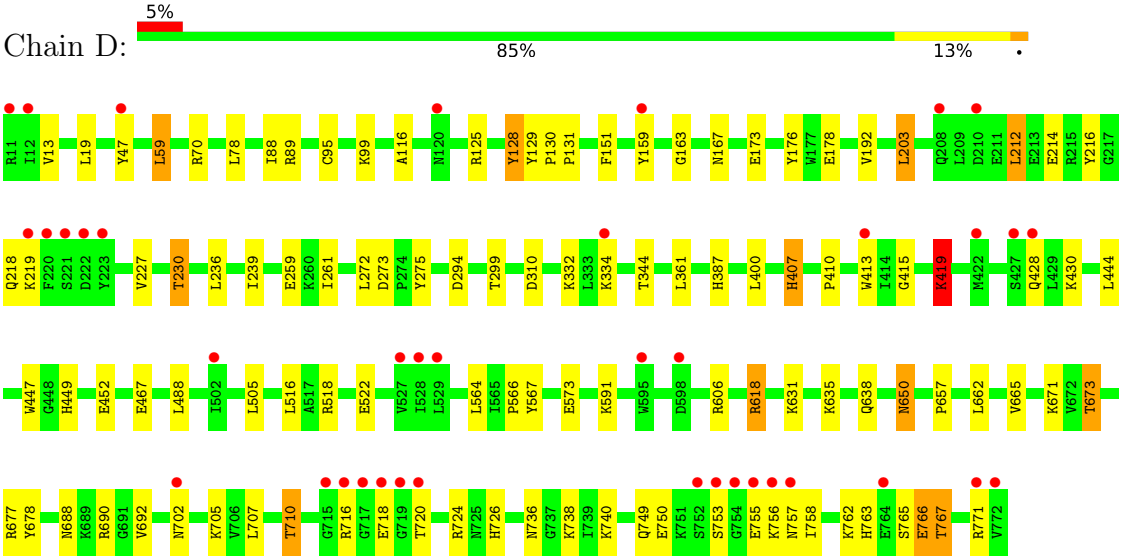
• Molecule 1: Beta-galactosidase

Chain C:



• Molecule 1: Beta-galactosidase

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	85.13Å 149.60Å 147.31Å 90.00° 102.07° 90.00°	Depositor
Resolution (Å)	30.00 – 1.75 29.96 – 1.75	Depositor EDS
% Data completeness (in resolution range)	98.0 (30.00-1.75) 98.1 (29.96-1.75)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.96 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.148 , 0.220 0.154 , 0.229	Depositor DCC
R_{free} test set	17963 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	18.8	Xtriage
Anisotropy	0.788	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 47.7	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	0.98	EDS
Total number of atoms	27343	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 2.96% 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: CA, 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	0.92	10/6508 (0.2%)	1.04	9/8835 (0.1%)
1	B	0.85	4/6503 (0.1%)	0.99	4/8828 (0.0%)
1	C	0.90	4/6525 (0.1%)	0.99	5/8859 (0.1%)
1	D	0.85	6/6517 (0.1%)	0.97	8/8849 (0.1%)
All	All	0.88	24/26053 (0.1%)	1.00	26/35371 (0.1%)

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	2

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	404	GLU	CD-OE2	-13.07	1.11	1.25
1	C	749	GLN	CD-NE2	12.75	1.64	1.32
1	A	61	ASP	CG-OD1	9.09	1.46	1.25
1	B	399	GLY	C-O	7.89	1.36	1.23
1	D	419	LYS	C-O	7.80	1.38	1.23

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	61	ASP	CB-CG-OD1	-9.44	109.80	118.30
1	A	61	ASP	CB-CG-OD2	-8.15	110.97	118.30
1	A	618	ARG	CG-CD-NE	-7.73	95.56	111.80
1	D	720	THR	CA-CB-OG1	7.46	124.67	109.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	70	ARG	NE-CZ-NH1	6.96	123.78	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	166	ILE	Mainchain
1	A	61	ASP	Sidechain

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	6326	0	6257	73	0
1	B	6321	0	6256	65	0
1	C	6344	0	6265	62	0
1	D	6330	0	6259	66	0
2	A	1	0	0	0	0
2	C	1	0	0	0	0
3	A	16	0	28	4	0
3	B	16	0	28	7	0
3	C	16	0	28	8	0
3	D	16	0	28	4	0
4	A	432	0	0	21	0
4	B	488	0	0	18	0
4	C	532	0	0	13	0
4	D	504	0	0	15	0
All	All	27343	0	25149	273	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 273 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:424:PHE:O	1:C:427:SER:HB2	1.48	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:294:ASP:HB2	4:D:1371:HOH:O	1.62	0.98
3:D:902:MPD:HM3	4:D:1003:HOH:O	1.63	0.97
1:D:95:CYS:SG	3:D:902:MPD:H13	2.10	0.91
1:D:766:GLU:HG2	4:D:1391:HOH:O	1.74	0.88

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	762/762 (100%)	727 (95%)	34 (4%)	1 (0%)	51	33
1	B	761/762 (100%)	726 (95%)	35 (5%)	0	100	100
1	C	763/762 (100%)	733 (96%)	29 (4%)	1 (0%)	51	33
1	D	762/762 (100%)	726 (95%)	35 (5%)	1 (0%)	51	33
All	All	3048/3048 (100%)	2912 (96%)	133 (4%)	3 (0%)	51	33

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	758	ILE
1	C	718	GLU
1	A	702	ASN

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	684/682 (100%)	649 (95%)	35 (5%)	24	6
1	B	683/682 (100%)	645 (94%)	38 (6%)	21	5
1	C	685/682 (100%)	650 (95%)	35 (5%)	24	6
1	D	684/682 (100%)	650 (95%)	34 (5%)	24	6
All	All	2736/2728 (100%)	2594 (95%)	142 (5%)	23	6

5 of 142 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	212	LEU
1	D	230	THR
1	D	650	ASN
1	B	505	LEU
1	B	488	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	167	ASN
1	C	421	ASN
1	D	650	ASN
1	C	407	HIS
1	C	428	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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	$\#\|Z\| > 2$
3	MPD	B	902	-	7,7,7	0.63	0	9,10,10	1.00	1 (11%)
3	MPD	D	902	-	7,7,7	1.43	2 (28%)	9,10,10	1.41	1 (11%)
3	MPD	D	901	-	7,7,7	0.41	0	9,10,10	0.37	0
3	MPD	B	901	-	7,7,7	0.34	0	9,10,10	0.77	0
3	MPD	A	802	-	7,7,7	1.03	1 (14%)	9,10,10	0.86	0
3	MPD	A	803	-	7,7,7	0.36	0	9,10,10	0.41	0
3	MPD	C	801	-	7,7,7	0.83	0	9,10,10	1.21	1 (11%)
3	MPD	C	803	-	7,7,7	0.98	0	9,10,10	0.73	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	MPD	B	902	-	-	2/5/5/5	-
3	MPD	D	902	-	-	2/5/5/5	-
3	MPD	D	901	-	-	3/5/5/5	-
3	MPD	B	901	-	-	4/5/5/5	-
3	MPD	A	802	-	-	2/5/5/5	-
3	MPD	A	803	-	-	0/5/5/5	-
3	MPD	C	801	-	-	0/5/5/5	-
3	MPD	C	803	-	-	3/5/5/5	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	902	MPD	O4-C4	2.55	1.54	1.43
3	D	902	MPD	O2-C2	2.20	1.50	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	802	MPD	O2-C2	2.02	1.49	1.44

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	902	MPD	O4-C4-C3	3.21	124.33	111.36
3	C	801	MPD	C5-C4-C3	2.17	121.92	111.69
3	B	902	MPD	O2-C2-CM	2.11	114.86	108.08

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	802	MPD	C2-C3-C4-C5
3	B	901	MPD	O2-C2-C3-C4
3	B	901	MPD	CM-C2-C3-C4
3	C	803	MPD	O2-C2-C3-C4
3	B	902	MPD	C2-C3-C4-C5

There are no ring outliers.

6 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	902	MPD	4	0
3	D	902	MPD	4	0
3	B	901	MPD	3	0
3	A	802	MPD	4	0
3	C	801	MPD	3	0
3	C	803	MPD	5	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	762/762 (100%)	0.02	42 (5%)	25	31	20, 36, 68, 109	0
1	B	762/762 (100%)	-0.06	42 (5%)	25	31	19, 32, 67, 117	0
1	C	762/762 (100%)	-0.23	24 (3%)	49	55	19, 29, 66, 95	0
1	D	762/762 (100%)	-0.08	39 (5%)	28	34	21, 33, 68, 107	0
All	All	3048/3048 (100%)	-0.09	147 (4%)	30	36	19, 32, 67, 117	0

The worst 5 of 147 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	11	ARG	7.1
1	B	11	ARG	5.2
1	B	718	GLU	5.2
1	D	221	SER	4.9
1	B	425	ILE	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, 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
3	MPD	B	902	8/8	0.62	0.26	32,47,54,63	0
3	MPD	C	801	8/8	0.75	0.25	46,53,65,99	0
3	MPD	A	802	8/8	0.77	0.20	45,50,55,60	0
3	MPD	C	803	8/8	0.79	0.23	43,52,68,70	0
3	MPD	A	803	8/8	0.86	0.18	32,38,60,62	0
3	MPD	D	902	8/8	0.86	0.16	36,42,58,69	0
3	MPD	D	901	8/8	0.96	0.09	24,32,35,39	0
3	MPD	B	901	8/8	0.96	0.07	31,34,36,38	0
2	CA	A	801	1/1	0.99	0.07	38,38,38,38	0
2	CA	C	802	1/1	0.99	0.03	47,47,47,47	0

6.5 Other polymers (i)

There are no such residues in this entry.