



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 19, 2017 – 01:20 PM EST

PDB ID : 4BDV
Title : CRYSTAL STRUCTURE OF A TRUNCATED B-DOMAIN HUMAN FACTOR VIII
Authors : Svensson, L.A.; Thim, L.; Olsen, O.H.; Nicolaisen, E.M.
Deposited on : 2012-10-08
Resolution : 3.98 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

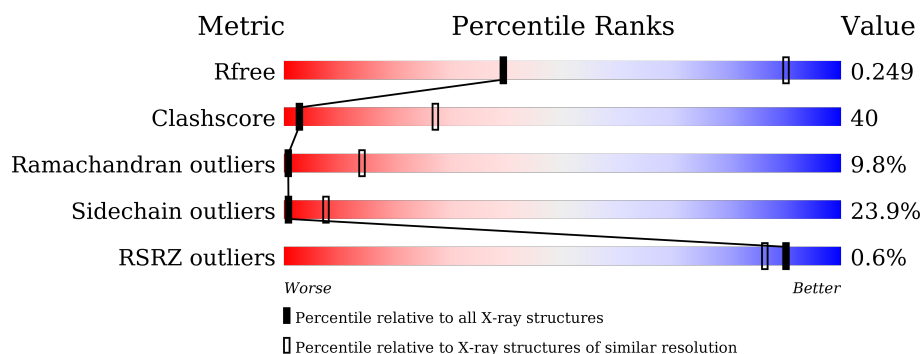
The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20028442
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20028442

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X-RAY DIFFRACTION

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}	91344	1009 (4.40-3.56)
Clashscore	102246	1033 (4.36-3.60)
Ramachandran outliers	100387	1012 (4.38-3.58)
Sidechain outliers	100360	1002 (4.38-3.58)
RSRZ outliers	91569	1012 (4.40-3.56)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	760	<div> <div> <div></div> <div>25%</div> <div>38%</div> <div>15%</div> <div>•</div> <div>19%</div> </div> </div>
2	B	685	<div> <div> <div></div> <div>32%</div> <div>41%</div> <div>14%</div> <div>•</div> <div>12%</div> </div> </div>

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
5	NAG	A	1755	X	-	-	X
6	EDO	A	3333	-	-	-	X
6	EDO	B	3333	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 9973 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 FACTOR VIIIA HEAVY CHAIN, 92 KDA ISOFORM, B DOMAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	612	Total	C	N	O	S	0	0	0
			4944	3194	826	900	24			

- Molecule 2 is a protein called FACTOR VIIIA LIGHT CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	606	Total	C	N	O	S	0	0	0
			4929	3175	841	885	28			

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca	0	0
			1	1		

- Molecule 5 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		
6	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is COPPER (I) ION (three-letter code: CU1) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total	Cu	0	0
			1	1		

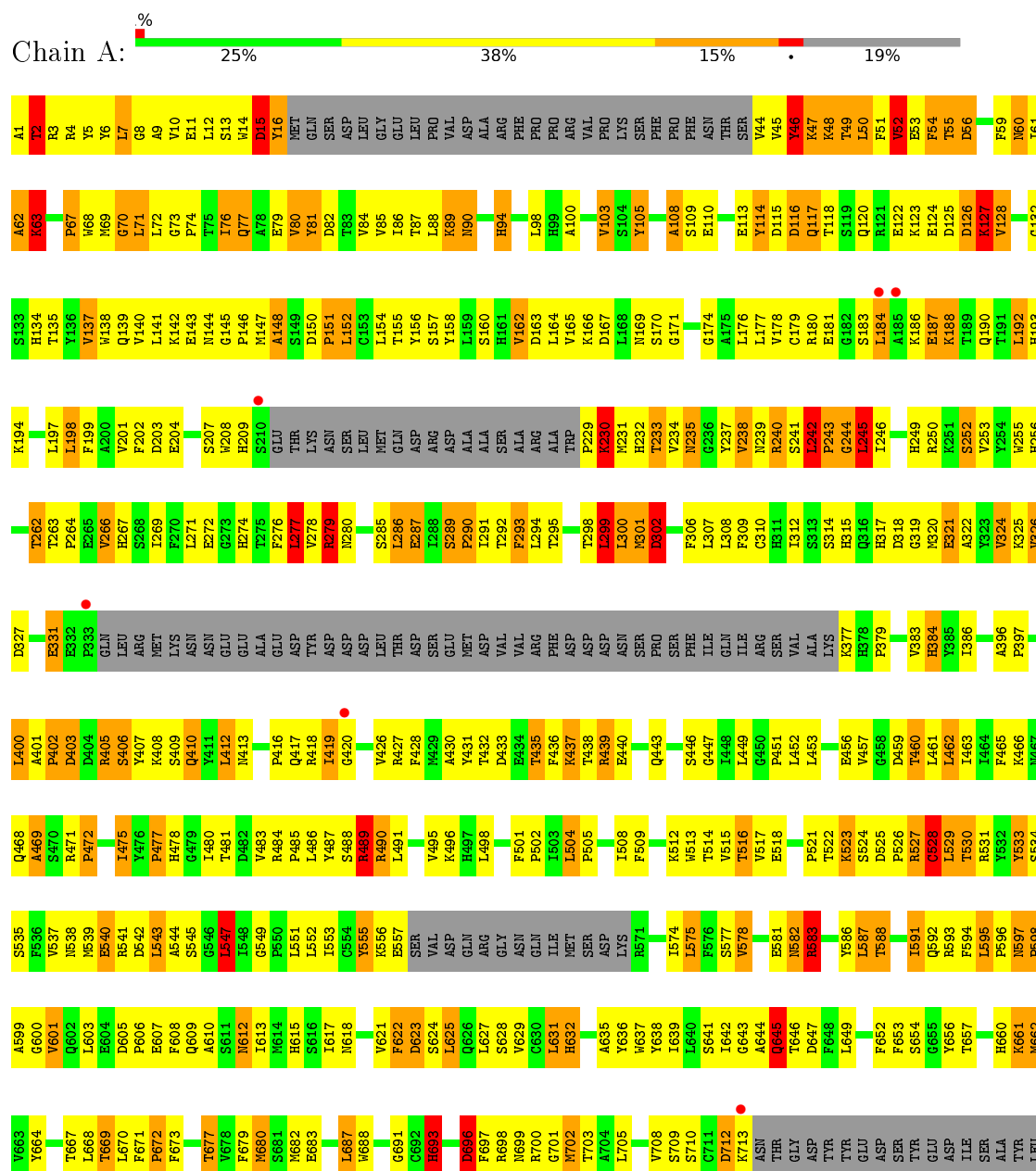
- Molecule 8 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	B	5	Total	C	N	O	0	0
			61	34	2	25		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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.

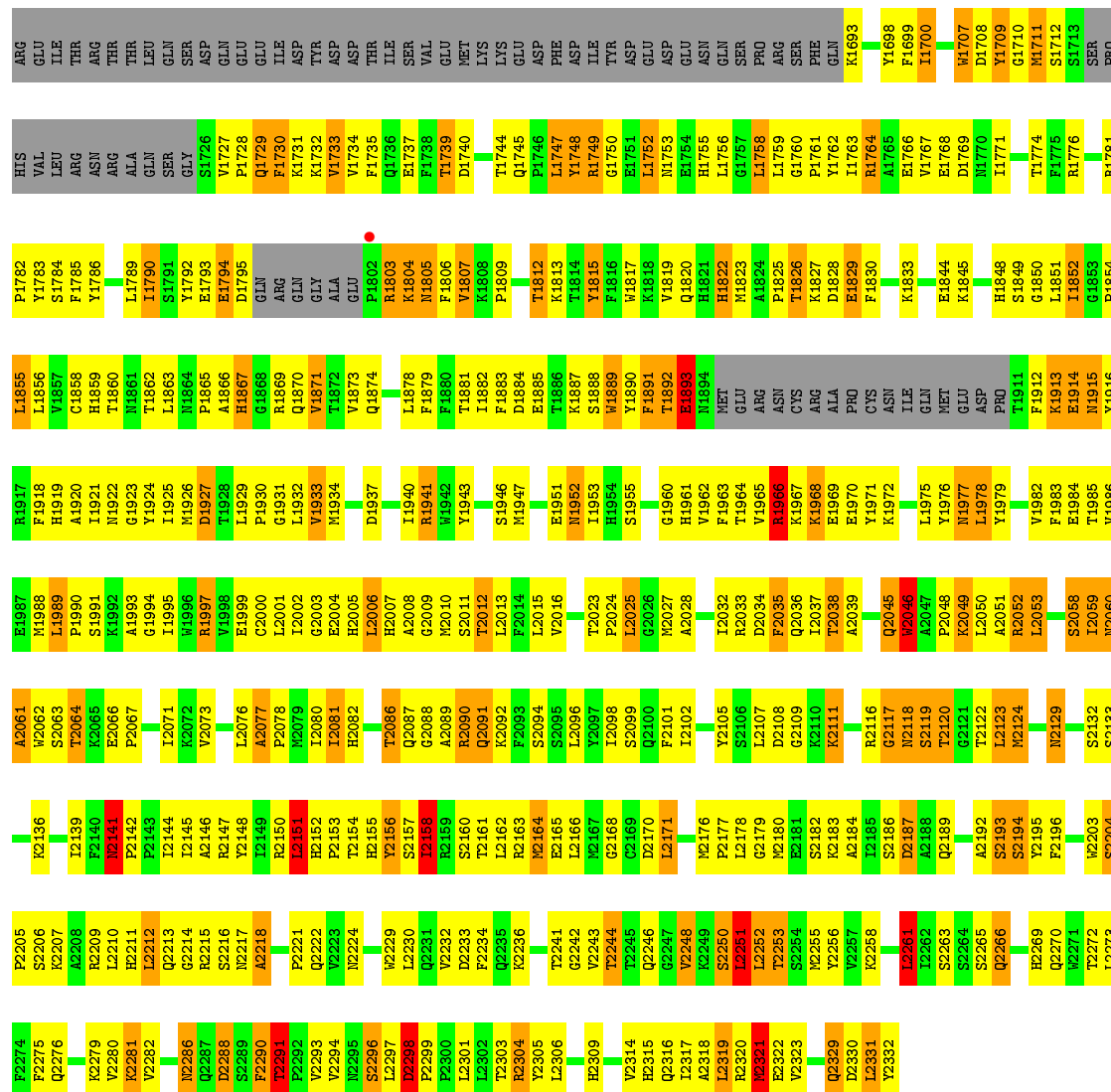
- Molecule 1: FACTOR VIIIA HEAVY CHAIN, 92 KDA ISOFORM, B DOMAIN



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PRO
SER
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GLN
HIS

• Molecule 2: FACTOR VIIIA LIGHT CHAIN

Chain B: 32% 41% 14% • 12%



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	133.84Å 133.84Å 355.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.98 19.99 – 3.98	Depositor EDS
% Data completeness (in resolution range)	98.8 (20.00-3.98) 99.9 (19.99-3.98)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.33 (at 3.94Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.162 , 0.246 0.166 , 0.249	Depositor DCC
R_{free} test set	1458 reflections (5.42%)	DCC
Wilson B-factor (Å ²)	134.1	Xtriage
Anisotropy	0.066	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 120.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9973	wwPDB-VP
Average B, all atoms (Å ²)	160.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.18% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, BMA, NAG, CU1, CA, EDO

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	0.68	1/5085 (0.0%)	1.00	18/6901 (0.3%)
2	B	0.64	0/5070	0.94	10/6864 (0.1%)
All	All	0.66	1/10155 (0.0%)	0.97	28/13765 (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	5
2	B	0	3
5	A	1	0
All	All	1	8

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	46	TYR	N-CA	5.60	1.57	1.46

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2261	LEU	CA-CB-CG	-9.31	93.89	115.30
1	A	489	ARG	NE-CZ-NH1	8.95	124.78	120.30
1	A	46	TYR	N-CA-C	7.75	131.93	111.00
1	A	184	LEU	CA-CB-CG	7.14	131.73	115.30
1	A	15	ASP	N-CA-C	7.09	130.16	111.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	A	1755	NAG	C1

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	108	ALA	Peptide
1	A	436	PHE	Peptide
1	A	547	LEU	Peptide
1	A	583	ARG	Peptide
1	A	693	HIS	Peptide

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	4944	0	4834	414	0
2	B	4929	0	4812	393	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	28	0	25	2	0
6	A	4	0	6	2	0
6	B	4	0	6	0	0
7	B	1	0	0	0	0
8	B	61	0	52	3	0
All	All	9973	0	9735	793	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 40.

The worst 5 of 793 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:A:530:THR:HG22	1:A:677:THR:HB	1.26	1.17
2:B:1733:VAL:HG22	2:B:1890:TYR:HE2	1.12	1.13
1:A:523:LYS:HD3	1:A:523:LYS:H	1.05	1.13
2:B:2266:GLN:HE21	2:B:2266:GLN:HA	1.01	1.11
2:B:1859:HIS:O	2:B:1862:THR:HG22	1.55	1.05

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	602/760 (79%)	440 (73%)	97 (16%)	65 (11%)	0	11
2	B	598/685 (87%)	445 (74%)	101 (17%)	52 (9%)	1	17
All	All	1200/1445 (83%)	885 (74%)	198 (16%)	117 (10%)	1	14

5 of 117 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	15	ASP
1	A	46	TYR
1	A	54	PHE
1	A	56	ASP
1	A	62	ALA

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	544/680 (80%)	404 (74%)	140 (26%)	0	6
2	B	539/613 (88%)	420 (78%)	119 (22%)	1	10
All	All	1083/1293 (84%)	824 (76%)	259 (24%)	1	7

5 of 259 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	612	ASN
2	B	1731	LYS
2	B	2261	LEU
1	A	627	LEU
1	A	680	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	1822	HIS
2	B	1950	ASN
2	B	2235	GLN
2	B	1870	GLN
2	B	1952	ASN

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 ⓘ

7 carbohydrates 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	$\# Z > 2$
5	NAG	A	1755	1,5	14,14,15	1.14	1 (7%)	15,19,21	2.36	6 (40%)
5	NAG	A	1756	5	14,14,15	0.61	0	15,19,21	2.10	3 (20%)
8	NAG	B	2334	8,2	14,14,15	0.78	0	15,19,21	1.88	4 (26%)
8	NAG	B	2335	8	14,14,15	1.18	2 (14%)	15,19,21	2.99	7 (46%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	BMA	B	2336	8	11,11,12	0.88	1 (9%)	15,15,17	1.64	2 (13%)
8	BMA	B	2337	8	11,11,12	0.98	1 (9%)	15,15,17	1.60	2 (13%)
8	BMA	B	2338	8	11,11,12	0.75	0	15,15,17	1.10	2 (13%)

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
5	NAG	A	1755	1,5	1/1/5/7	0/6/23/26	0/1/1/1
5	NAG	A	1756	5	-	0/6/23/26	0/1/1/1
8	NAG	B	2334	8,2	-	0/6/23/26	0/1/1/1
8	NAG	B	2335	8	-	0/6/23/26	0/1/1/1
8	BMA	B	2336	8	-	0/2/19/22	0/1/1/1
8	BMA	B	2337	8	-	0/2/19/22	0/1/1/1
8	BMA	B	2338	8	-	0/2/19/22	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	B	2336	BMA	C2-C3	2.01	1.55	1.52
8	B	2335	NAG	C2-N2	2.36	1.50	1.46
8	B	2335	NAG	C1-C2	2.57	1.56	1.52
5	A	1755	NAG	C1-C2	2.57	1.56	1.52
8	B	2337	BMA	C2-C3	2.61	1.56	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	2334	NAG	O7-C7-C8	-3.01	116.53	122.07
5	A	1755	NAG	O3-C3-C4	-2.26	105.26	110.36
8	B	2336	BMA	C1-C2-C3	-2.26	106.81	109.55
5	A	1755	NAG	O7-C7-C8	-2.22	117.98	122.07
8	B	2335	NAG	O7-C7-C8	-2.19	118.05	122.07

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	A	1755	NAG	C1

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1756	NAG	2	0
8	B	2334	NAG	2	0
8	B	2335	NAG	1	0
8	B	2336	BMA	1	0
8	B	2338	BMA	1	0

5.6 Ligand geometry

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 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	$\# Z > 2$
6	EDO	A	3333	-	3,3,3	0.47	0	2,2,2	0.33	0
6	EDO	B	3333	-	3,3,3	0.56	0	2,2,2	0.11	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
6	EDO	A	3333	-	-	0/1/1/1	0/0/0/0
6	EDO	B	3333	-	-	0/1/1/1	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	3333	EDO	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	612/760 (80%)	-0.60	6 (0%) 84 77	98, 154, 230, 309	0
2	B	606/685 (88%)	-0.64	1 (0%) 95 94	99, 155, 213, 290	0
All	All	1218/1445 (84%)	-0.62	7 (0%) 90 86	98, 154, 223, 309	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	333	PRO	4.2
1	A	185	ALA	2.8
1	A	713	LYS	2.6
1	A	420	GLY	2.3
2	B	1802	PRO	2.2

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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
5	NAG	A	1755	14/15	0.89	0.40	1.69	197,223,245,258	0
8	NAG	B	2335	14/15	0.91	0.24	0.63	164,205,234,248	0
8	NAG	B	2334	14/15	0.94	0.20	-0.37	151,173,209,221	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	NAG	A	1756	14/15	0.71	0.46	-	217,256,320,356	0
8	BMA	B	2336	11/12	0.92	0.28	-	202,237,263,297	0
8	BMA	B	2338	11/12	0.82	0.26	-	211,251,269,270	0
8	BMA	B	2337	11/12	0.78	0.28	-	221,270,291,291	0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
6	EDO	A	3333	4/4	0.70	0.43	9.41	170,174,186,187	0
6	EDO	B	3333	4/4	0.74	0.48	1.98	129,134,141,143	0
7	CU1	B	1	1/1	0.98	0.16	-0.25	133,133,133,133	0
3	ZN	A	800	1/1	0.99	0.14	-0.61	144,144,144,144	0
4	CA	A	801	1/1	0.97	0.10	-1.48	130,130,130,130	0

6.5 Other polymers [i](#)

There are no such residues in this entry.