



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:29 AM UTC

PDB ID : 3EHM / pdb_00003ehm
Title : Structure of BT1043
Authors : Koropatkin, N.M.; Smith, T.J.
Deposited on : 2008-09-13
Resolution : 2.00 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

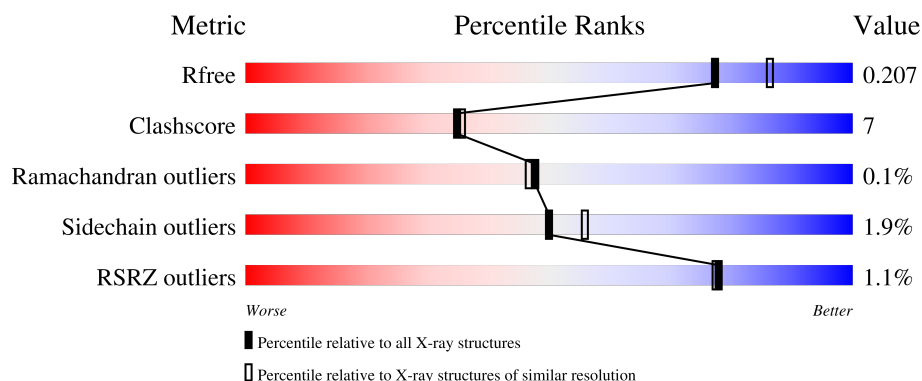
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	532	% 79% 15% ..
1	B	532	% 77% 17% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8719 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 SusD homolog.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	510	Total	C	N	O	S	Se	0	0	0
			4027	2563	672	779	1	12			
1	B	510	Total	C	N	O	S	Se	0	0	0
			4025	2563	671	778	1	12			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MSE	-	expression tag	UNP Q8A8X4
A	0	ALA	-	expression tag	UNP Q8A8X4
A	1	SER	-	expression tag	UNP Q8A8X4
A	210	VAL	ALA	conflict	UNP Q8A8X4
B	-1	MSE	-	expression tag	UNP Q8A8X4
B	0	ALA	-	expression tag	UNP Q8A8X4
B	1	SER	-	expression tag	UNP Q8A8X4
B	210	VAL	ALA	conflict	UNP Q8A8X4

- Molecule 2 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	340	Total	O	0	0
			340	340		
3	B	323	Total	O	0	0
			323	323		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	60.28Å 102.23Å 175.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.00 50.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.8 (50.00-2.00) 97.8 (50.00-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.53 (at 1.94Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.171 , 0.207 0.172 , 0.207	Depositor DCC
R_{free} test set	7349 reflections (9.35%)	wwPDB-VP
Wilson B-factor (Å ²)	18.8	Xtriage
Anisotropy	0.844	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 35.3	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	0.95	EDS
Total number of atoms	8719	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.15% 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: 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	0.35	0/4121	0.90	18/5582 (0.3%)
1	B	0.35	0/4119	0.90	19/5579 (0.3%)
All	All	0.35	0/8240	0.90	37/11161 (0.3%)

There are no bond length outliers.

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	55	LEU	N-CA-C	10.24	122.39	111.03
1	B	55	LEU	N-CA-C	10.16	122.31	111.03
1	B	529	ASN	N-CA-C	8.02	133.45	111.00
1	B	95	SER	N-CA-C	7.95	119.95	111.28
1	A	95	SER	N-CA-C	6.95	119.88	111.82
1	A	132	LEU	N-CA-C	-6.83	103.91	111.36
1	A	64	TYR	N-CA-C	-6.74	104.01	111.36
1	B	64	TYR	N-CA-C	-6.74	104.02	111.36
1	B	487	PHE	N-CA-C	-6.71	100.59	110.52
1	B	132	LEU	N-CA-C	-6.62	104.15	111.36
1	A	482	ARG	N-CA-C	-6.58	105.16	113.72
1	B	54	ASP	N-CA-C	6.56	121.12	112.72
1	A	54	ASP	N-CA-C	6.32	120.81	112.72
1	B	482	ARG	N-CA-C	-6.31	105.61	113.38
1	B	463	MSE	N-CA-C	-6.00	101.39	110.28
1	A	447	ALA	N-CA-C	5.96	117.78	111.28
1	A	463	MSE	N-CA-C	-5.83	101.66	110.28
1	B	518	TRP	N-CA-C	5.81	118.36	111.33
1	A	109	LYS	N-CA-C	5.78	119.14	111.75
1	A	487	PHE	N-CA-C	-5.77	101.98	110.52
1	B	337	LEU	N-CA-C	-5.76	100.02	109.40
1	A	337	LEU	N-CA-C	-5.75	100.03	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	447	ALA	N-CA-C	5.69	117.16	111.07
1	B	87	ASN	N-CA-C	-5.65	105.20	111.36
1	A	518	TRP	N-CA-C	5.58	118.08	111.33
1	B	508	GLY	N-CA-C	-5.39	106.78	115.08
1	A	508	GLY	N-CA-C	-5.32	106.88	115.08
1	A	290	PHE	N-CA-C	5.26	117.68	109.52
1	A	421	TYR	N-CA-C	5.18	117.41	109.07
1	B	152	ALA	CA-C-N	5.12	125.12	119.90
1	B	152	ALA	C-N-CA	5.12	125.12	119.90
1	A	87	ASN	N-CA-C	-5.12	105.78	111.36
1	A	503	ILE	CB-CA-C	-5.09	108.86	113.70
1	A	157	SER	N-CA-C	-5.07	103.84	110.53
1	B	497	ASN	CA-C-N	5.07	124.85	119.28
1	B	497	ASN	C-N-CA	5.07	124.85	119.28
1	B	402	TYR	N-CA-C	5.03	118.49	111.30

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	4027	0	3879	57	0
1	B	4025	0	3877	61	0
2	B	4	0	6	0	0
3	A	340	0	0	0	0
3	B	323	0	0	5	0
All	All	8719	0	7762	118	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 7.

All (118) 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:312:ASN:HA	1:A:466:MSE:HE3	1.32	1.07
1:A:309:ALA:HB3	1:A:466:MSE:HE2	1.30	1.06
1:B:413:ASN:HD22	1:B:414:THR:H	1.15	0.94
1:B:218:GLU:HG2	1:B:222:LYS:HE3	1.56	0.88
1:A:69:ASN:HD22	1:A:70:ASN:H	1.17	0.87
1:B:69:ASN:HD22	1:B:70:ASN:H	1.21	0.85
1:B:266:ASN:HD22	1:B:269:ARG:HH22	1.25	0.85
1:A:413:ASN:HD22	1:A:414:THR:H	1.28	0.78
1:A:309:ALA:HB3	1:A:466:MSE:CE	2.10	0.77
1:A:309:ALA:CB	1:A:466:MSE:HE2	2.15	0.76
1:A:69:ASN:HD22	1:A:70:ASN:N	1.84	0.74
1:A:312:ASN:ND2	1:A:314:LYS:H	1.85	0.73
1:A:266:ASN:HD22	1:A:269:ARG:HH22	1.33	0.73
1:A:247:LYS:HB3	1:A:336:PRO:HB3	1.72	0.71
1:B:91:GLN:HA	1:B:95:SER:OG	1.92	0.70
1:B:99:LEU:HB2	1:B:100:PRO:HD3	1.74	0.69
1:B:69:ASN:HD22	1:B:70:ASN:N	1.88	0.69
1:A:208:ARG:HD3	1:A:344:GLU:OE2	1.93	0.69
1:B:413:ASN:HD22	1:B:414:THR:N	1.91	0.67
1:B:247:LYS:HB3	1:B:336:PRO:HB3	1.79	0.65
1:A:69:ASN:ND2	1:A:71:TRP:H	1.95	0.65
1:B:312:ASN:ND2	1:B:314:LYS:H	1.96	0.64
1:A:312:ASN:HD22	1:A:313:SER:N	1.95	0.64
1:A:372:ILE:O	1:A:376:GLU:HG3	1.98	0.63
1:A:91:GLN:HA	1:A:95:SER:OG	1.98	0.63
1:B:200:LYS:HE3	3:B:964:HOH:O	1.99	0.62
1:B:69:ASN:ND2	1:B:71:TRP:H	1.98	0.61
1:B:413:ASN:ND2	1:B:414:THR:H	1.95	0.61
1:B:380:SER:HB2	3:B:1114:HOH:O	2.01	0.60
1:B:312:ASN:HD22	1:B:313:SER:N	2.00	0.59
1:A:69:ASN:ND2	1:A:70:ASN:H	1.95	0.59
1:B:237:ILE:O	1:B:345:THR:HG21	2.02	0.59
1:A:207:LEU:O	1:A:210:VAL:HG22	2.01	0.59
1:B:427:LYS:O	1:B:431:GLN:HG3	2.03	0.58
1:A:312:ASN:HA	1:A:466:MSE:CE	2.20	0.58
1:B:240:ILE:O	1:B:243:GLU:HG2	2.04	0.58
1:A:63:GLY:HA3	1:A:273:THR:HB	1.86	0.57
1:B:69:ASN:ND2	1:B:70:ASN:H	1.95	0.57
1:A:192:ASN:HD22	1:A:251:LYS:NZ	2.03	0.57
1:A:79:TRP:N	1:A:79:TRP:CD1	2.74	0.56
1:B:207:LEU:O	1:B:210:VAL:HG22	2.06	0.56
1:A:192:ASN:HD22	1:A:251:LYS:HZ3	1.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:372:ILE:O	1:B:376:GLU:HG3	2.05	0.55
1:B:470:ALA:HB3	1:B:471:PRO:HD3	1.88	0.55
1:B:63:GLY:HA3	1:B:273:THR:HB	1.87	0.55
1:A:29:ASN:HD21	1:A:33:ARG:HE	1.55	0.55
1:B:255:LEU:HD11	1:B:259:LEU:HD12	1.86	0.55
1:A:312:ASN:HD22	1:A:313:SER:H	1.55	0.54
1:A:368:GLN:NE2	1:A:368:GLN:HA	2.21	0.54
1:B:218:GLU:CG	1:B:222:LYS:HE3	2.34	0.54
1:B:51:GLN:HA	1:B:55:LEU:HB2	1.89	0.54
1:B:368:GLN:O	1:B:372:ILE:HG12	2.07	0.54
1:A:503:ILE:HB	1:A:504:PRO:HD3	1.90	0.54
1:A:312:ASN:HD21	1:A:314:LYS:HB2	1.74	0.53
1:A:278:LEU:HD13	1:A:286:LEU:HA	1.92	0.52
1:B:270:MSE:HE3	1:B:307:PRO:HB3	1.92	0.51
1:B:68:ASN:O	1:B:69:ASN:HB2	2.11	0.51
1:B:502:GLU:HG2	1:B:506:LEU:HG	1.93	0.51
1:A:69:ASN:ND2	1:A:70:ASN:N	2.57	0.50
1:A:427:LYS:O	1:A:431:GLN:HG3	2.11	0.50
1:B:99:LEU:CB	1:B:100:PRO:HD3	2.40	0.50
1:B:79:TRP:CD1	1:B:79:TRP:N	2.79	0.50
1:B:312:ASN:HD22	1:B:313:SER:H	1.59	0.50
1:B:516:LYS:HD3	1:B:520:VAL:HG11	1.93	0.49
1:A:470:ALA:HB3	1:A:471:PRO:HD3	1.94	0.49
1:B:206:MSE:O	1:B:210:VAL:HG13	2.12	0.49
1:A:295:TYR:CD1	1:A:401:LYS:HD3	2.47	0.49
1:B:29:ASN:HD21	1:B:33:ARG:HE	1.60	0.49
1:B:456:ARG:O	1:B:521:ARG:HG2	2.12	0.49
1:B:66:GLY:HA3	1:B:308:VAL:HB	1.95	0.49
1:A:502:GLU:HG2	1:A:506:LEU:HG	1.94	0.48
1:A:208:ARG:HD2	1:A:449:GLU:OE2	2.13	0.48
1:A:87:ASN:O	1:A:91:GLN:HG3	2.13	0.48
1:B:383:ALA:HB3	3:B:1049:HOH:O	2.14	0.48
1:A:413:ASN:HD22	1:A:414:THR:N	2.04	0.48
1:A:29:ASN:O	1:A:33:ARG:HG2	2.14	0.47
1:B:62:ILE:HG21	1:B:451:TRP:HA	1.97	0.47
1:B:69:ASN:ND2	1:B:70:ASN:N	2.58	0.46
1:A:206:MSE:O	1:A:210:VAL:HG13	2.15	0.46
1:A:368:GLN:HA	1:A:368:GLN:HE21	1.81	0.46
1:A:468:GLU:O	1:A:478:ILE:HD11	2.16	0.46
1:B:317:SER:HB3	1:B:322:SER:HB2	1.96	0.46
1:A:232:LYS:NZ	1:A:233:ASN:HD21	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:159:GLU:HG3	1:B:518:TRP:CZ2	2.51	0.45
1:B:95:SER:O	1:B:99:LEU:HD23	2.17	0.45
1:B:310:PRO:HD3	3:B:1113:HOH:O	2.16	0.45
1:B:29:ASN:O	1:B:33:ARG:HG2	2.16	0.45
1:B:297:SER:CA	1:B:301:ALA:HB2	2.48	0.44
1:B:222:LYS:HE2	3:B:1188:HOH:O	2.17	0.44
1:A:260:ALA:O	1:A:264:GLU:HB2	2.17	0.44
1:A:95:SER:O	1:A:99:LEU:HD23	2.18	0.44
1:A:79:TRP:N	1:A:79:TRP:HD1	2.16	0.43
1:B:197:ASN:HD22	1:B:197:ASN:HA	1.67	0.43
1:A:129:ILE:HD11	1:A:201:LEU:HD21	2.01	0.43
1:A:255:LEU:O	1:A:256:ASN:C	2.60	0.42
1:A:317:SER:HB3	1:A:322:SER:HB2	2.02	0.42
1:B:216:ILE:HG13	1:B:519:TRP:HA	2.00	0.42
1:A:500:MSE:O	1:A:503:ILE:HG12	2.19	0.42
1:B:102:ASN:O	1:B:106:GLU:HG3	2.20	0.42
1:A:51:GLN:HA	1:A:55:LEU:HB2	2.01	0.42
1:A:66:GLY:HA3	1:A:308:VAL:HB	2.02	0.42
1:B:371:ASN:ND2	1:B:375:GLN:HE21	2.18	0.42
1:B:278:LEU:HD13	1:B:286:LEU:HA	2.02	0.42
1:A:312:ASN:ND2	1:A:313:SER:N	2.66	0.42
1:B:398:SER:OG	1:B:399:ASN:N	2.53	0.42
1:B:524:ARG:HA	1:B:525:PRO:HD3	1.93	0.41
1:A:197:ASN:HD22	1:A:197:ASN:HA	1.61	0.41
1:A:270:MSE:HE2	1:A:327:SER:HB2	2.02	0.41
1:A:68:ASN:O	1:A:69:ASN:HB2	2.20	0.41
1:A:207:LEU:HA	1:A:210:VAL:HG22	2.03	0.41
1:A:468:GLU:HB3	1:A:478:ILE:HD13	2.03	0.41
1:B:382:VAL:HG13	1:B:383:ALA:N	2.36	0.41
1:A:216:ILE:HG13	1:A:519:TRP:HA	2.02	0.41
1:B:32:GLN:HB3	1:B:37:ILE:O	2.21	0.41
1:B:255:LEU:CD1	1:B:259:LEU:HD12	2.51	0.41
1:B:297:SER:HA	1:B:301:ALA:HB2	2.02	0.41
1:B:395:LEU:HD12	1:B:395:LEU:HA	1.90	0.40
1:B:266:ASN:HD22	1:B:269:ARG:NH2	2.05	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	508/532 (96%)	489 (96%)	18 (4%)	1 (0%)	43	42
1	B	508/532 (96%)	494 (97%)	14 (3%)	0	100	100
All	All	1016/1064 (96%)	983 (97%)	32 (3%)	1 (0%)	48	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	479	GLU

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	430/435 (99%)	422 (98%)	8 (2%)	50	56
1	B	429/435 (99%)	421 (98%)	8 (2%)	50	56
All	All	859/870 (99%)	843 (98%)	16 (2%)	50	56

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	ASN
1	A	174	GLU
1	A	177	ASN
1	A	413	ASN
1	A	441	LEU

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Mol	Chain	Res	Type
1	A	445	PRO
1	A	479	GLU
1	A	487	PHE
1	B	110	ASP
1	B	177	ASN
1	B	197	ASN
1	B	395	LEU
1	B	399	ASN
1	B	413	ASN
1	B	445	PRO
1	B	528	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	ASN
1	A	51	GLN
1	A	69	ASN
1	A	74	ASN
1	A	80	ASN
1	A	96	GLN
1	A	177	ASN
1	A	186	GLN
1	A	192	ASN
1	A	197	ASN
1	A	233	ASN
1	A	263	ASN
1	A	266	ASN
1	A	312	ASN
1	A	368	GLN
1	A	371	ASN
1	A	377	GLN
1	A	399	ASN
1	A	407	HIS
1	A	413	ASN
1	A	433	GLN
1	A	495	ASN
1	B	29	ASN
1	B	51	GLN
1	B	69	ASN
1	B	74	ASN
1	B	78	ASN

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Mol	Chain	Res	Type
1	B	80	ASN
1	B	91	GLN
1	B	96	GLN
1	B	144	ASN
1	B	177	ASN
1	B	186	GLN
1	B	192	ASN
1	B	197	ASN
1	B	233	ASN
1	B	266	ASN
1	B	312	ASN
1	B	371	ASN
1	B	375	GLN
1	B	399	ASN
1	B	407	HIS
1	B	413	ASN
1	B	431	GLN
1	B	495	ASN
1	B	499	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	EDO	B	600	-	3,3,3	0.73	0	2,2,2	0.38	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	EDO	B	600	-	-	0/1/1/1	-

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.

No monomer is involved in short contacts.

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	498/532 (93%)	-0.31	7 (1%) 73 73	11, 17, 27, 35	0
1	B	498/532 (93%)	-0.22	4 (0%) 82 82	12, 19, 27, 35	0
All	All	996/1064 (93%)	-0.26	11 (1%) 78 77	11, 18, 27, 35	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	480	ASP	4.0
1	B	397	GLY	3.9
1	B	398	SER	3.7
1	A	481	CYS	2.9
1	A	478	ILE	2.8
1	A	398	SER	2.6
1	A	479	GLU	2.5
1	B	529	ASN	2.4
1	A	397	GLY	2.3
1	B	20	PRO	2.2
1	A	112	ASP	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($\text{\AA}^2$)	Q<0.9
2	EDO	B	600	4/4	0.90	0.11	24,26,29,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.