



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:21 PM UTC

PDB ID : 5OGZ / pdb_00005ogz
Title : Crystal structure of Ruminiclostridium Thermocellum beta-Glucosidase A
Authors : Salama-Alber, O.; Bayer, E.
Deposited on : 2017-07-13
Resolution : 1.60 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

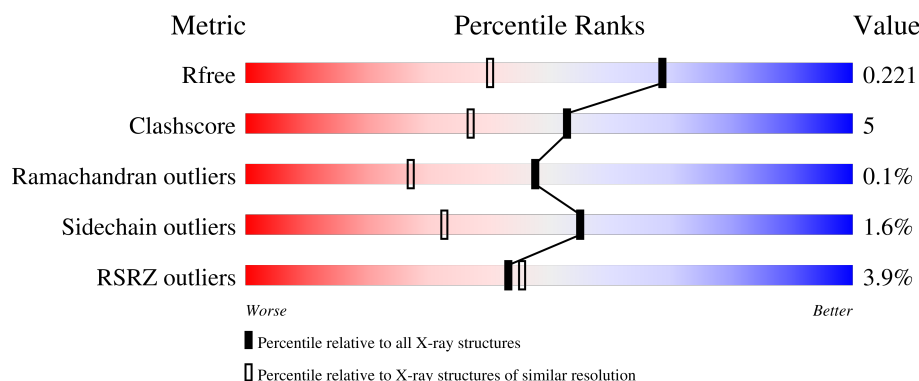
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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	456	
1	B	456	

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
3	EDO	B	503	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7900 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-glucosidase A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	449	Total	C	N	O	S	11	5	0
			3701	2395	611	689	6			
1	B	449	Total	C	N	O	S	11	5	0
			3701	2395	611	689	6			

There are 20 discrepancies between the modelled and reference sequences:

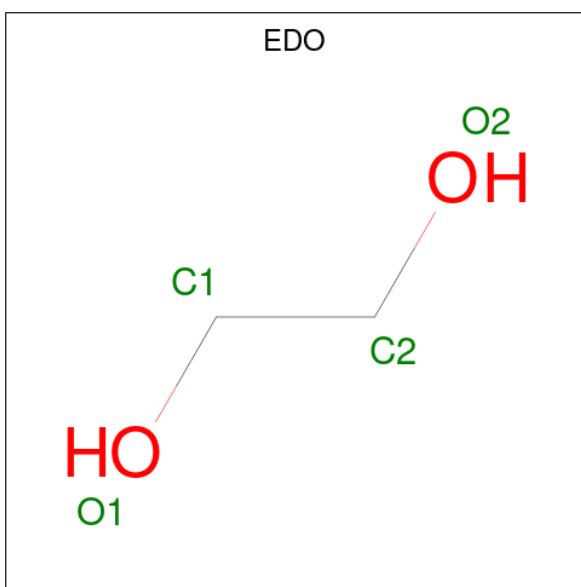
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P26208
A	2	ALA	-	expression tag	UNP P26208
A	449	LEU	-	expression tag	UNP P26208
A	450	GLU	-	expression tag	UNP P26208
A	451	HIS	-	expression tag	UNP P26208
A	452	HIS	-	expression tag	UNP P26208
A	453	HIS	-	expression tag	UNP P26208
A	454	HIS	-	expression tag	UNP P26208
A	455	HIS	-	expression tag	UNP P26208
A	456	HIS	-	expression tag	UNP P26208
B	1	MET	-	initiating methionine	UNP P26208
B	2	ALA	-	expression tag	UNP P26208
B	449	LEU	-	expression tag	UNP P26208
B	450	GLU	-	expression tag	UNP P26208
B	451	HIS	-	expression tag	UNP P26208
B	452	HIS	-	expression tag	UNP P26208
B	453	HIS	-	expression tag	UNP P26208
B	454	HIS	-	expression tag	UNP P26208
B	455	HIS	-	expression tag	UNP P26208
B	456	HIS	-	expression tag	UNP P26208

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

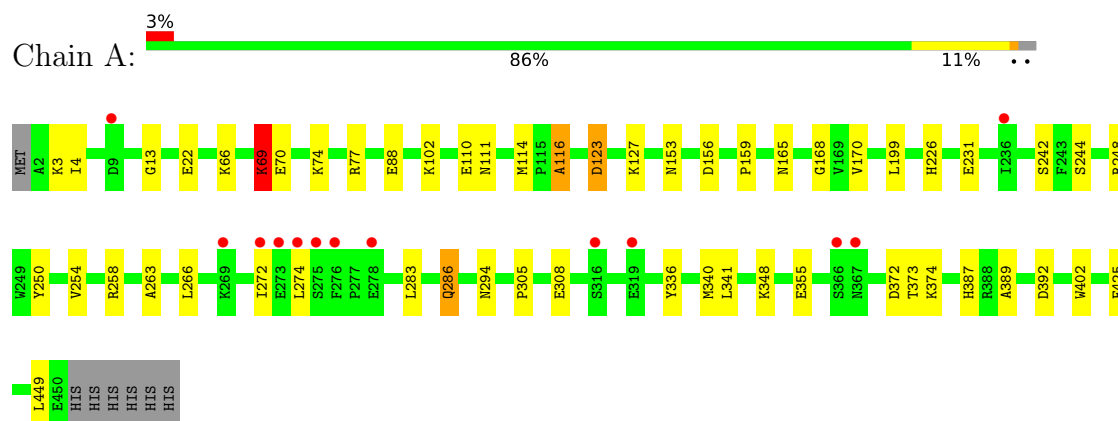
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	273	Total 273	O 273	0	0
4	B	206	Total 206	O 206	0	0

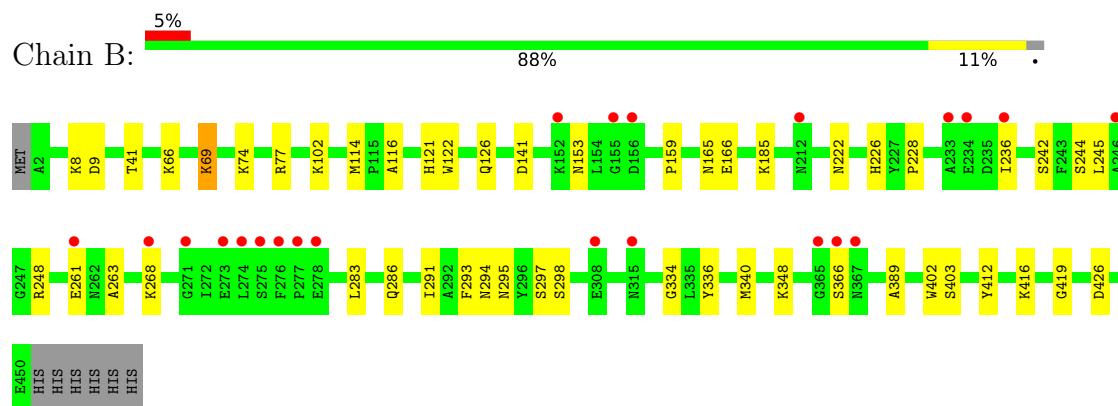
3 Residue-property plots [i](#)

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-glucosidase A



• Molecule 1: Beta-glucosidase A



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.67Å 56.22Å 94.50Å 90.00° 100.20° 90.00°	Depositor
Resolution (Å)	93.01 – 1.60 93.01 – 1.60	Depositor EDS
% Data completeness (in resolution range)	94.6 (93.01-1.60) 94.6 (93.01-1.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.27 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.183 , 0.216 0.193 , 0.221	Depositor DCC
R_{free} test set	5902 reflections (4.72%)	wwPDB-VP
Wilson B-factor (Å ²)	15.8	Xtriage
Anisotropy	0.280	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 35.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.053 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7900	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 7.98% 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: EDO, SO4

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	1.35	13/3803 (0.3%)	1.21	6/5143 (0.1%)
1	B	1.28	7/3803 (0.2%)	1.19	6/5143 (0.1%)
All	All	1.32	20/7606 (0.3%)	1.20	12/10286 (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	B	0	1

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	355	GLU	N-CA	8.86	1.56	1.46
1	A	348	LYS	CA-CB	5.94	1.56	1.52
1	B	348	LYS	C-O	-5.59	1.21	1.23
1	B	166	GLU	N-CA	5.58	1.50	1.46
1	A	374	LYS	C-O	-5.53	1.17	1.24
1	A	170	VAL	CA-C	5.50	1.59	1.52
1	A	425	PHE	C-O	-5.48	1.16	1.24
1	A	110	GLU	N-CA	5.41	1.53	1.46
1	A	372	ASP	CA-C	-5.41	1.47	1.53
1	A	263	ALA	C-O	-5.40	1.17	1.24
1	B	419	GLY	CA-C	5.33	1.57	1.52
1	B	126	GLN	N-CA	-5.33	1.40	1.46
1	A	286	GLN	N-CA	5.32	1.51	1.45
1	A	254	VAL	C-O	5.20	1.29	1.24
1	B	141	ASP	N-CA	-5.17	1.39	1.46
1	A	156	ASP	C-O	5.12	1.30	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	13	GLY	CA-C	-5.10	1.47	1.52
1	A	116	ALA	CA-CB	-5.07	1.45	1.53
1	B	293	PHE	N-CA	-5.04	1.39	1.45
1	B	291	ILE	CA-CB	5.01	1.60	1.54

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	41	THR	CB-CA-C	8.14	119.13	109.85
1	A	69	LYS	CD-CE-NZ	7.21	134.98	111.90
1	B	348	LYS	CA-C-N	6.50	126.47	120.03
1	B	348	LYS	C-N-CA	6.50	126.47	120.03
1	B	41	THR	CA-C-N	-6.44	113.34	119.85
1	B	41	THR	C-N-CA	-6.44	113.34	119.85
1	A	373	THR	N-CA-C	6.33	118.18	111.28
1	A	69	LYS	CA-CB-CG	6.29	126.68	114.10
1	A	22	GLU	N-CA-C	5.79	117.67	111.36
1	B	69	LYS	CD-CE-NZ	5.54	129.63	111.90
1	A	402	TRP	CA-C-O	-5.54	114.23	120.43
1	A	305	PRO	N-CA-C	5.18	120.57	113.84

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	121	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	3701	0	3603	38	0
1	B	3701	0	3603	35	1
2	A	5	0	0	0	0
2	B	10	0	0	0	0
3	B	4	0	5	11	0
4	A	273	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	206	0	0	1	0
All	All	7900	0	7211	73	1

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.

All (73) 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:102:LYS:HD3	4:A:793:HOH:O	1.54	1.05
1:A:336:TYR:CE1	1:A:340:MET:HE3	2.01	0.95
1:B:336:TYR:CE1	1:B:340:MET:HE3	2.09	0.87
1:A:340:MET:CE	1:A:389:ALA:HA	2.07	0.84
1:B:298:SER:OG	3:B:503:EDO:C1	2.30	0.80
1:B:340:MET:CE	1:B:389:ALA:HA	2.12	0.79
1:B:298:SER:OG	3:B:503:EDO:H12	1.88	0.74
1:B:298:SER:OG	3:B:503:EDO:H11	1.91	0.71
1:A:102:LYS:CE	1:A:153:ASN:HD22	2.04	0.70
1:A:102:LYS:HG2	4:A:844:HOH:O	1.91	0.69
1:B:295:ASN:ND2	3:B:503:EDO:H21	2.08	0.68
1:A:340:MET:HE2	1:A:389:ALA:HA	1.76	0.68
1:B:77:ARG:HH22	1:B:165:ASN:HD22	1.41	0.68
1:A:102:LYS:HE3	1:A:153:ASN:HD22	1.57	0.66
1:A:340:MET:HE1	1:A:392:ASP:HB2	1.77	0.65
1:B:334:GLY:C	3:B:503:EDO:H22	2.23	0.64
1:A:102:LYS:HE3	1:A:153:ASN:ND2	2.13	0.64
1:B:295:ASN:HD21	3:B:503:EDO:H21	1.62	0.64
1:B:102:LYS:HE2	1:B:153:ASN:HD22	1.62	0.63
1:A:77:ARG:HH22	1:A:165:ASN:HD22	1.47	0.61
1:B:114:MET:HG3	1:B:159:PRO:HG2	1.83	0.60
1:B:334:GLY:HA3	3:B:503:EDO:H11	1.81	0.60
1:B:228:PRO:HG3	1:B:236:ILE:HD13	1.84	0.59
1:A:165:ASN:HD21	1:A:294:ASN:HD21	1.50	0.58
1:B:340:MET:HE2	1:B:389:ALA:CB	2.35	0.57
1:A:341:LEU:C	1:A:341:LEU:HD23	2.30	0.57
1:B:165:ASN:HD21	1:B:294:ASN:HD21	1.52	0.56
1:B:283:LEU:O	1:B:286:GLN:HG2	2.05	0.56
1:B:244:SER:HA	1:B:248[B]:ARG:HB3	1.86	0.56
1:B:222:ASN:ND2	4:B:605:HOH:O	2.39	0.56
1:A:340:MET:HE1	1:A:389:ALA:HA	1.88	0.54
1:B:226:HIS:HD2	1:B:242:SER:OG	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:283:LEU:O	1:A:286:GLN:HG2	2.08	0.53
1:B:77:ARG:HH22	1:B:165:ASN:ND2	2.06	0.53
1:A:69:LYS:CE	1:A:111:ASN:OD1	2.59	0.50
1:B:334:GLY:O	3:B:503:EDO:H22	2.10	0.50
1:A:226:HIS:HD2	1:A:242:SER:OG	1.94	0.50
1:A:70:GLU:OE1	4:A:601:HOH:O	2.20	0.49
1:B:340:MET:HE1	1:B:389:ALA:HA	1.91	0.49
1:A:114:MET:HG3	1:A:159:PRO:HG2	1.95	0.48
1:A:244:SER:HA	1:A:248[B]:ARG:HB3	1.95	0.48
1:A:77:ARG:HH22	1:A:165:ASN:ND2	2.10	0.48
1:A:66:LYS:HA	1:A:69:LYS:HE3	1.96	0.48
1:B:102:LYS:CE	1:B:153:ASN:ND2	2.77	0.48
1:B:102:LYS:CE	1:B:153:ASN:HD22	2.25	0.47
1:A:308:GLU:OE1	1:A:308:GLU:N	2.44	0.47
1:B:334:GLY:CA	3:B:503:EDO:H11	2.45	0.47
1:A:69:LYS:HE2	1:A:111:ASN:OD1	2.15	0.47
1:A:199:LEU:HD11	1:A:283:LEU:HD23	1.96	0.46
1:B:245:LEU:HD23	1:B:263:ALA:HB1	1.96	0.46
1:A:336:TYR:CZ	1:A:340:MET:HE3	2.46	0.46
1:A:102:LYS:CD	4:A:793:HOH:O	2.36	0.45
1:B:9:ASP:OD1	1:B:9:ASP:N	2.46	0.45
1:B:77:ARG:HA	1:B:116:ALA:O	2.16	0.45
1:B:340:MET:HE2	1:B:389:ALA:HB1	1.98	0.45
1:B:340:MET:CE	1:B:389:ALA:CA	2.88	0.44
1:A:258:ARG:HG3	1:A:258:ARG:HH21	1.84	0.43
1:A:226:HIS:CD2	1:A:242:SER:OG	2.72	0.43
1:B:412:TYR:CD1	1:B:416[A]:LYS:HE2	2.54	0.43
1:B:334:GLY:C	3:B:503:EDO:C2	2.91	0.42
1:A:340:MET:HE2	1:A:389:ALA:CA	2.47	0.42
1:B:402:TRP:HA	1:B:403:SER:HA	1.85	0.42
1:B:297:SER:O	3:B:503:EDO:H12	2.20	0.42
1:A:336:TYR:CE1	1:A:340:MET:CE	2.89	0.41
1:A:165:ASN:ND2	1:A:294:ASN:HD21	2.16	0.41
1:A:168:GLY:HA2	1:A:250:TYR:CZ	2.56	0.41
1:A:77:ARG:HA	1:A:116:ALA:O	2.20	0.41
1:A:258:ARG:HG3	1:A:258:ARG:NH2	2.35	0.41
1:A:3:LYS:HA	1:A:449:LEU:HD23	2.03	0.41
1:B:66:LYS:HA	1:B:69:LYS:HE3	2.03	0.41
1:A:4:ILE:HG23	1:A:387:HIS:CG	2.57	0.40
1:A:123:ASP:OD1	1:A:123:ASP:N	2.54	0.40
1:A:88:GLU:HB3	1:A:127:LYS:HD3	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:261:GLU:OE1	1:B:426:ASP:OD2[1_565]	2.08	0.12

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	452/456 (99%)	442 (98%)	10 (2%)	0	100	100
1	B	452/456 (99%)	446 (99%)	5 (1%)	1 (0%)	43	24
All	All	904/912 (99%)	888 (98%)	15 (2%)	1 (0%)	48	27

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	122	TRP

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	392/394 (100%)	384 (98%)	8 (2%)	48	24
1	B	392/394 (100%)	386 (98%)	6 (2%)	57	35
All	All	784/788 (100%)	770 (98%)	14 (2%)	55	28

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	LYS
1	A	74[A]	LYS
1	A	74[B]	LYS
1	A	123	ASP
1	A	231	GLU
1	A	266	LEU
1	A	272	ILE
1	A	274	LEU
1	B	8	LYS
1	B	74[A]	LYS
1	B	74[B]	LYS
1	B	185	LYS
1	B	268	LYS
1	B	366	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	129	GLN
1	A	153	ASN
1	A	165	ASN
1	A	226	HIS
1	A	295	ASN
1	A	387	HIS
1	A	391	GLN
1	B	126	GLN
1	B	129	GLN
1	B	153	ASN
1	B	165	ASN
1	B	222	ASN
1	B	226	HIS
1	B	295	ASN
1	B	367	ASN
1	B	387	HIS
1	B	391	GLN
1	B	445	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	SO4	B	502	-	4,4,4	0.49	0	6,6,6	0.99	0
2	SO4	A	501	-	4,4,4	0.41	0	6,6,6	0.53	0
3	EDO	B	503	-	3,3,3	1.75	1 (33%)	2,2,2	1.83	1 (50%)
2	SO4	B	501	-	4,4,4	0.46	0	6,6,6	0.37	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	EDO	B	503	-	-	0/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	503	EDO	O1-C1	-2.88	1.27	1.42

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	B	503	EDO	O1-C1-C2	-2.55	92.99	112.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	503	EDO	11	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	247:GLY	C	248[A]:ARG	N	1.20

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, 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	448/456 (98%)	0.04	13 (2%) 53 56	6, 15, 35, 55	4 (0%)
1	B	448/456 (98%)	0.44	22 (4%) 35 36	7, 20, 40, 63	4 (0%)
All	All	896/912 (98%)	0.24	35 (3%) 43 45	6, 17, 37, 63	8 (0%)

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	276	PHE	5.5
1	B	274	LEU	5.1
1	B	271	GLY	4.8
1	B	277	PRO	4.1
1	B	276	PHE	4.0
1	A	316	SER	3.9
1	A	272	ILE	3.7
1	B	236	ILE	3.7
1	B	278	GLU	3.3
1	A	274	LEU	3.3
1	A	366	SER	3.0
1	B	365	GLY	3.0
1	B	261	GLU	2.7
1	B	233	ALA	2.7
1	A	319	GLU	2.6
1	A	278	GLU	2.6
1	B	308	GLU	2.6
1	A	269	LYS	2.5
1	B	367	ASN	2.5
1	B	156	ASP	2.5
1	A	236	ILE	2.4
1	B	155	GLY	2.4
1	B	212	ASN	2.3
1	B	273	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	275	SER	2.3
1	A	367	ASN	2.2
1	B	234	GLU	2.2
1	B	152	LYS	2.2
1	B	246	ALA	2.1
1	B	366	SER	2.1
1	A	273	GLU	2.1
1	A	9	ASP	2.1
1	A	275	SER	2.1
1	B	268	LYS	2.1
1	B	315	ASN	2.0

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
2	SO4	A	501	5/5	0.88	0.13	38,38,44,44	0
2	SO4	B	502	5/5	0.88	0.11	48,48,52,53	0
2	SO4	B	501	5/5	0.90	0.09	43,45,49,53	0
3	EDO	B	503	4/4	0.90	0.15	19,21,23,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.