



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 2, 2025 – 01:39 am GMT

PDB ID : 9GOX
Title : Crystal structure of Fab B6-D9 in complex with CD38
Authors : Dreyfus, C.; Freier, R.
Deposited on : 2024-09-06
Resolution : 1.84 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.003 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

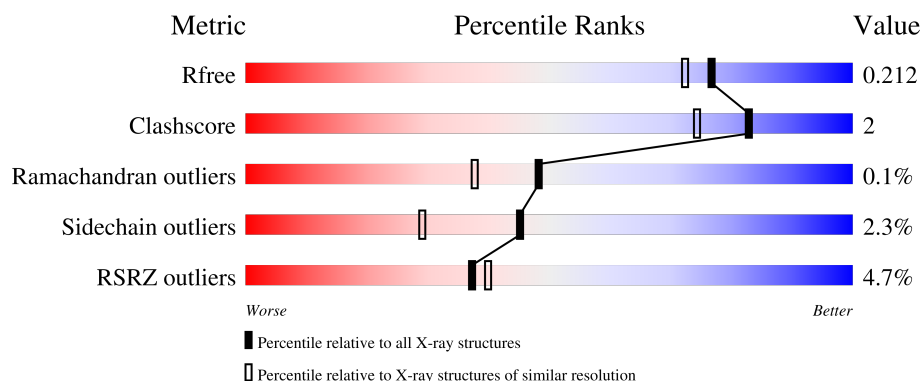
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.84 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}	164625	1150 (1.84-1.84)
Clashscore	180529	1248 (1.84-1.84)
Ramachandran outliers	177936	1240 (1.84-1.84)
Sidechain outliers	177891	1240 (1.84-1.84)
RSRZ outliers	164620	1149 (1.84-1.84)

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	H	224	<div> <div>5%</div> <div> <div></div> <div>90%</div> <div>9%</div> </div> </div>
2	L	214	<div> <div>5%</div> <div> <div></div> <div>95%</div> <div>5%</div> </div> </div>
3	A	264	<div> <div>4%</div> <div> <div></div> <div>86%</div> <div>8%</div> <div>6%</div> </div> </div>

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 6331 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 Fab B6-D9 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	223	Total	C	N	O	S	12	11	0
			1739	1103	286	341	9			

- Molecule 2 is a protein called Fab B6-D9 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	214	Total	C	N	O	S	3	8	0
			1677	1053	281	336	7			

- Molecule 3 is a protein called ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	249	Total	C	N	O	S	25	14	0
			2104	1327	365	395	17			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	301	HIS	-	expression tag	UNP P28907
A	302	HIS	-	expression tag	UNP P28907
A	303	HIS	-	expression tag	UNP P28907
A	304	HIS	-	expression tag	UNP P28907
A	305	HIS	-	expression tag	UNP P28907
A	306	HIS	-	expression tag	UNP P28907
A	307	HIS	-	expression tag	UNP P28907
A	308	HIS	-	expression tag	UNP P28907

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



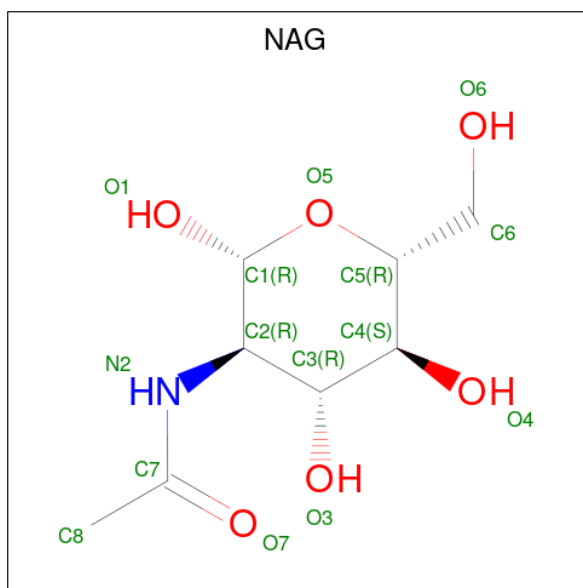
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	H	1	Total	C	O	0	0
			4	2	2		
5	L	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	L	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



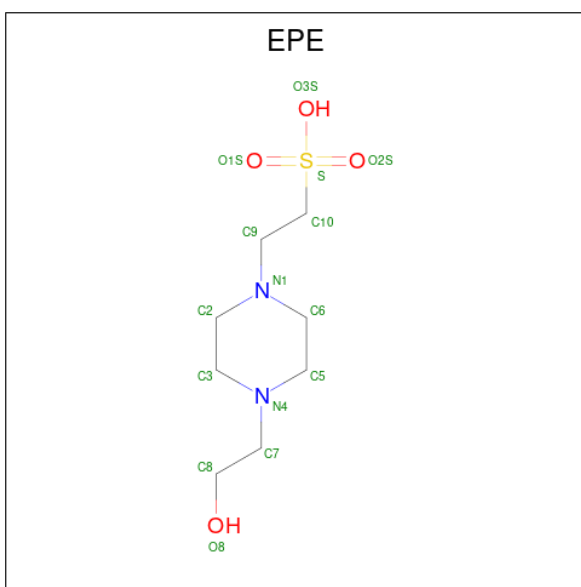
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 9 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

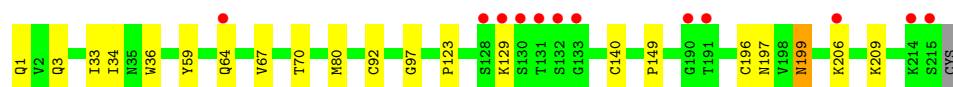
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	H	210	Total	O	0	0
			210	210		
10	L	207	Total	O	0	0
			207	207		
10	A	279	Total	O	0	2
			281	281		

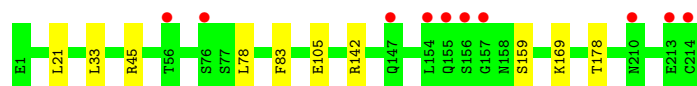
3 Residue-property plots

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.

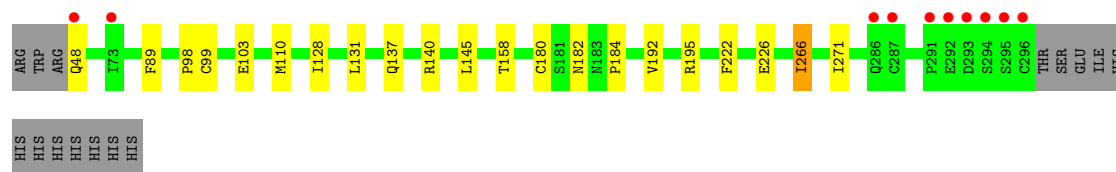
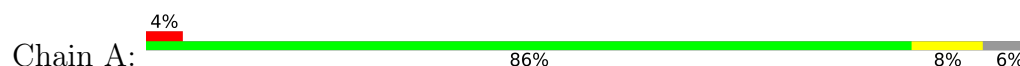
- Molecule 1: Fab B6-D9 heavy chain



- Molecule 2: Fab B6-D9 light chain



- Molecule 3: ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	166.04Å 166.04Å 78.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	71.27 – 1.84 71.27 – 1.84	Depositor EDS
% Data completeness (in resolution range)	77.0 (71.27-1.84) 77.0 (71.27-1.84)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 1.84Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.174 , 0.208 0.182 , 0.212	Depositor DCC
R_{free} test set	4742 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	32.8	Xtriage
Anisotropy	0.018	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 43.5	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	0.96	EDS
Total number of atoms	6331	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.82% 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: NAG, ACT, EPE, EDO, SO4, GOL

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	H	0.64	0/1799	0.86	0/2446
2	L	0.64	0/1738	0.81	0/2362
3	A	0.64	0/2168	0.77	0/2936
All	All	0.64	0/5705	0.81	0/7744

There are no bond length outliers.

There are no bond angle outliers.

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	H	1739	0	1713	9	0
2	L	1677	0	1650	4	0
3	A	2104	0	2052	12	0
4	A	5	0	0	0	0
4	H	5	0	0	0	0
5	A	24	0	36	1	0
5	H	4	0	6	0	0
5	L	8	0	12	0	0
6	A	42	0	39	0	0
7	A	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	A	4	0	3	0	0
9	A	15	0	18	0	0
10	A	281	0	0	2	0
10	H	210	0	0	2	0
10	L	207	0	0	1	0
All	All	6331	0	5537	25	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 2.

All (25) 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)
3:A:180[B]:CYS:SG	3:A:182[B]:ASN:O	1.93	1.25
3:A:180[B]:CYS:SG	3:A:182[B]:ASN:C	2.53	0.86
3:A:48:GLN:NE2	10:A:501:HOH:O	2.14	0.75
1:H:3:GLN:OE1	10:H:401:HOH:O	2.09	0.69
1:H:199[B]:ASN:OD1	1:H:206[B]:LYS:HG3	1.98	0.63
3:A:158[B]:THR:HG22	10:A:719:HOH:O	1.97	0.63
3:A:110:MET:O	3:A:195:ARG:NH2	2.34	0.61
1:H:70[A]:THR:HG21	10:H:472:HOH:O	2.03	0.58
3:A:145:LEU:HD11	3:A:192[B]:VAL:HG12	1.86	0.56
3:A:103:GLU:HG3	5:A:405:EDO:H12	1.94	0.49
3:A:266[A]:ILE:HD12	3:A:271:ILE:O	2.15	0.47
3:A:222:PHE:HA	3:A:226:GLU:HB2	1.98	0.46
2:L:78:LEU:HD23	2:L:83:PHE:CE1	2.52	0.43
1:H:59:TYR:CD1	1:H:67:VAL:HG13	2.54	0.43
2:L:78:LEU:HD23	2:L:83:PHE:CZ	2.54	0.43
3:A:98:PRO:O	3:A:184:PRO:HD3	2.18	0.43
1:H:140[B]:CYS:HB3	1:H:196:CYS:SG	2.59	0.42
1:H:123:PRO:HD3	1:H:209:LYS:HD3	2.02	0.42
2:L:159:SER:HA	2:L:178:THR:O	2.19	0.42
3:A:99:CYS:SG	3:A:180[B]:CYS:CB	3.07	0.42
3:A:137:GLN:O	3:A:140:ARG:NH1	2.53	0.42
1:H:34:ILE:HG23	1:H:92[A]:CYS:SG	2.60	0.42
1:H:36:TRP:CE2	1:H:80[B]:MET:HB3	2.56	0.40
1:H:33:ILE:HD12	1:H:97:GLY:HA2	2.03	0.40
2:L:45:ARG:HD2	10:L:575:HOH:O	2.21	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	H	232/224 (104%)	227 (98%)	5 (2%)	0	100	100
2	L	220/214 (103%)	213 (97%)	7 (3%)	0	100	100
3	A	261/264 (99%)	255 (98%)	5 (2%)	1 (0%)	30	18
All	All	713/702 (102%)	695 (98%)	17 (2%)	1 (0%)	48	38

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	128	ILE

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	H	199/189 (105%)	191 (96%)	8 (4%)	27	10
2	L	193/185 (104%)	188 (97%)	5 (3%)	41	24
3	A	244/245 (100%)	240 (98%)	4 (2%)	58	44
All	All	636/619 (103%)	619 (97%)	17 (3%)	45	22

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	1	GLN
1	H	64[A]	GLN

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Mol	Chain	Res	Type
1	H	64[B]	GLN
1	H	129	LYS
1	H	149	PRO
1	H	197	ASN
1	H	199[A]	ASN
1	H	199[B]	ASN
2	L	21	LEU
2	L	33	LEU
2	L	105	GLU
2	L	142	ARG
2	L	169	LYS
3	A	89	PHE
3	A	131	LEU
3	A	266[A]	ILE
3	A	266[B]	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
2	L	32	ASN
2	L	92	ASN
2	L	137	ASN
2	L	138	ASN
3	A	244	HIS

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

17 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	$\# Z > 2$
7	GOL	A	407	-	5,5,5	0.14	0	5,5,5	0.36	0
5	EDO	A	405	-	3,3,3	0.28	0	2,2,2	0.69	0
5	EDO	A	411	-	3,3,3	0.07	0	2,2,2	0.27	0
4	SO4	A	404	-	4,4,4	0.31	0	6,6,6	0.10	0
6	NAG	A	402	3	14,14,15	0.63	0	17,19,21	1.31	1 (5%)
9	EPE	A	413	-	15,15,15	0.59	1 (6%)	18,20,20	0.83	1 (5%)
5	EDO	A	409	-	3,3,3	0.06	0	2,2,2	0.20	0
5	EDO	H	302	-	3,3,3	0.08	0	2,2,2	0.23	0
6	NAG	A	403	3	14,14,15	0.39	0	17,19,21	0.84	0
5	EDO	L	301	-	3,3,3	0.12	0	2,2,2	0.34	0
8	ACT	A	410	-	3,3,3	0.99	0	3,3,3	0.82	0
5	EDO	L	302	-	3,3,3	0.16	0	2,2,2	0.52	0
4	SO4	H	301	-	4,4,4	0.36	0	6,6,6	0.04	0
5	EDO	A	412	-	3,3,3	0.18	0	2,2,2	0.33	0
5	EDO	A	406	-	3,3,3	0.11	0	2,2,2	0.19	0
5	EDO	A	408	-	3,3,3	0.18	0	2,2,2	0.49	0
6	NAG	A	401	3	14,14,15	0.63	0	17,19,21	1.31	1 (5%)

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
7	GOL	A	407	-	-	0/4/4/4	-
5	EDO	A	405	-	-	1/1/1/1	-
5	EDO	A	411	-	-	0/1/1/1	-
6	NAG	A	402	3	-	2/6/23/26	0/1/1/1
9	EPE	A	413	-	-	1/9/19/19	0/1/1/1
5	EDO	A	409	-	-	0/1/1/1	-
5	EDO	H	302	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	A	403	3	-	1/6/23/26	0/1/1/1
5	EDO	L	301	-	-	0/1/1/1	-
5	EDO	L	302	-	-	0/1/1/1	-
5	EDO	A	412	-	-	0/1/1/1	-
5	EDO	A	406	-	-	1/1/1/1	-
5	EDO	A	408	-	-	1/1/1/1	-
6	NAG	A	401	3	-	3/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	413	EPE	O3S-S	2.21	1.55	1.47

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	402	NAG	C1-O5-C5	4.45	118.22	112.19
6	A	401	NAG	O5-C1-C2	-3.20	106.24	111.29
9	A	413	EPE	O3S-S-C10	-2.34	101.98	105.77

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	H	302	EDO	O1-C1-C2-O2
6	A	402	NAG	C4-C5-C6-O6
6	A	401	NAG	C4-C5-C6-O6
6	A	402	NAG	O5-C5-C6-O6
6	A	401	NAG	O5-C5-C6-O6
5	A	405	EDO	O1-C1-C2-O2
5	A	408	EDO	O1-C1-C2-O2
6	A	401	NAG	C1-C2-N2-C7
6	A	403	NAG	C3-C2-N2-C7
9	A	413	EPE	N4-C7-C8-O8
5	A	406	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	405	EDO	1	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, 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	H	223/224 (99%)	0.14	12 (5%)	32	35	14, 32, 66, 96	16 (7%)
2	L	214/214 (100%)	0.34	10 (4%)	37	40	17, 37, 57, 104	10 (4%)
3	A	249/264 (94%)	0.09	10 (4%)	43	46	13, 30, 58, 99	25 (10%)
All	All	686/702 (97%)	0.19	32 (4%)	37	40	13, 34, 60, 104	51 (7%)

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	295[A]	SER	7.0
2	L	214	CYS	6.1
1	H	130	SER	4.5
3	A	292	GLU	4.3
3	A	296	CYS	4.1
1	H	129	LYS	4.1
1	H	214	LYS	4.1
2	L	154	LEU	4.1
3	A	294	SER	3.4
1	H	132	SER	3.2
1	H	64[A]	GLN	3.1
1	H	215	SER	3.0
2	L	157	GLY	2.8
1	H	133	GLY	2.7
1	H	128	SER	2.7
3	A	48	GLN	2.7
2	L	155	GLN	2.6
3	A	291	PRO	2.4
3	A	286	GLN	2.4
2	L	56	THR	2.3
2	L	213	GLU	2.3
1	H	131	THR	2.3
2	L	76	SER	2.3

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Mol	Chain	Res	Type	RSRZ
2	L	210	ASN	2.2
1	H	191	THR	2.2
2	L	147	GLN	2.2
3	A	293	ASP	2.2
1	H	190	GLY	2.1
3	A	73	ILE	2.1
2	L	156	SER	2.1
1	H	206[A]	LYS	2.0
3	A	287	CYS	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 monosaccharides 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
6	NAG	A	401	14/15	0.72	0.17	55,58,63,64	0
5	EDO	A	406	4/4	0.73	0.28	65,67,68,69	0
6	NAG	A	402	14/15	0.73	0.15	50,70,73,74	0
8	ACT	A	410	4/4	0.74	0.21	47,53,53,57	0
5	EDO	A	409	4/4	0.84	0.18	77,78,78,79	0
5	EDO	A	405	4/4	0.85	0.19	46,46,49,53	0
4	SO4	A	404	5/5	0.85	0.14	54,61,75,75	0
5	EDO	A	408	4/4	0.87	0.20	57,60,60,61	0
5	EDO	A	411	4/4	0.88	0.18	72,72,73,74	0
4	SO4	H	301	5/5	0.88	0.13	89,89,92,97	0
5	EDO	L	301	4/4	0.90	0.19	64,66,66,67	0
7	GOL	A	407	6/6	0.90	0.14	47,48,51,54	0
5	EDO	L	302	4/4	0.90	0.15	44,48,52,54	0
5	EDO	A	412	4/4	0.91	0.14	59,60,63,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	NAG	A	403	14/15	0.91	0.10	39,43,46,46	0
5	EDO	H	302	4/4	0.92	0.14	37,44,51,55	0
9	EPE	A	413	15/15	0.92	0.12	38,40,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.