



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 3, 2025 – 12:39 PM EST

PDB ID : 9NPC / pdb_00009npc
Title : Crystal structure of the inactive conformation of a glycoside hydrolase (CapGH2b) from the GH2 family in the space group I212121 at 2.65 Å
Authors : Martins, M.P.; Spadeto, J.P.M.; Miyamoto, R.Y.; Morais, M.A.B.; Murakami, M.T.
Deposited on : 2025-03-11
Resolution : 2.65 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 ⓘ 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 : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

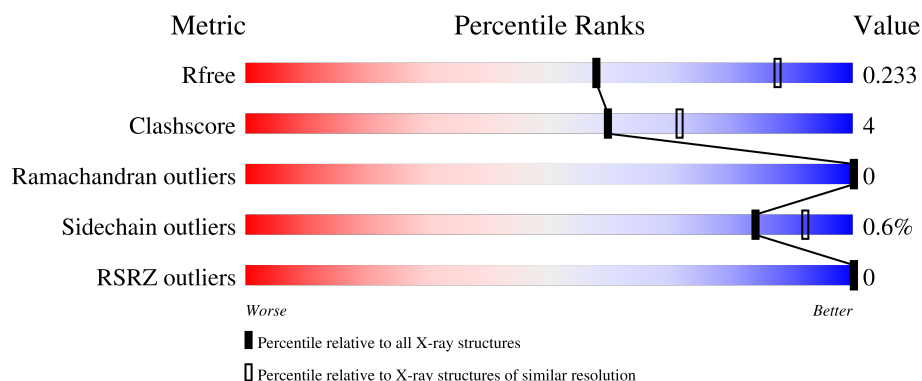
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION




The reported resolution of this entry is 2.65 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	1003 (2.66-2.66)
Clashscore	180529	1063 (2.66-2.66)
Ramachandran outliers	177936	1052 (2.66-2.66)
Sidechain outliers	177891	1052 (2.66-2.66)
RSRZ outliers	164620	1003 (2.66-2.66)

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	798	 80% 12% 8%
1	B	798	 81% 12% 8%
1	C	798	 82% 10% 8%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 18386 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 Glycoside hydrolase family 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	737	Total	C	N	O	S	Se	0	1	0
			5928	3786	1013	1098	8	23			
1	B	737	Total	C	N	O	S	Se	0	1	0
			5928	3786	1013	1098	8	23			
1	C	736	Total	C	N	O	S	Se	0	1	0
			5920	3780	1012	1097	8	23			

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

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

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



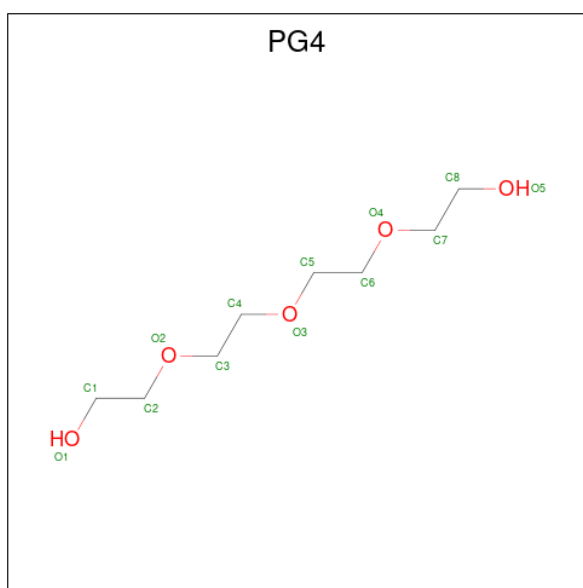
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		
3	A	1	Total	C	O	0	0
			7	4	3		
3	A	1	Total	C	O	0	0
			7	4	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		
3	B	1	Total	C	O	0	0
			7	4	3		
3	B	1	Total	C	O	0	0
			7	4	3		
3	B	1	Total	C	O	0	0
			7	4	3		
3	C	1	Total	C	O	0	0
			7	4	3		

- Molecule 4 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	8	5		
4	B	1	Total	C	O	0	0
			13	8	5		
4	B	1	Total	C	O	0	0
			13	8	5		
4	C	1	Total	C	O	0	0
			13	8	5		
4	C	1	Total	C	O	0	0
			13	8	5		

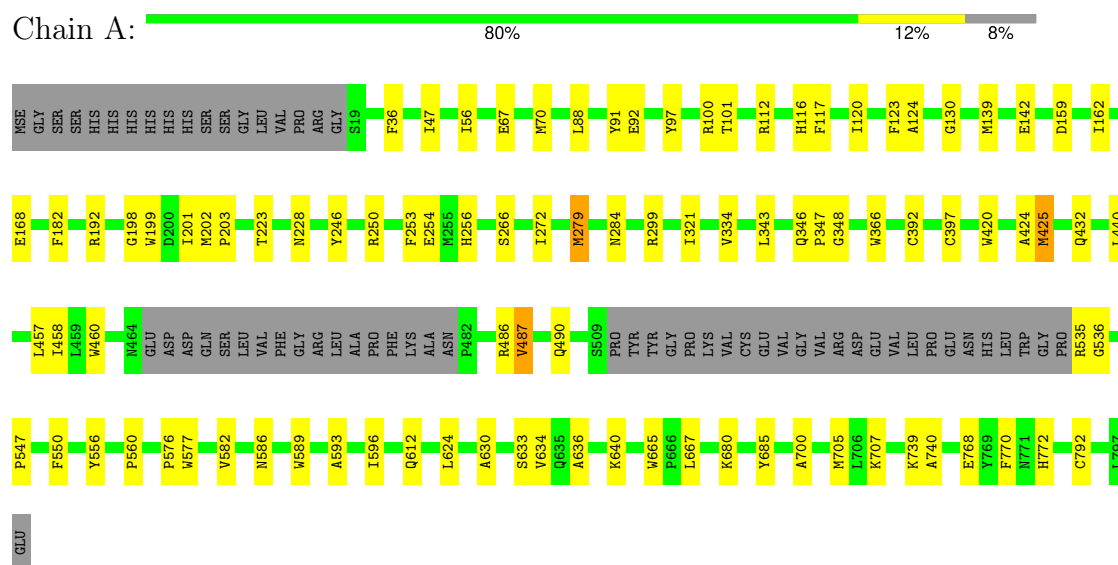
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	157	Total 157	O 157	0	0
5	B	136	Total 136	O 136	0	0
5	C	141	Total 141	O 141	0	0

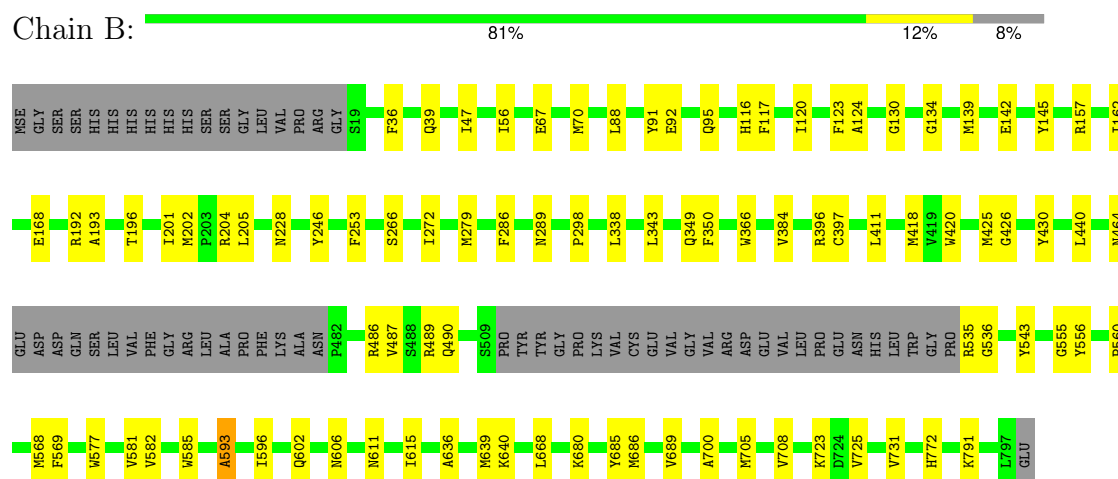
3 Residue-property plots

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.

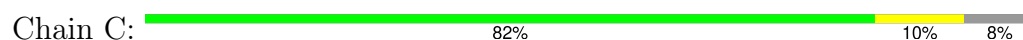
- Molecule 1: Glycoside hydrolase family 2



- Molecule 1: Glycoside hydrolase family 2



- Molecule 1: Glycoside hydrolase family 2



MSE	GLY	SER	HIS	HIS	HIS	HIS	SER	SER	GLY	LEU	VAL	PRO	ARG	GLY	S19	F36	Q39	I56	E67	M70	L88	Y91	E92	Q95	W96	Y97	A104	H116	F117	I120	F123	E142	N156	D159	R163	P203	R204	L205						
T223	N228	Y246	R250	F253	S266	I272	L273	R274	M279	F286	R332	L343	Q346	W366	R396	C397	W420	A424	M425	L440	Y464	GLU	ASP	GLN	SER	LEU	VAL	PHE	GLY	ARG	LEU	ALA	PRO	PHE	LYS	ALA	ASN	P482	R486	V487				
S488	R489	Q490	R494	L506	F507	S508	S509	PRO	TYR	TYR	GLY	PRO	LYS	VAL	CYS	GLU	VAL	VAL	PRO	GLU	ASN	HIS	LEU	TRP	GLY	PRO	R535	G536	Y543	G555	Y556	P560	W588	W585	A593	W594	R595	I596	Y597	N606	Q612	V613		
V620	V634	Q635	A636	M639	I661	W665	P666	L667	I672	K680	Y685	M686	A700	M705	M757	Y762	E768	Y769	F770	C792	E796	LEU	GLU																					

4 Data and refinement statistics

Property	Value	Source
Space group	I 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	191.85Å 192.00Å 191.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.25 – 2.65 45.25 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.8 (45.25-2.65) 99.6 (45.25-2.65)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.27 (at 2.65Å)	Xtriage
Refinement program	PHENIX (1.21.2_5419: ???)	Depositor
R, R_{free}	0.203 , 0.233 0.203 , 0.233	Depositor DCC
R_{free} test set	5117 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	59.7	Xtriage
Anisotropy	0.255	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 34.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.011 for -h,-l,-k 0.009 for k,h,-l 0.008 for -l,-k,-h 0.448 for l,-h,-k 0.448 for -k,-l,h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	18386	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.51% 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: PG4, PO4, PEG

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	1/6060 (0.0%)	0.54	1/8190 (0.0%)
1	B	0.30	0/6060	0.49	0/8190
1	C	0.35	0/6052	0.55	1/8179 (0.0%)
All	All	0.34	1/18172 (0.0%)	0.53	2/24559 (0.0%)

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
1	B	0	2
1	C	0	3
All	All	0	7

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	633	SER	C-N	-5.21	1.27	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	487	VAL	N-CA-CB	-5.21	105.15	110.62
1	C	672	ILE	N-CA-C	-5.06	107.82	112.83

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	112	ARG	Sidechain
1	A	593	ALA	Peptide
1	B	489	ARG	Sidechain
1	B	593	ALA	Peptide
1	C	332	ARG	Sidechain

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	5928	0	5749	53	0
1	B	5928	0	5749	51	0
1	C	5920	0	5738	47	0
2	A	25	0	0	0	0
2	B	20	0	0	0	0
2	C	10	0	0	0	0
3	A	28	0	40	1	0
3	B	21	0	30	1	0
3	C	7	0	10	0	0
4	A	13	0	18	0	0
4	B	26	0	36	3	0
4	C	26	0	36	1	0
5	A	157	0	0	2	0
5	B	136	0	0	0	0
5	C	141	0	0	0	0
All	All	18386	0	17406	150	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 4.

The worst 5 of 150 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:568:MSE:HG2	1:C:666:PRO:HB2	1.79	0.64
1:A:346:GLN:HB3	1:A:347:PRO:HD2	1.82	0.61
1:B:366:TRP:HB3	1:B:397:CYS:HA	1.83	0.61
1:B:396:ARG:HG3	1:B:420:TRP:CG	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:366:TRP:HB3	1:C:397:CYS:HA	1.83	0.60

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	732/798 (92%)	707 (97%)	25 (3%)	0	100	100
1	B	732/798 (92%)	705 (96%)	27 (4%)	0	100	100
1	C	731/798 (92%)	709 (97%)	22 (3%)	0	100	100
All	All	2195/2394 (92%)	2121 (97%)	74 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	638/666 (96%)	634 (99%)	4 (1%)	84	92
1	B	638/666 (96%)	634 (99%)	4 (1%)	84	92
1	C	637/666 (96%)	634 (100%)	3 (0%)	86	94
All	All	1913/1998 (96%)	1902 (99%)	11 (1%)	84	92

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	708	VAL
1	C	205	LEU
1	C	792	CYS
1	C	762	TYR
1	B	205	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	B	421	GLN
1	B	557	HIS
1	C	421	GLN
1	B	549	GLN
1	B	602	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

24 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	PO4	A	804	-	4,4,4	1.62	1 (25%)	6,6,6	0.47	0
4	PG4	C	805	-	12,12,12	0.13	0	11,11,11	0.12	0
3	PEG	C	803	-	6,6,6	0.10	0	5,5,5	0.09	0
3	PEG	A	809	-	6,6,6	0.10	0	5,5,5	0.10	0
3	PEG	A	807	-	6,6,6	0.10	0	5,5,5	0.09	0
4	PG4	B	808	-	12,12,12	0.13	0	11,11,11	0.12	0
3	PEG	A	808	-	6,6,6	0.12	0	5,5,5	0.07	0
2	PO4	B	803	-	4,4,4	1.58	1 (25%)	6,6,6	0.48	0
2	PO4	A	801	-	4,4,4	1.60	1 (25%)	6,6,6	0.45	0
2	PO4	B	801	-	4,4,4	1.61	1 (25%)	6,6,6	0.47	0
2	PO4	A	803	-	4,4,4	1.58	1 (25%)	6,6,6	0.50	0
2	PO4	C	802	-	4,4,4	1.58	1 (25%)	6,6,6	0.51	0
3	PEG	B	806	-	6,6,6	0.11	0	5,5,5	0.08	0
2	PO4	C	801	-	4,4,4	1.58	1 (25%)	6,6,6	0.44	0
3	PEG	B	807	-	6,6,6	0.10	0	5,5,5	0.09	0
4	PG4	B	809	-	12,12,12	0.12	0	11,11,11	0.14	0
3	PEG	B	805	-	6,6,6	0.11	0	5,5,5	0.10	0
4	PG4	A	810	-	12,12,12	0.29	0	11,11,11	0.16	0
2	PO4	A	805	-	4,4,4	0.74	0	6,6,6	0.46	0
3	PEG	A	806	-	6,6,6	0.11	0	5,5,5	0.08	0
2	PO4	B	802	-	4,4,4	1.59	1 (25%)	6,6,6	0.47	0
2	PO4	B	804	-	4,4,4	0.79	0	6,6,6	0.43	0
4	PG4	C	804	-	12,12,12	0.12	0	11,11,11	0.14	0
2	PO4	A	802	-	4,4,4	1.59	1 (25%)	6,6,6	0.47	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
4	PG4	A	810	-	-	5/10/10/10	-
4	PG4	C	805	-	-	3/10/10/10	-
4	PG4	C	804	-	-	7/10/10/10	-
3	PEG	C	803	-	-	0/4/4/4	-
4	PG4	B	808	-	-	3/10/10/10	-
3	PEG	A	809	-	-	1/4/4/4	-
3	PEG	A	806	-	-	0/4/4/4	-
3	PEG	A	807	-	-	1/4/4/4	-
3	PEG	A	808	-	-	1/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PEG	B	806	-	-	2/4/4/4	-
3	PEG	B	807	-	-	1/4/4/4	-
4	PG4	B	809	-	-	6/10/10/10	-
3	PEG	B	805	-	-	1/4/4/4	-

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	804	PO4	P-O1	2.80	1.57	1.50
2	A	801	PO4	P-O1	2.80	1.57	1.50
2	B	802	PO4	P-O1	2.79	1.57	1.50
2	C	801	PO4	P-O1	2.78	1.57	1.50
2	B	801	PO4	P-O1	2.77	1.57	1.50

There are no bond angle outliers.

There are no chirality outliers.

5 of 31 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	810	PG4	O2-C3-C4-O3
4	C	805	PG4	O3-C5-C6-O4
4	B	809	PG4	C4-C3-O2-C2
4	C	804	PG4	C6-C5-O3-C4
3	B	807	PEG	O2-C3-C4-O4

There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	808	PG4	1	0
3	A	808	PEG	1	0
3	B	806	PEG	1	0
4	B	809	PG4	2	0
4	C	804	PG4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	715/798 (89%)	-1.70	0 100 100	38, 60, 93, 110	0
1	B	715/798 (89%)	-1.70	0 100 100	40, 60, 92, 110	0
1	C	714/798 (89%)	-1.72	0 100 100	42, 59, 91, 109	0
All	All	2144/2394 (89%)	-1.71	0 100 100	38, 60, 92, 110	0

There are no RSRZ outliers to report.

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	PO4	A	805	5/5	0.97	0.06	85,93,97,126	0
2	PO4	B	804	5/5	0.97	0.07	73,77,106,118	0
3	PEG	A	809	7/7	0.97	0.06	71,74,79,80	0
2	PO4	B	801	5/5	0.98	0.04	93,94,109,133	0
2	PO4	A	804	5/5	0.98	0.07	55,67,84,89	5

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	PEG	A	806	7/7	0.98	0.05	79,85,89,93	0
3	PEG	A	808	7/7	0.98	0.06	58,70,80,83	0
2	PO4	A	803	5/5	0.98	0.04	103,109,120,131	0
3	PEG	B	806	7/7	0.98	0.05	75,77,83,92	0
3	PEG	C	803	7/7	0.98	0.05	73,77,83,90	0
4	PG4	A	810	13/13	0.98	0.06	63,74,86,86	0
4	PG4	B	808	13/13	0.98	0.05	61,81,94,96	0
4	PG4	B	809	13/13	0.98	0.05	61,76,87,89	0
4	PG4	C	805	13/13	0.98	0.06	69,78,88,90	0
2	PO4	C	802	5/5	0.99	0.04	72,73,76,95	0
3	PEG	B	807	7/7	0.99	0.07	58,67,73,75	0
2	PO4	B	802	5/5	0.99	0.03	51,53,56,64	0
3	PEG	A	807	7/7	0.99	0.04	69,75,82,82	0
2	PO4	B	803	5/5	0.99	0.03	73,78,83,96	0
2	PO4	A	802	5/5	0.99	0.04	70,72,79,102	0
4	PG4	C	804	13/13	0.99	0.03	63,72,86,90	0
3	PEG	B	805	7/7	0.99	0.04	72,74,78,80	0
2	PO4	A	801	5/5	1.00	0.02	54,54,55,60	0
2	PO4	C	801	5/5	1.00	0.02	52,53,59,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.