



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 30, 2026 – 10:23 AM UTC

PDB ID : 9NPF / pdb_00009npf
Title : Crystal structure of the inactive conformation of a glycoside hydrolase (CapGH2b) from the GH2 family in the space group P1 at 2.15 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 : 2.15 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	:	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

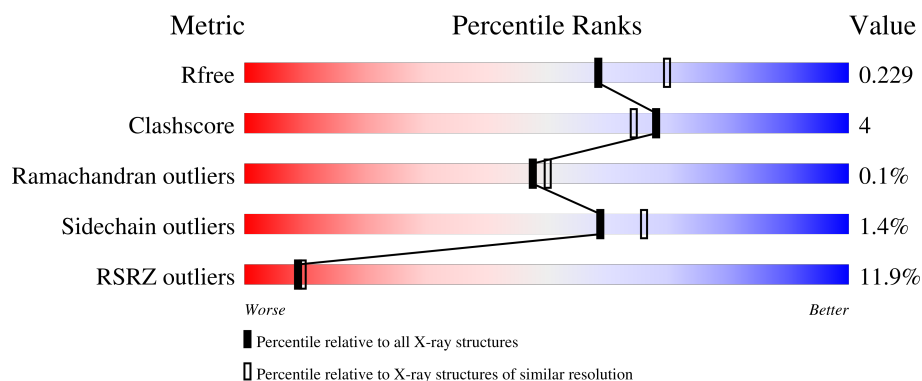
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	<div> <div>7%</div> <div> <div></div> <div>83%</div> <div>9%</div> <div>8%</div> </div> </div>
1	B	798	<div> <div>6%</div> <div> <div></div> <div>83%</div> <div>9%</div> <div>8%</div> </div> </div>
1	C	798	<div> <div>16%</div> <div> <div></div> <div>83%</div> <div>8%</div> <div>8%</div> </div> </div>
1	D	798	<div> <div>5%</div> <div> <div></div> <div>84%</div> <div>7%</div> <div>8%</div> </div> </div>
1	E	798	<div> <div>8%</div> <div> <div></div> <div>84%</div> <div>8%</div> <div>8%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	798	<div><div></div><div>22%</div><div></div><div>78%</div><div></div><div>12%</div><div></div><div>9%</div></div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 37135 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	736	Total	C	N	O	S	Se	0	0	0
			5917	3782	1011	1094	8	22			
1	B	736	Total	C	N	O	S	Se	0	0	0
			5917	3786	1008	1093	8	22			
1	C	731	Total	C	N	O	S	Se	0	0	0
			5879	3755	1005	1089	8	22			
1	D	733	Total	C	N	O	S	Se	0	0	0
			5891	3766	1007	1089	8	21			
1	E	733	Total	C	N	O	S	Se	0	0	0
			5898	3773	1007	1088	8	22			
1	F	728	Total	C	N	O	S	Se	0	0	0
			5859	3742	1001	1086	8	22			

- 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	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		
2	C	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



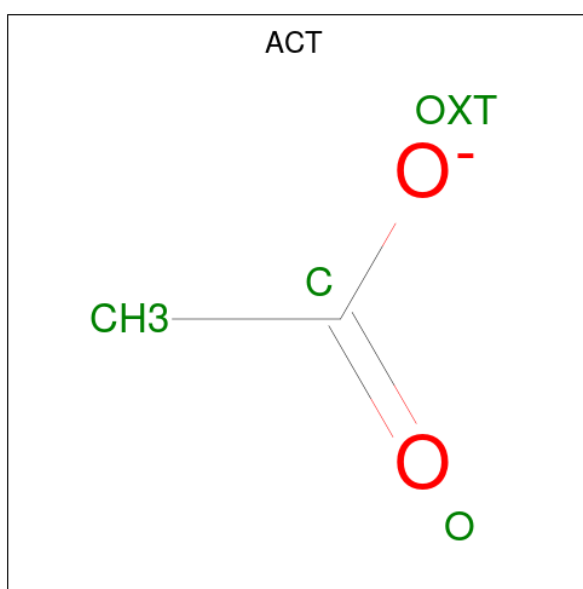
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	E	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	F	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 5 is water.

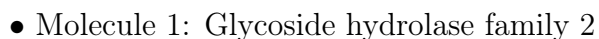
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	357	Total	O	0	0
			357	357		
5	B	331	Total	O	0	0
			331	331		
5	C	194	Total	O	0	0
			194	194		

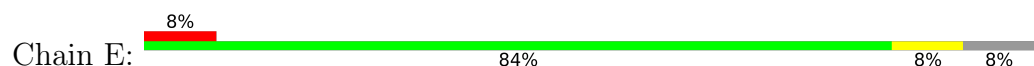
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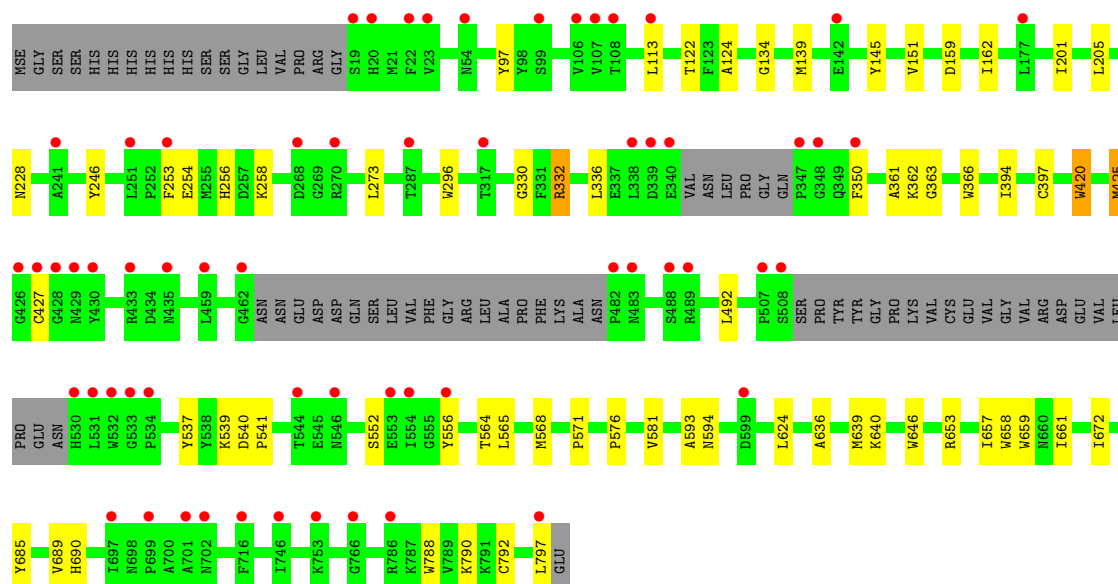
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	305	Total 305	O 305	0	0
5	E	288	Total 288	O 288	0	0
5	F	113	Total 113	O 113	0	0

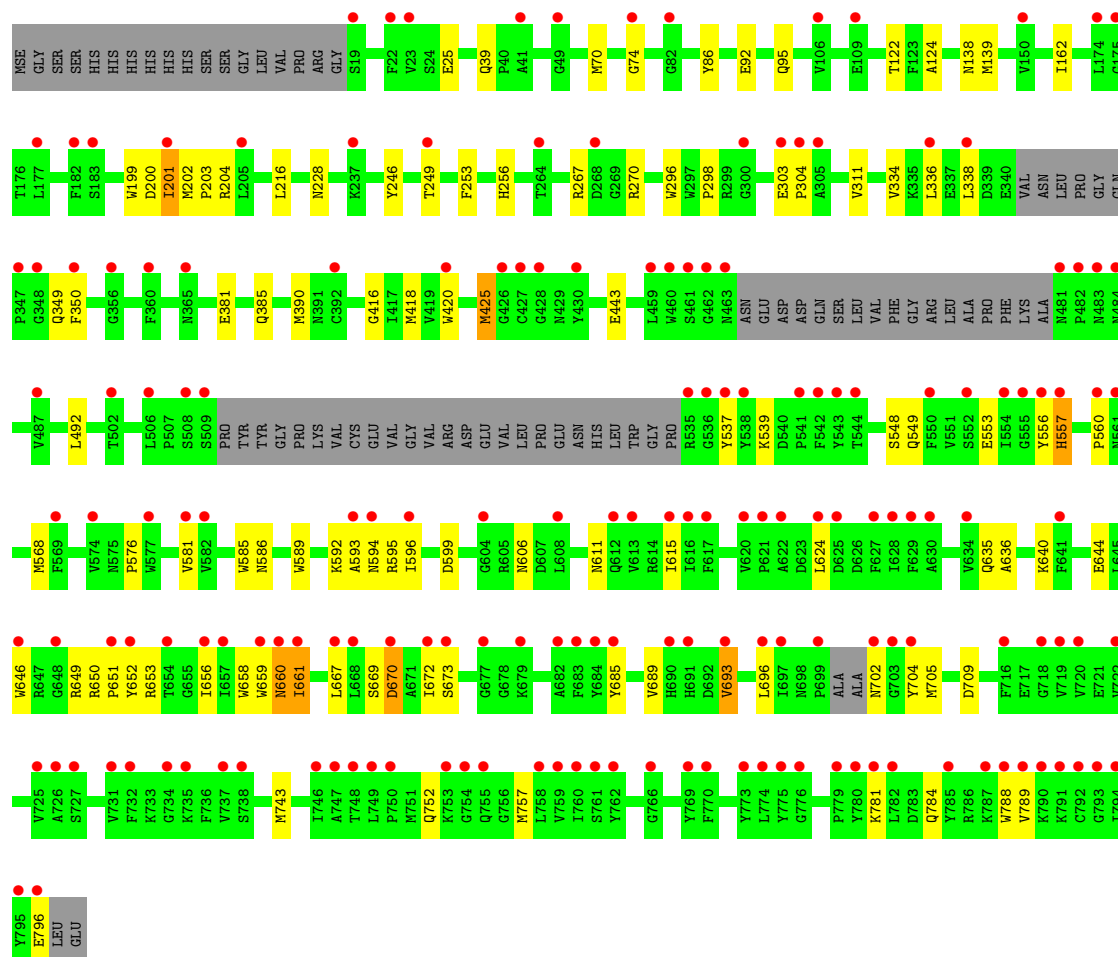
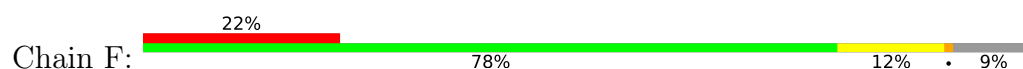
- Molecule 1: Glycoside hydrolase family 2







• Molecule 1: Glycoside hydrolase family 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	121.70Å 123.57Å 133.24Å 89.44° 117.29° 103.20°	Depositor
Resolution (Å)	49.00 – 2.15 49.00 – 2.15	Depositor EDS
% Data completeness (in resolution range)	90.1 (49.00-2.15) 90.1 (49.00-2.15)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.30 (at 2.16Å)	Xtriage
Refinement program	PHENIX (1.21.2_5419: ???)	Depositor
R, R_{free}	0.207 , 0.228 0.208 , 0.229	Depositor DCC
R_{free} test set	16398 reflections (4.52%)	wwPDB-VP
Wilson B-factor (Å ²)	47.1	Xtriage
Anisotropy	0.447	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 51.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	37135	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.57% 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: PO4, ACT, 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	A	0.28	0/6050	0.47	2/8176 (0.0%)
1	B	0.25	0/6051	0.43	0/8180
1	C	0.31	5/6008 (0.1%)	0.43	0/8117
1	D	0.26	0/6025	0.45	0/8148
1	E	0.26	0/6032	0.47	2/8151 (0.0%)
1	F	0.30	3/5988 (0.1%)	0.47	4/8088 (0.0%)
All	All	0.28	8/36154 (0.0%)	0.45	8/48860 (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	C	0	1
1	D	0	1
All	All	0	4

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	743	MSE	C-N	9.12	1.45	1.33
1	F	70	MSE	C-N	7.26	1.43	1.33
1	C	757	MSE	C-N	7.14	1.43	1.33
1	C	639	MSE	C-N	-6.80	1.25	1.33
1	F	425	MSE	C-N	-5.59	1.26	1.33

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	23	VAL	N-CA-C	-8.76	104.76	112.12
1	E	425	MSE	CA-C-N	8.08	127.15	121.65
1	E	425	MSE	C-N-CA	8.08	127.15	121.65
1	F	661	ILE	N-CA-C	-7.17	104.40	113.22
1	F	670	ASP	N-CA-C	-5.38	106.59	112.72

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	217	ARG	Sidechain
1	A	763	ARG	Sidechain
1	C	593	ALA	Peptide
1	D	593	ALA	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	5917	0	5733	41	0
1	B	5917	0	5741	43	0
1	C	5879	0	5699	39	0
1	D	5891	0	5713	35	0
1	E	5898	0	5718	36	0
1	F	5859	0	5674	64	0
2	A	10	0	0	0	0
2	B	10	0	0	0	0
2	C	15	0	0	0	0
2	D	10	0	0	0	0
2	E	15	0	0	0	0
2	F	10	0	0	0	0
3	A	30	0	40	1	0
3	B	18	0	24	0	0
3	C	6	0	8	0	0
3	D	24	0	32	2	0
3	E	24	0	32	1	0
3	F	6	0	8	0	0
4	A	4	0	3	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	4	0	3	0	0
5	A	357	0	0	0	0
5	B	331	0	0	0	0
5	C	194	0	0	0	0
5	D	305	0	0	0	0
5	E	288	0	0	0	0
5	F	113	0	0	0	0
All	All	37135	0	34428	251	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 251 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:F:425:MSE:HE1	1:F:492:LEU:HD11	1.79	0.63
1:B:593:ALA:N	1:B:594:ASN:HA	2.12	0.63
1:B:425:MSE:HE1	1:B:492:LEU:HD11	1.80	0.62
1:F:640:LYS:HG3	1:F:689:VAL:HG21	1.80	0.62
1:F:649:ARG:HE	1:F:653:ARG:HE	1.48	0.62

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	728/798 (91%)	708 (97%)	20 (3%)	0	100	100
1	B	730/798 (92%)	712 (98%)	18 (2%)	0	100	100
1	C	723/798 (91%)	701 (97%)	22 (3%)	0	100	100
1	D	727/798 (91%)	709 (98%)	17 (2%)	1 (0%)	48	50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	725/798 (91%)	706 (97%)	18 (2%)	1 (0%)	48	50
1	F	718/798 (90%)	691 (96%)	26 (4%)	1 (0%)	48	50
All	All	4351/4788 (91%)	4227 (97%)	121 (3%)	3 (0%)	48	50

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	427	CYS
1	F	660	ASN
1	E	427	CYS

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	635/666 (95%)	628 (99%)	7 (1%)	65	72
1	B	635/666 (95%)	625 (98%)	10 (2%)	55	61
1	C	632/666 (95%)	626 (99%)	6 (1%)	70	77
1	D	632/666 (95%)	620 (98%)	12 (2%)	50	56
1	E	633/666 (95%)	627 (99%)	6 (1%)	70	77
1	F	631/666 (95%)	618 (98%)	13 (2%)	47	52
All	All	3798/3996 (95%)	3744 (99%)	54 (1%)	59	66

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	420	TRP
1	E	205	LEU
1	F	656	ILE
1	D	484	ASN
1	D	670	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such

sidechains are listed below:

Mol	Chain	Res	Type
1	C	464	ASN
1	D	575	ASN
1	F	681	GLN
1	E	435	ASN
1	B	575	ASN

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](#)

34 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	$\# Z > 2$
3	GOL	B	803	-	5,5,5	0.36	0	5,5,5	0.61	0
3	GOL	A	806	-	5,5,5	0.37	0	5,5,5	0.52	0
2	PO4	A	801	-	4,4,4	1.52	1 (25%)	6,6,6	0.49	0
2	PO4	D	802	-	4,4,4	0.77	0	6,6,6	0.46	0
3	GOL	A	805	-	5,5,5	0.35	0	5,5,5	0.48	0
3	GOL	C	804	-	5,5,5	0.31	0	5,5,5	0.39	0
3	GOL	F	803	-	5,5,5	0.32	0	5,5,5	0.42	0
4	ACT	A	808	-	3,3,3	1.16	0	3,3,3	1.21	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PO4	F	801	-	4,4,4	1.56	1 (25%)	6,6,6	0.51	0
2	PO4	F	802	-	4,4,4	1.58	1 (25%)	6,6,6	0.52	0
3	GOL	D	804	-	5,5,5	0.36	0	5,5,5	0.56	0
3	GOL	E	804	-	5,5,5	0.34	0	5,5,5	0.51	0
3	GOL	E	807	-	5,5,5	0.39	0	5,5,5	0.57	0
2	PO4	E	802	-	4,4,4	0.78	0	6,6,6	0.46	0
3	GOL	B	805	-	5,5,5	0.34	0	5,5,5	0.51	0
3	GOL	D	803	-	5,5,5	0.35	0	5,5,5	0.43	0
3	GOL	E	805	-	5,5,5	0.33	0	5,5,5	0.42	0
2	PO4	C	801	-	4,4,4	1.59	1 (25%)	6,6,6	0.55	0
3	GOL	D	806	-	5,5,5	0.34	0	5,5,5	0.44	0
3	GOL	E	806	-	5,5,5	0.34	0	5,5,5	0.42	0
2	PO4	B	802	-	4,4,4	0.79	0	6,6,6	0.45	0
3	GOL	A	807	-	5,5,5	0.33	0	5,5,5	0.46	0
3	GOL	B	804	-	5,5,5	0.34	0	5,5,5	0.35	0
2	PO4	C	802	-	4,4,4	0.85	0	6,6,6	0.43	0
2	PO4	D	801	-	4,4,4	1.49	1 (25%)	6,6,6	0.55	0
3	GOL	D	805	-	5,5,5	0.32	0	5,5,5	0.41	0
3	GOL	A	803	-	5,5,5	0.34	0	5,5,5	0.43	0
2	PO4	C	803	-	4,4,4	0.80	0	6,6,6	0.49	0
3	GOL	A	804	-	5,5,5	0.34	0	5,5,5	0.47	0
2	PO4	B	801	-	4,4,4	1.55	1 (25%)	6,6,6	0.50	0
4	ACT	B	806	-	3,3,3	1.16	0	3,3,3	1.18	0
2	PO4	E	803	-	4,4,4	0.79	0	6,6,6	0.45	0
2	PO4	E	801	-	4,4,4	1.54	1 (25%)	6,6,6	0.54	0
2	PO4	A	802	-	4,4,4	0.80	0	6,6,6	0.44	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	GOL	B	803	-	-	0/4/4/4	-
3	GOL	D	805	-	-	0/4/4/4	-
3	GOL	D	806	-	-	0/4/4/4	-
3	GOL	E	806	-	-	0/4/4/4	-
3	GOL	A	803	-	-	1/4/4/4	-
3	GOL	D	804	-	-	0/4/4/4	-
3	GOL	E	804	-	-	3/4/4/4	-
3	GOL	E	807	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	806	-	-	0/4/4/4	-
3	GOL	A	804	-	-	0/4/4/4	-
3	GOL	A	807	-	-	2/4/4/4	-
3	GOL	A	805	-	-	2/4/4/4	-
3	GOL	B	804	-	-	0/4/4/4	-
3	GOL	B	805	-	-	3/4/4/4	-
3	GOL	D	803	-	-	0/4/4/4	-
3	GOL	C	804	-	-	0/4/4/4	-
3	GOL	F	803	-	-	1/4/4/4	-
3	GOL	E	805	-	-	0/4/4/4	-

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	802	PO4	P-O1	2.81	1.57	1.50
2	C	801	PO4	P-O1	2.78	1.57	1.50
2	F	801	PO4	P-O1	2.71	1.56	1.50
2	A	801	PO4	P-O1	2.69	1.56	1.50
2	B	801	PO4	P-O1	2.68	1.56	1.50

There are no bond angle outliers.

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	807	GOL	O1-C1-C2-O2
3	A	807	GOL	O1-C1-C2-C3
3	E	804	GOL	C1-C2-C3-O3
3	A	805	GOL	C1-C2-C3-O3
3	B	805	GOL	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	807	GOL	1	0
3	D	803	GOL	1	0
3	D	806	GOL	1	0
3	A	804	GOL	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 [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	714/798 (89%)	0.62	55 (7%) 19 22	36, 53, 75, 90	0
1	B	714/798 (89%)	0.57	47 (6%) 24 27	35, 53, 83, 98	0
1	C	709/798 (88%)	1.06	127 (17%) 3 4	39, 65, 117, 147	0
1	D	712/798 (89%)	0.60	43 (6%) 27 31	35, 54, 85, 100	0
1	E	711/798 (89%)	0.76	61 (8%) 16 17	37, 57, 80, 89	0
1	F	706/798 (88%)	1.34	174 (24%) 2 2	41, 76, 138, 172	0
All	All	4266/4788 (89%)	0.83	507 (11%) 9 9	35, 58, 107, 172	0

The worst 5 of 507 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	347	PRO	5.7
1	F	726	ALA	5.5
1	F	651	PRO	5.3
1	B	427	CYS	5.2
1	C	343	LEU	5.1

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 ⓘ

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	E	803	5/5	0.49	0.20	112,135,145,296	0
3	GOL	B	804	6/6	0.74	0.17	57,64,66,68	0
4	ACT	B	806	4/4	0.76	0.23	58,62,67,71	0
2	PO4	C	803	5/5	0.77	0.20	53,56,56,68	5
3	GOL	D	806	6/6	0.79	0.17	59,68,70,74	0
3	GOL	D	805	6/6	0.79	0.17	60,71,75,76	0
4	ACT	A	808	4/4	0.83	0.20	48,52,55,62	0
3	GOL	E	807	6/6	0.83	0.16	49,55,59,61	0
3	GOL	A	807	6/6	0.84	0.17	64,66,68,72	0
2	PO4	B	802	5/5	0.86	0.18	58,61,66,66	5
2	PO4	C	802	5/5	0.86	0.18	48,52,54,61	5
3	GOL	E	806	6/6	0.86	0.13	51,55,57,62	0
3	GOL	F	803	6/6	0.87	0.14	62,65,67,69	0
2	PO4	F	802	5/5	0.87	0.17	59,61,64,71	5
3	GOL	A	803	6/6	0.87	0.12	46,57,63,65	0
3	GOL	B	805	6/6	0.89	0.13	56,58,63,68	0
3	GOL	C	804	6/6	0.89	0.12	56,58,62,64	0
3	GOL	D	803	6/6	0.89	0.12	59,60,64,64	0
3	GOL	B	803	6/6	0.89	0.14	39,45,48,53	0
2	PO4	D	802	5/5	0.89	0.24	77,80,103,262	0
3	GOL	A	806	6/6	0.90	0.13	53,55,56,61	0
3	GOL	D	804	6/6	0.90	0.13	42,47,49,50	0
2	PO4	A	802	5/5	0.90	0.17	60,60,65,71	5
2	PO4	E	802	5/5	0.91	0.12	65,67,70,72	5
3	GOL	A	804	6/6	0.92	0.14	47,51,56,60	0
3	GOL	E	805	6/6	0.93	0.11	53,57,62,73	0
2	PO4	C	801	5/5	0.93	0.14	52,56,58,65	0
3	GOL	A	805	6/6	0.93	0.11	51,52,54,57	0
2	PO4	E	801	5/5	0.94	0.08	61,62,64,65	0
3	GOL	E	804	6/6	0.94	0.10	52,59,60,60	0
2	PO4	F	801	5/5	0.94	0.10	64,64,65,66	0
2	PO4	A	801	5/5	0.94	0.12	58,58,60,61	0
2	PO4	B	801	5/5	0.97	0.10	49,53,58,59	0
2	PO4	D	801	5/5	0.97	0.09	53,54,57,60	0

6.5 Other polymers [i](#)

There are no such residues in this entry.