



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 09:13 PM GMT

PDB ID : 2XAD
Title : Crystal structure of deacetylase-teicoplanincomplex in biosynthesis pathway of teicoplanin
Authors : Chan, H.C.; Huang, Y.T.; Lyu, S.Y.; Huang, C.J.; Li, Y.S.; Liu, Y.C.; Chou, C.C.; Tsai, M.D.; Li, T.L.
Deposited on : 2010-03-31
Resolution : 1.70 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

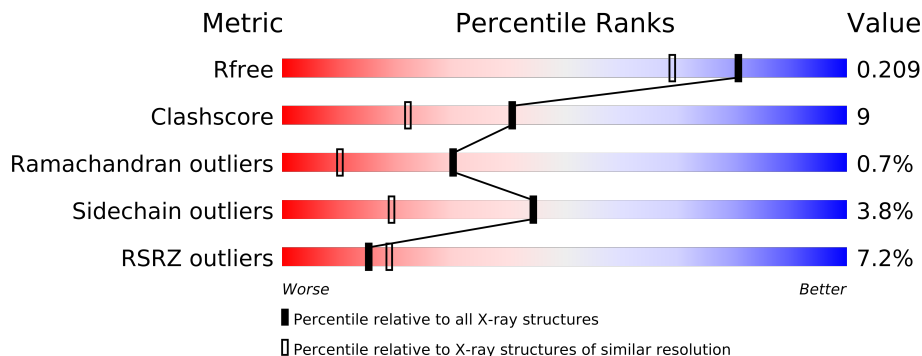
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.70 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}	66092	2456 (1.70-1.70)
Clashscore	79885	2929 (1.70-1.70)
Ramachandran outliers	78287	2878 (1.70-1.70)
Sidechain outliers	78261	2878 (1.70-1.70)
RSRZ outliers	66119	2456 (1.70-1.70)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	273	
1	B	273	
1	C	273	
1	D	273	
2	E	7	
2	F	7	
2	G	7	
2	H	7	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	BMA	E	708	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Geometry	Electron density
3	BMA	F	708	-	X
3	BMA	G	708	-	X
3	BMA	H	708	-	X
4	NAG	E	709	-	X
4	NAG	F	709	-	X
4	NAG	H	709	-	X
6	T55	H	711	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 9379 atoms, of which 0 are hydrogen and 0 are deuterium.

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 N-ACYL GLM PEUDO-TEICOPLANIN DEACETYLASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	259	Total	C	N	O	S	Se	0	0	0
			2018	1263	366	385	1	3			
1	B	258	Total	C	N	O	S	Se	0	0	1
			2006	1255	365	382	1	3			
1	C	258	Total	C	N	O	S	Se	0	0	1
			2008	1257	365	382	1	3			
1	D	257	Total	C	N	O	S	Se	0	0	0
			2006	1255	364	383	1	3			

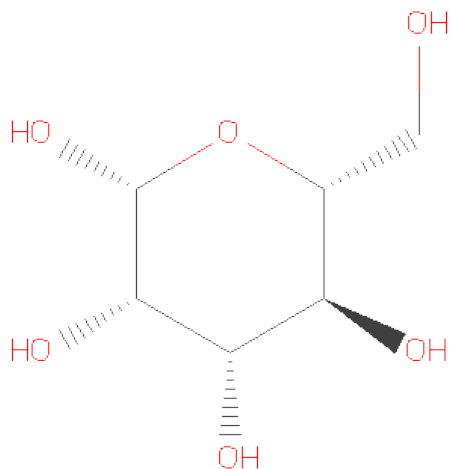
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	164	ASN	HIS	ENGINEERED MUTATION	UNP Q6ZZJ1
B	164	ASN	HIS	ENGINEERED MUTATION	UNP Q6ZZJ1
C	164	ASN	HIS	ENGINEERED MUTATION	UNP Q6ZZJ1
D	164	ASN	HIS	ENGINEERED MUTATION	UNP Q6ZZJ1

- Molecule 2 is a protein called TEICOPLANIN.

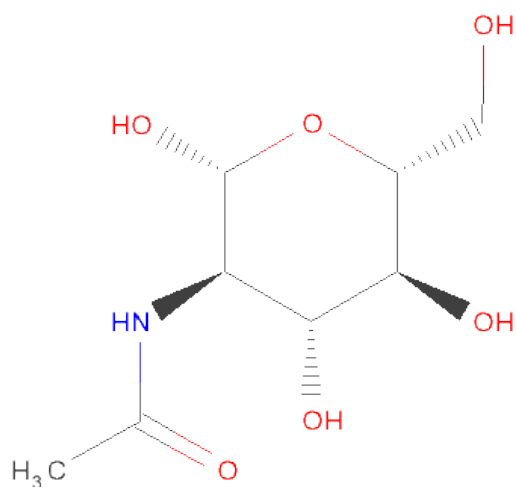
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	7	Total	C	Cl	N	O	0	0	0
			84	58	2	7	17			
2	F	7	Total	C	Cl	N	O	0	0	0
			85	58	2	7	18			
2	G	7	Total	C	Cl	N	O	0	0	0
			85	58	2	7	18			
2	H	7	Total	C	Cl	N	O	0	0	0
			85	58	2	7	18			

- Molecule 3 is SUGAR (BETA-D-MANNOSE) (three-letter code: BMA) (formula: C₆H₁₂O₆).



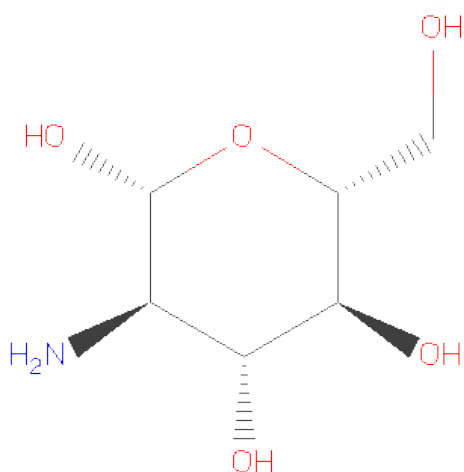
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	E	1	Total	C	O	0	0
			11	6	5		
3	F	1	Total	C	O	0	0
			11	6	5		
3	G	1	Total	C	O	0	0
			11	6	5		
3	H	1	Total	C	O	0	0
			11	6	5		

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



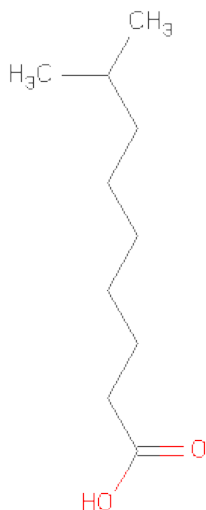
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	E	1	Total	C	N	O	0	0
			14	8	1	5		
4	F	1	Total	C	N	O	0	0
			14	8	1	5		
4	G	1	Total	C	N	O	0	0
			14	8	1	5		
4	H	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is SUGAR (D-GLUCOSAMINE) (three-letter code: GCS) (formula: $C_6H_{13}NO_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	E	1	Total	C	N	O	0	0
			11	6	1	4		
5	F	1	Total	C	N	O	0	0
			11	6	1	4		
5	G	1	Total	C	N	O	0	0
			11	6	1	4		
5	H	1	Total	C	N	O	0	0
			11	6	1	4		

- Molecule 6 is 8-METHYLNONANOIC ACID (three-letter code: T55) (formula: $C_{10}H_{20}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	E	1	Total	C	O	0	0
			11	10	1		
6	F	1	Total	C	O	0	0
			11	10	1		
6	G	1	Total	C	O	0	0
			11	10	1		
6	H	1	Total	C	O	0	0
			11	10	1		

- Molecule 7 is water.

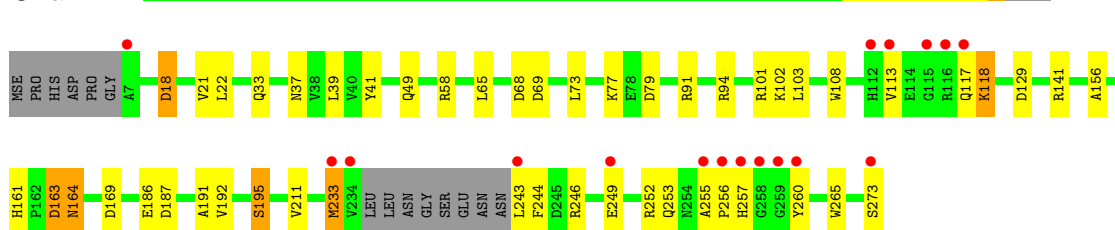
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	204	Total	O	0	0
			204	204		
7	B	200	Total	O	0	0
			200	200		
7	C	158	Total	O	0	0
			158	158		
7	D	221	Total	O	0	0
			221	221		
7	E	4	Total	O	0	0
			4	4		
7	F	13	Total	O	0	0
			13	13		
7	G	4	Total	O	0	0
			4	4		
7	H	10	Total	O	0	0
			10	10		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: N-ACYL GLM PEUDO-TEICOPLANIN DEACETYLASE

Chain A:



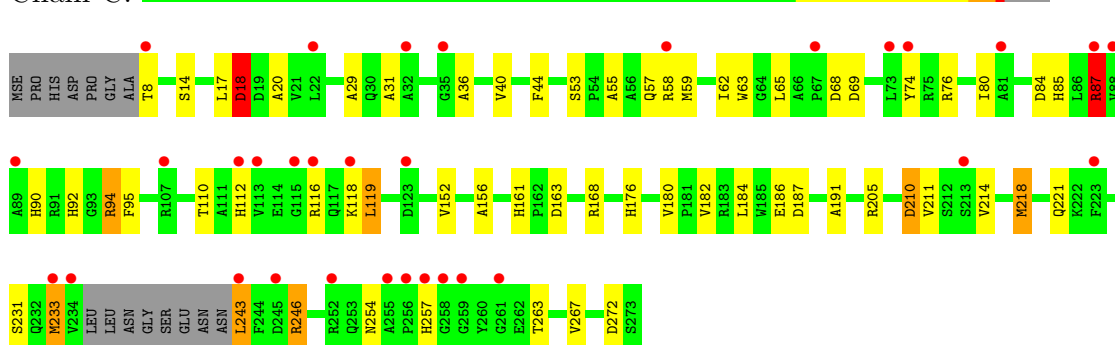
• Molecule 1: N-ACYL GLM PEUDO-TEICOPLANIN DEACETYLASE

Chain B:



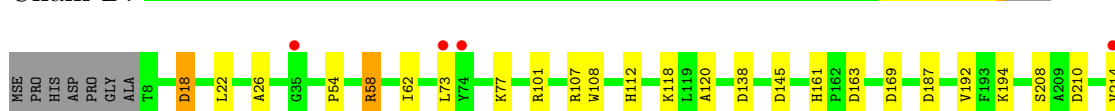
• Molecule 1: N-ACYL GLM PEUDO-TEICOPLANIN DEACETYLASE

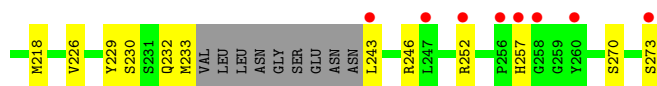
Chain C:



• Molecule 1: N-ACYL GLM PEUDO-TEICOPLANIN DEACETYLASE

Chain D:





- Molecule 2: TEICOPLANIN

Chain E:



- Molecule 2: TEICOPLANIN

Chain F:



- Molecule 2: TEICOPLANIN

Chain G:



- Molecule 2: TEICOPLANIN

Chain H:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	58.77Å 70.71Å 76.31Å 113.89° 108.29° 98.20°	Depositor
Resolution (Å)	20.00 – 1.70 19.94 – 1.70	Depositor EDS
% Data completeness (in resolution range)	95.8 (20.00-1.70) 93.7 (19.94-1.70)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.37 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.201 , 0.237 0.191 , 0.209	Depositor DCC
R_{free} test set	5379 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	18.4	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 30.8	EDS
Estimated twinning fraction	0.125 for -h,-k,h+k+l	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 106831 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9379	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 59.45 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.7616e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, GHP, NAG, 3MY, T55, GCS, 3FG, OMY

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	1.25	8/2064 (0.4%)	1.34	12/2805 (0.4%)
1	B	1.17	4/2052 (0.2%)	1.08	7/2789 (0.3%)
1	C	1.20	3/2054 (0.1%)	1.13	11/2792 (0.4%)
1	D	1.14	1/2052 (0.0%)	1.09	9/2788 (0.3%)
All	All	1.19	16/8222 (0.2%)	1.16	39/11174 (0.3%)

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	21	VAL	CB-CG1	7.31	1.68	1.52
1	A	265	TRP	CG-CD1	6.90	1.46	1.36
1	C	44	PHE	CE2-CZ	6.50	1.49	1.37
1	A	101	ARG	CD-NE	-6.16	1.35	1.46
1	A	41	TYR	CE1-CZ	6.12	1.46	1.38

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	101	ARG	NE-CZ-NH2	-31.52	104.54	120.30
1	A	101	ARG	NE-CZ-NH1	24.14	132.37	120.30
1	A	101	ARG	CD-NE-CZ	10.92	138.88	123.60
1	C	205	ARG	NE-CZ-NH2	-10.55	115.02	120.30
1	C	205	ARG	NE-CZ-NH1	9.81	125.20	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2018	0	1935	30	1
1	B	2006	0	1921	19	0
1	C	2008	0	1925	66	1
1	D	2006	0	1921	30	0
2	E	84	0	34	2	0
2	F	85	0	35	4	0
2	G	85	0	35	3	0
2	H	85	0	34	5	0
3	E	11	0	10	0	0
3	F	11	0	10	1	0
3	G	11	0	10	0	0
3	H	11	0	10	4	0
4	E	14	0	13	2	0
4	F	14	0	11	0	0
4	G	14	0	13	1	0
4	H	14	0	13	0	0
5	E	11	0	9	0	0
5	F	11	0	9	0	0
5	G	11	0	9	0	0
5	H	11	0	9	0	0
6	E	11	0	19	4	0
6	F	11	0	19	4	0
6	G	11	0	19	3	0
6	H	11	0	19	12	0
7	A	204	0	0	4	0
7	B	200	0	0	0	0
7	C	158	0	0	2	0
7	D	221	0	0	4	0
7	E	4	0	0	0	0
7	F	13	0	0	2	0
7	G	4	0	0	0	0
7	H	10	0	0	0	0
All	All	9379	0	8042	154	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including

hydrogens) of the entry. The overall clashscore for this entry is 9.

The worst 5 of 154 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:29:ALA:CB	1:C:218:MSE:HE2	1.57	1.34
1:C:29:ALA:HB1	1:C:218:MSE:CE	1.66	1.26
1:D:233:MSE:HE2	7:D:2200:HOH:O	1.45	1.17
1:D:233:MSE:HE3	6:H:711:T55:CAF	1.76	1.15
1:C:243:LEU:HD22	6:G:711:T55:HAF1	1.32	1.11

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	Distance(Å)	Clash(Å)
1:A:195:SER:O	1:C:58:ARG:NH2[1_544]	2.15	0.05

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	255/273 (93%)	247 (97%)	6 (2%)	2 (1%)	27	8
1	B	254/273 (93%)	249 (98%)	3 (1%)	2 (1%)	27	8
1	C	254/273 (93%)	241 (95%)	12 (5%)	1 (0%)	43	22
1	D	253/273 (93%)	246 (97%)	5 (2%)	2 (1%)	27	8
All	All	1016/1092 (93%)	983 (97%)	26 (3%)	7 (1%)	30	10

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	18	ASP
1	B	18	ASP
1	B	257	HIS
1	C	18	ASP
1	D	18	ASP

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	210/218 (96%)	201 (96%)	9 (4%)	40	16
1	B	208/218 (95%)	200 (96%)	8 (4%)	44	19
1	C	209/218 (96%)	199 (95%)	10 (5%)	35	13
1	D	209/218 (96%)	204 (98%)	5 (2%)	61	39
All	All	836/872 (96%)	804 (96%)	32 (4%)	44	19

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	217	GLU
1	C	8	THR
1	D	187	ASP
1	B	253	GLN
1	C	69	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	122	ASN
1	C	161	HIS
1	D	122	ASN
1	C	90	HIS
1	C	117	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

28 non-standard protein/DNA/RNA residues 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	GHP	E	701	2	11,11,12	6.17	2 (18%)	12,14,16	6.69	2 (16%)
2	3MY	E	702	2	13,13,14	6.84	4 (30%)	15,17,19	3.73	9 (60%)
2	3FG	E	703	2	11,11,13	5.59	2 (18%)	10,14,18	14.58	3 (30%)
2	GHP	E	704	2,5	11,11,12	5.48	6 (54%)	12,14,16	1.59	2 (16%)
2	GHP	E	705	2	11,11,12	5.96	5 (45%)	12,14,16	21.99	4 (33%)
2	OMY	E	706	2,4	14,14,15	5.23	5 (35%)	17,19,21	3.51	6 (35%)
2	3FG	E	707	3,2	13,13,13	2.31	2 (15%)	18,18,18	2.16	4 (22%)
2	GHP	F	701	2	11,11,12	6.68	2 (18%)	12,14,16	16.35	3 (25%)
2	3MY	F	702	2	13,13,14	4.92	3 (23%)	15,17,19	4.20	5 (33%)
2	3FG	F	703	2	12,12,13	6.38	2 (16%)	14,16,18	24.82	2 (14%)
2	GHP	F	704	2,5	11,11,12	6.24	5 (45%)	12,14,16	9.77	5 (41%)
2	GHP	F	705	2	11,11,12	5.53	4 (36%)	12,14,16	23.52	6 (50%)
2	OMY	F	706	2,4	14,14,15	5.60	3 (21%)	17,19,21	3.41	3 (17%)
2	3FG	F	707	3,2	13,13,13	2.35	2 (15%)	18,18,18	2.13	6 (33%)
2	GHP	G	701	2	11,11,12	6.34	2 (18%)	12,14,16	3.71	4 (33%)
2	3MY	G	702	2	13,13,14	5.65	2 (15%)	15,17,19	3.84	9 (60%)
2	3FG	G	703	2	12,12,13	5.62	2 (16%)	14,16,18	5.03	1 (7%)
2	GHP	G	704	2,5	11,11,12	6.26	3 (27%)	12,14,16	4.48	3 (25%)
2	GHP	G	705	2	11,11,12	6.01	4 (36%)	12,14,16	30.04	5 (41%)
2	OMY	G	706	2,4	14,14,15	4.90	4 (28%)	17,19,21	3.24	5 (29%)
2	3FG	G	707	3,2	13,13,13	2.30	3 (23%)	18,18,18	2.40	7 (38%)
2	GHP	H	701	2	11,11,12	6.46	3 (27%)	12,14,16	6.67	3 (25%)
2	3MY	H	702	2	13,13,14	6.19	3 (23%)	15,17,19	3.90	5 (33%)
2	3FG	H	703	2	12,12,13	5.87	3 (25%)	14,16,18	1.27	2 (14%)
2	GHP	H	704	2,5	11,11,12	6.07	4 (36%)	12,14,16	1.81	1 (8%)
2	GHP	H	705	2	11,11,12	6.74	2 (18%)	12,14,16	24.73	5 (41%)
2	OMY	H	706	2,4	14,14,15	4.97	8 (57%)	17,19,21	3.25	7 (41%)
2	3FG	H	707	3,2	13,13,13	2.02	2 (15%)	18,18,18	2.26	6 (33%)

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	GHP	E	701	2	-	0/4/6/8	0/1/1/1
2	3MY	E	702	2	-	0/4/6/8	0/1/1/1
2	3FG	E	703	2	-	0/4/6/8	0/1/1/1
2	GHP	E	704	2,5	-	0/4/6/8	0/1/1/1
2	GHP	E	705	2	-	0/4/6/8	0/1/1/1
2	OMY	E	706	2,4	-	0/8/10/12	0/1/1/1
2	3FG	E	707	3,2	-	0/8/8/8	0/1/1/1
2	GHP	F	701	2	-	0/4/6/8	0/1/1/1
2	3MY	F	702	2	-	0/4/6/8	0/1/1/1
2	3FG	F	703	2	-	0/4/6/8	0/1/1/1
2	GHP	F	704	2,5	-	0/4/6/8	0/1/1/1
2	GHP	F	705	2	-	0/4/6/8	0/1/1/1
2	OMY	F	706	2,4	-	0/8/10/12	0/1/1/1
2	3FG	F	707	3,2	-	0/8/8/8	0/1/1/1
2	GHP	G	701	2	-	0/4/6/8	0/1/1/1
2	3MY	G	702	2	-	0/4/6/8	0/1/1/1
2	3FG	G	703	2	-	0/4/6/8	0/1/1/1
2	GHP	G	704	2,5	-	0/4/6/8	0/1/1/1
2	GHP	G	705	2	-	0/4/6/8	0/1/1/1
2	OMY	G	706	2,4	-	0/8/10/12	0/1/1/1
2	3FG	G	707	3,2	-	0/8/8/8	0/1/1/1
2	GHP	H	701	2	-	0/4/6/8	0/1/1/1
2	3MY	H	702	2	-	0/4/6/8	0/1/1/1
2	3FG	H	703	2	-	0/4/6/8	0/1/1/1
2	GHP	H	704	2,5	-	0/4/6/8	0/1/1/1
2	GHP	H	705	2	-	0/4/6/8	0/1/1/1
2	OMY	H	706	2,4	-	0/8/10/12	0/1/1/1
2	3FG	H	707	3,2	-	0/8/8/8	0/1/1/1

The worst 5 of 92 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	702	3MY	O-C	23.76	1.27	1.11
2	F	701	GHP	O-C	21.65	1.26	1.11
2	H	702	3MY	O-C	21.51	1.26	1.11
2	H	705	GHP	O-C	20.34	1.25	1.11
2	G	702	3MY	O-C	20.07	1.25	1.11

The worst 5 of 123 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	705	GHP	C-CA-N	-103.81	101.51	113.27
2	F	703	3FG	C-CA-N	92.79	123.78	113.27
2	H	705	GHP	C-CA-N	-85.31	103.60	113.27
2	F	705	GHP	C-CA-N	-81.20	104.07	113.27
2	E	705	GHP	C-CA-N	-75.79	104.68	113.27

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

16 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	BMA	E	708	2	10,11,12	1.28	1 (10%)	11,15,17	2.13	3 (27%)
4	NAG	E	709	2	12,14,15	1.45	3 (25%)	15,19,21	2.12	2 (13%)
5	GCS	E	710	2,6	9,11,12	1.02	0	11,15,17	2.57	6 (54%)
6	T55	E	711	5	10,10,11	6.46	2 (20%)	8,10,12	1.68	2 (25%)
3	BMA	F	708	2	10,11,12	1.00	0	11,15,17	0.93	0
4	NAG	F	709	2	12,14,15	1.91	4 (33%)	15,19,21	4.10	6 (40%)
5	GCS	F	710	2,6	9,11,12	1.78	1 (11%)	11,15,17	2.28	5 (45%)
6	T55	F	711	5	10,10,11	5.78	1 (10%)	8,10,12	0.73	0
3	BMA	G	708	2	10,11,12	2.04	4 (40%)	11,15,17	2.01	3 (27%)
4	NAG	G	709	2	12,14,15	1.29	2 (16%)	15,19,21	2.77	2 (13%)
5	GCS	G	710	2,6	9,11,12	1.34	2 (22%)	11,15,17	1.23	1 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	T55	G	711	5	10,10,11	5.04	2 (20%)	8,10,12	1.04	1 (12%)
3	BMA	H	708	2	10,11,12	0.86	0	11,15,17	2.84	6 (54%)
4	NAG	H	709	2	12,14,15	1.72	1 (8%)	15,19,21	2.43	5 (33%)
5	GCS	H	710	2,6	9,11,12	1.18	2 (22%)	11,15,17	1.64	4 (36%)
6	T55	H	711	5	10,10,11	6.89	2 (20%)	8,10,12	0.32	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	BMA	E	708	2	-	0/2/19/22	0/1/1/1
4	NAG	E	709	2	-	0/6/23/26	0/1/1/1
5	GCS	E	710	2,6	-	0/2/19/22	0/1/1/1
6	T55	E	711	5	-	0/7/8/9	0/0/0/0
3	BMA	F	708	2	-	0/2/19/22	0/1/1/1
4	NAG	F	709	2	1/1/5/7	0/6/23/26	0/1/1/1
5	GCS	F	710	2,6	-	0/2/19/22	0/1/1/1
6	T55	F	711	5	-	0/7/8/9	0/0/0/0
3	BMA	G	708	2	-	0/2/19/22	0/1/1/1
4	NAG	G	709	2	-	0/6/23/26	0/1/1/1
5	GCS	G	710	2,6	-	0/2/19/22	0/1/1/1
6	T55	G	711	5	-	0/7/8/9	0/0/0/0
3	BMA	H	708	2	-	0/2/19/22	0/1/1/1
4	NAG	H	709	2	-	0/6/23/26	0/1/1/1
5	GCS	H	710	2,6	-	0/2/19/22	0/1/1/1
6	T55	H	711	5	-	0/7/8/9	0/0/0/0

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	H	711	T55	O-C	21.40	1.26	1.11
6	E	711	T55	O-C	20.15	1.25	1.11
6	F	711	T55	O-C	18.20	1.23	1.11
6	G	711	T55	O-C	15.70	1.22	1.11
4	H	709	NAG	C2-N2	4.79	1.52	1.46

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	G	709	NAG	O5-C5-C6	10.03	117.50	106.98
4	F	709	NAG	C3-C4-C5	9.40	126.99	110.20
4	F	709	NAG	C2-N2-C7	7.29	135.34	123.09
4	F	709	NAG	O3-C3-C2	6.29	122.30	109.09
4	F	709	NAG	O3-C3-C4	5.90	123.58	110.35

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	F	709	NAG	C3

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

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 ⓘ

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	259/273 (94%)	0.30	17 (6%) 18 22	8, 18, 45, 61	0
1	B	258/273 (94%)	0.25	14 (5%) 25 29	9, 19, 46, 60	0
1	C	258/273 (94%)	0.71	32 (12%) 5 6	10, 26, 47, 63	0
1	D	257/273 (94%)	0.24	12 (4%) 30 34	8, 19, 37, 62	0
2	E	7/7 (100%)	0.40	0 100 100	20, 31, 37, 42	0
2	F	7/7 (100%)	0.15	0 100 100	20, 30, 33, 35	0
2	G	7/7 (100%)	0.80	1 (14%) 3 5	22, 30, 39, 49	0
2	H	7/7 (100%)	-0.33	0 100 100	14, 21, 23, 26	0
All	All	1060/1120 (94%)	0.37	76 (7%) 15 19	8, 20, 46, 63	0

The worst 5 of 76 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	234	VAL	8.4
1	C	243	LEU	8.0
1	C	259	GLY	6.1
1	C	257	HIS	6.0
1	A	256	PRO	5.9

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	GHP	G	701	11/12	0.59	15.47	37,50,56,56	0
2	GHP	E	701	11/12	0.17	5.03	32,33,37,40	0
2	3MY	E	702	13/14	0.11	1.76	13,19,29,30	0
2	3MY	F	702	13/14	0.10	0.41	11,16,27,30	0
2	3MY	G	702	13/14	0.10	0.08	12,21,34,36	0
2	GHP	F	701	11/12	0.13	0.07	27,31,36,40	0
2	3FG	G	703	12/13	0.14	-0.01	27,39,48,50	0
2	3FG	F	703	12/13	0.12	-0.09	19,31,36,38	0
2	OMY	G	706	14/15	0.17	-0.10	23,28,41,43	0
2	3FG	G	707	13/13	0.13	-0.16	28,32,39,43	0
2	3FG	E	707	13/13	0.14	-0.17	38,41,44,49	0
2	OMY	F	706	14/15	0.15	-0.24	21,28,35,38	0
2	OMY	E	706	14/15	0.16	-0.26	18,29,39,43	0
2	GHP	H	701	11/12	0.08	-0.33	18,20,23,24	0
2	3FG	H	707	13/13	0.11	-0.37	20,24,31,32	0
2	OMY	H	706	14/15	0.11	-0.40	14,20,26,42	0
2	3FG	H	703	12/13	0.09	-0.45	15,21,27,30	0
2	GHP	H	704	11/12	0.09	-0.50	10,15,18,20	0
2	3FG	E	703	11/13	0.12	-0.62	26,30,39,41	0
2	3FG	F	707	13/13	0.11	-0.81	30,33,38,42	0
2	3MY	H	702	13/14	0.07	-0.88	8,12,18,18	0
2	GHP	F	704	11/12	0.09	-0.89	16,18,22,24	0
2	GHP	E	704	11/12	0.08	-0.93	11,18,27,27	0
2	GHP	G	704	11/12	0.08	-1.02	16,21,26,28	0
2	GHP	G	705	11/12	0.11	-2.02	25,31,34,36	0
2	GHP	E	705	11/12	0.19	-2.54	30,34,42,45	0
2	GHP	H	705	11/12	0.08	-2.56	19,23,26,27	0
2	GHP	F	705	11/12	0.15	-6.57	22,30,34,34	0

6.3 Carbohydrates ⓘ

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	NAG	H	709	14/15	0.40	5.22	39,51,56,56	0
3	BMA	E	708	11/12	0.37	4.35	57,62,64,66	0
4	NAG	F	709	14/15	0.46	4.32	4,47,55,58	0
3	BMA	H	708	11/12	0.29	3.78	36,46,53,53	0
3	BMA	G	708	11/12	0.27	3.12	43,47,50,50	0
3	BMA	F	708	11/12	0.31	2.94	51,56,59,63	0
4	NAG	E	709	14/15	0.41	2.58	56,64,67,67	0
6	T55	H	711	11/12	0.14	2.28	12,31,41,41	0
6	T55	F	711	11/12	0.17	1.75	19,34,38,39	0
5	GCS	H	710	11/12	0.10	1.37	4,9,11,12	0
6	T55	E	711	11/12	0.16	1.20	15,31,40,42	0
4	NAG	G	709	14/15	0.42	0.86	54,60,64,65	0
6	T55	G	711	11/12	0.18	0.40	19,31,43,46	0
5	GCS	F	710	11/12	0.08	-0.23	9,14,17,20	0
5	GCS	G	710	11/12	0.08	-0.70	10,14,17,17	0
5	GCS	E	710	11/12	0.06	-1.69	8,10,12,12	0

6.5 Other polymers ⓘ

There are no such residues in this entry.