



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:36 AM UTC

PDB ID : 8W0M / pdb_00008w0m
Title : Crystal structure of Acetyl-CoA synthetase 2 from *Candida albicans* in complex with a Acetyl Sulfamate AMP ester inhibitor
Authors : Seattle Structural Genomics Center for Infectious Disease; Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2024-02-13
Resolution : 3.10 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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

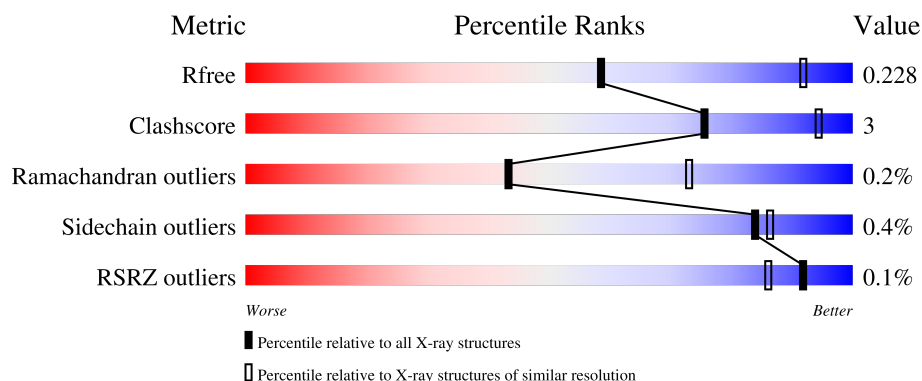
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	686	
1	B	686	
1	C	686	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13045 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 Acetyl-coenzyme A synthetase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	599	Total	C	N	O	S	0	0	0
			4674	2993	789	879	13			
1	B	525	Total	C	N	O	S	0	0	0
			4122	2645	693	771	13			
1	C	532	Total	C	N	O	S	0	0	0
			4171	2672	701	785	13			

There are 51 discrepancies between the modelled and reference sequences:

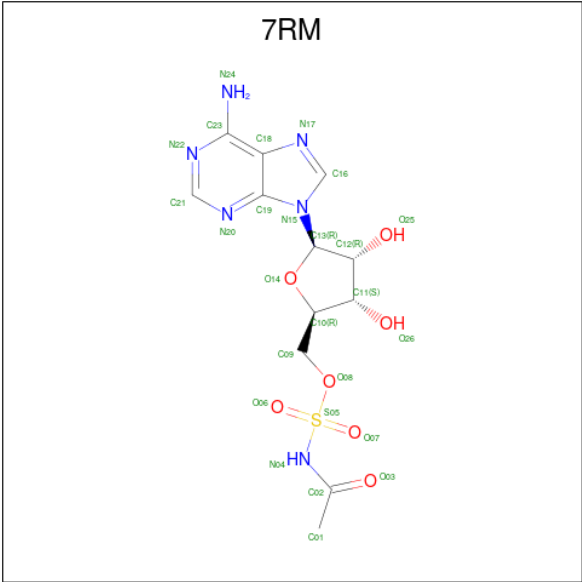
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q8NJJN3
A	2	HIS	-	expression tag	UNP Q8NJJN3
A	3	HIS	-	expression tag	UNP Q8NJJN3
A	4	HIS	-	expression tag	UNP Q8NJJN3
A	5	HIS	-	expression tag	UNP Q8NJJN3
A	6	HIS	-	expression tag	UNP Q8NJJN3
A	7	HIS	-	expression tag	UNP Q8NJJN3
A	8	HIS	-	expression tag	UNP Q8NJJN3
A	9	HIS	-	expression tag	UNP Q8NJJN3
A	10	GLU	-	expression tag	UNP Q8NJJN3
A	11	ASN	-	expression tag	UNP Q8NJJN3
A	12	LEU	-	expression tag	UNP Q8NJJN3
A	13	TYR	-	expression tag	UNP Q8NJJN3
A	14	PHE	-	expression tag	UNP Q8NJJN3
A	15	GLN	-	expression tag	UNP Q8NJJN3
A	16	GLY	-	expression tag	UNP Q8NJJN3
A	403	ALA	VAL	engineered mutation	UNP Q8NJJN3
B	1	MET	-	initiating methionine	UNP Q8NJJN3
B	2	HIS	-	expression tag	UNP Q8NJJN3
B	3	HIS	-	expression tag	UNP Q8NJJN3
B	4	HIS	-	expression tag	UNP Q8NJJN3
B	5	HIS	-	expression tag	UNP Q8NJJN3
B	6	HIS	-	expression tag	UNP Q8NJJN3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	7	HIS	-	expression tag	UNP Q8NJJ3
B	8	HIS	-	expression tag	UNP Q8NJJ3
B	9	HIS	-	expression tag	UNP Q8NJJ3
B	10	GLU	-	expression tag	UNP Q8NJJ3
B	11	ASN	-	expression tag	UNP Q8NJJ3
B	12	LEU	-	expression tag	UNP Q8NJJ3
B	13	TYR	-	expression tag	UNP Q8NJJ3
B	14	PHE	-	expression tag	UNP Q8NJJ3
B	15	GLN	-	expression tag	UNP Q8NJJ3
B	16	GLY	-	expression tag	UNP Q8NJJ3
B	403	ALA	VAL	engineered mutation	UNP Q8NJJ3
C	1	MET	-	initiating methionine	UNP Q8NJJ3
C	2	HIS	-	expression tag	UNP Q8NJJ3
C	3	HIS	-	expression tag	UNP Q8NJJ3
C	4	HIS	-	expression tag	UNP Q8NJJ3
C	5	HIS	-	expression tag	UNP Q8NJJ3
C	6	HIS	-	expression tag	UNP Q8NJJ3
C	7	HIS	-	expression tag	UNP Q8NJJ3
C	8	HIS	-	expression tag	UNP Q8NJJ3
C	9	HIS	-	expression tag	UNP Q8NJJ3
C	10	GLU	-	expression tag	UNP Q8NJJ3
C	11	ASN	-	expression tag	UNP Q8NJJ3
C	12	LEU	-	expression tag	UNP Q8NJJ3
C	13	TYR	-	expression tag	UNP Q8NJJ3
C	14	PHE	-	expression tag	UNP Q8NJJ3
C	15	GLN	-	expression tag	UNP Q8NJJ3
C	16	GLY	-	expression tag	UNP Q8NJJ3
C	403	ALA	VAL	engineered mutation	UNP Q8NJJ3

- Molecule 2 is 5'-O-(acetylsulfamoyl)adenosine (CCD ID: 7RM) (formula: C₁₂H₁₆N₆O₇S) (labeled as "Ligand of Interest" by depositor).

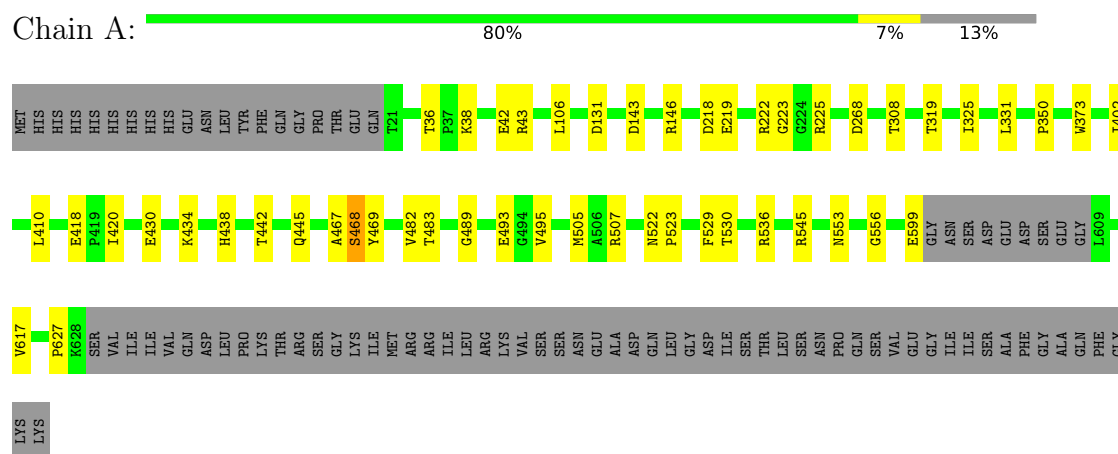


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			26	12	6	7	1		
2	B	1	Total	C	N	O	S	0	0
			26	12	6	7	1		
2	C	1	Total	C	N	O	S	0	0
			26	12	6	7	1		

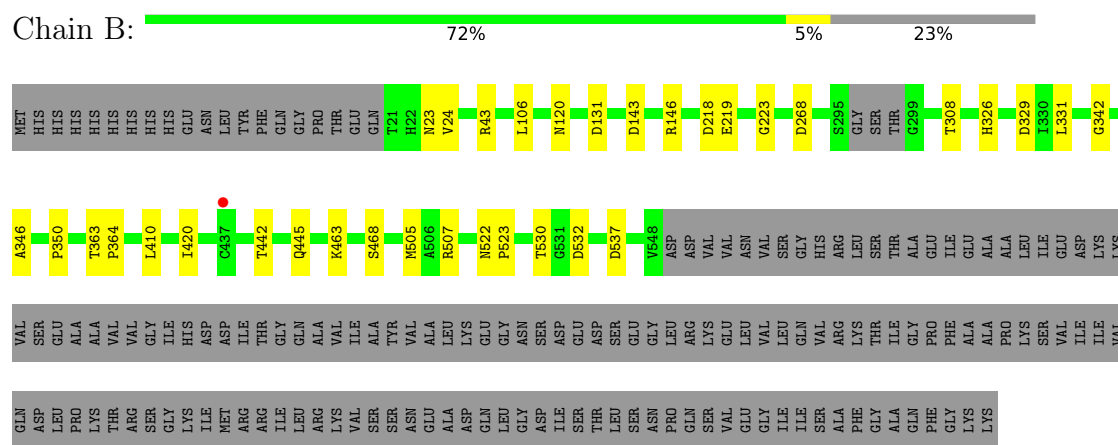
3 Residue-property plots

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.

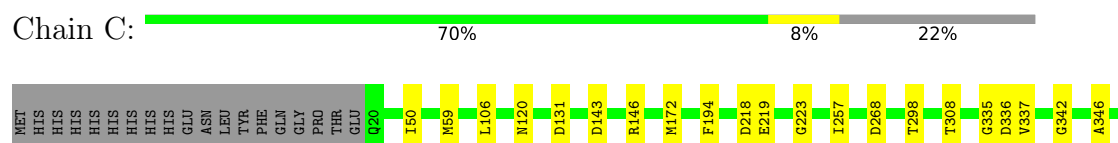
• Molecule 1: Acetyl-coenzyme A synthetase 2



• Molecule 1: Acetyl-coenzyme A synthetase 2



• Molecule 1: Acetyl-coenzyme A synthetase 2



I359	GLY	GLN	ILE
T363	HIS	VAL	SER
P364	ARG	ARG	ALA
A365	LEU	LYS	PHE
Y366	THR	ILE	GLY
Y369	ALA	GLY	ALA
L393	GLU	PRO	GLN
L413	ILE	PHE	PHE
Y428	ILE	GLY	GLY
I439	GLU	ALA	LYS
Q445	ASP	ALA	LYS
Q445	LYS	PRO	LYS
W462	VAL	LYS	LYS
S468	SER	GLN	ASP
D480	GLU	LEU	LEU
P481	ALA	PRO	LYS
E486	ALA	THR	ARG
I487	VAL	ARG	SER
E488	GLY	GLY	GLY
G489	ILE	ILE	LYS
A492	HIS	ILE	ILE
E493	ASP	ARG	ARG
G494	ASP	ILE	ILE
V495	ILE	LEU	LEU
K499	THR	ARG	LYS
W505	GLY	VAL	SER
A506	GLN	SER	SER
R507	ALA	ASN	GLU
T514	LEU	GLU	ALA
N522	LYS	ASP	ALA
P523	GLU	GLN	ASP
T530	ASP	LEU	ILE
R536	THR	SER	THR
R545	SER	LEU	LEU
D549	GLU	SER	SER
D550	GLY	ASN	ASN
V551	LEU	PRO	GLN
VAL	ARG	SER	SER
ASN	LYS	VAL	VAL
VAL	GLU	GLU	GLY
VAL	LEU	GLY	ILE
SER	LEU	ILE	

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	101.40Å 115.40Å 106.27Å 90.00° 116.40° 90.00°	Depositor
Resolution (Å)	47.59 – 3.10 47.59 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.59-3.10) 99.9 (47.59-3.10)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 3.12Å)	Xtriage
Refinement program	PHENIX (dev_5233: ???)	Depositor
R, R_{free}	0.188 , 0.230 0.191 , 0.228	Depositor DCC
R_{free} test set	2150 reflections (5.39%)	wwPDB-VP
Wilson B-factor (Å ²)	81.5	Xtriage
Anisotropy	0.158	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 72.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.008 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13045	wwPDB-VP
Average B, all atoms (Å ²)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.75% 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: 7RM

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	0.09	0/4799	0.27	0/6531
1	B	0.09	0/4241	0.27	0/5774
1	C	0.10	0/4291	0.29	0/5844
All	All	0.10	0/13331	0.28	0/18149

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

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	4674	0	4563	30	0
1	B	4122	0	3987	19	0
1	C	4171	0	4028	27	0
2	A	26	0	0	1	0
2	B	26	0	0	2	0
2	C	26	0	0	0	0
All	All	13045	0	12578	76	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 3.

All (76) 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:B:442:THR:O	2:B:701:7RM:N24	2.30	0.65
1:B:505:MET:O	1:B:507:ARG:NH1	2.33	0.61
1:A:505:MET:O	1:A:507:ARG:NH1	2.33	0.61
1:B:143:ASP:OD1	1:B:146:ARG:NH2	2.35	0.60
1:C:172:MET:HE3	1:C:335:GLY:O	2.02	0.59
1:A:38:LYS:NZ	1:A:42:GLU:OE2	2.34	0.59
1:A:493:GLU:OE1	1:A:545:ARG:NH1	2.34	0.59
1:A:553:ASN:O	1:A:553:ASN:ND2	2.37	0.57
1:C:505:MET:O	1:C:507:ARG:NH1	2.37	0.57
1:C:445:GLN:NE2	1:C:530:THR:O	2.37	0.57
1:C:218:ASP:OD1	1:C:219:GLU:N	2.38	0.56
1:C:172:MET:HE1	1:C:337:VAL:HG13	1.88	0.56
1:B:445:GLN:NE2	1:B:530:THR:O	2.39	0.55
1:C:493:GLU:OE1	1:C:545:ARG:NH1	2.40	0.55
1:A:445:GLN:NE2	1:A:530:THR:O	2.38	0.55
1:A:106:LEU:HD11	1:A:308:THR:HG22	1.88	0.54
1:A:218:ASP:OD1	1:A:219:GLU:N	2.41	0.53
1:B:131:ASP:OD1	1:B:223:GLY:N	2.41	0.53
1:B:463:LYS:NZ	1:B:537:ASP:OD2	2.42	0.52
1:C:486:GLU:OE1	1:C:499:LYS:NZ	2.41	0.52
1:A:331:LEU:HD23	1:A:350:PRO:HG3	1.92	0.52
1:C:489:GLY:O	1:C:536:ARG:NH2	2.38	0.52
1:A:131:ASP:OD1	1:A:223:GLY:N	2.44	0.51
1:B:106:LEU:HD11	1:B:308:THR:HG22	1.93	0.50
1:A:43:ARG:NH1	1:A:410:LEU:O	2.45	0.50
1:A:418:GLU:OE2	1:A:556:GLY:N	2.44	0.50
1:C:131:ASP:OD1	1:C:223:GLY:N	2.45	0.49
1:B:331:LEU:HD23	1:B:350:PRO:HG3	1.94	0.49
1:C:172:MET:CE	1:C:336:ASP:HA	2.43	0.49
1:C:522:ASN:N	1:C:523:PRO:HD2	2.26	0.49
1:C:549:ASP:O	1:C:550:ASP:CG	2.57	0.48
1:A:268:ASP:N	1:A:268:ASP:OD1	2.45	0.48
1:C:106:LEU:HD11	1:C:308:THR:HG22	1.94	0.48
1:C:480:ASP:HB2	1:C:487:ILE:HD11	1.95	0.48
1:C:268:ASP:N	1:C:268:ASP:OD1	2.46	0.48
1:C:550:ASP:OD1	1:C:550:ASP:C	2.57	0.48
1:B:218:ASP:OD1	1:B:219:GLU:N	2.42	0.48
1:B:268:ASP:N	1:B:268:ASP:OD1	2.47	0.47
1:C:439:ILE:O	1:C:462:ASN:ND2	2.48	0.47
1:A:442:THR:O	2:A:701:7RM:N24	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:468:SER:OG	1:A:469:TYR:N	2.48	0.47
1:C:487:ILE:HG21	1:C:492:ALA:HB1	1.96	0.46
1:C:143:ASP:OD1	1:C:146:ARG:NH2	2.48	0.46
1:C:172:MET:SD	1:C:359:ILE:HG23	2.55	0.46
1:C:363:THR:HG23	1:C:366:TYR:H	1.80	0.46
1:A:482:VAL:HG13	1:A:483:THR:HG23	1.98	0.46
1:A:599:GLU:N	1:A:599:GLU:OE1	2.49	0.46
1:B:532:ASP:OD1	2:B:701:7RM:O25	2.33	0.46
1:A:467:ALA:O	1:A:468:SER:OG	2.30	0.44
1:C:369:TYR:HE2	1:C:393:LEU:HD21	1.83	0.44
1:A:143:ASP:OD1	1:A:146:ARG:NH2	2.49	0.44
1:A:617:VAL:HG11	1:A:627:PRO:HD3	1.98	0.44
1:C:481:PRO:HG3	1:C:495:VAL:HG13	2.00	0.44
1:C:50:ILE:HG12	1:C:59:MET:HE1	1.99	0.43
1:A:36:THR:HG22	1:A:438:HIS:ND1	2.33	0.43
1:A:522:ASN:N	1:A:523:PRO:CD	2.81	0.43
1:B:522:ASN:N	1:B:523:PRO:CD	2.80	0.43
1:A:495:VAL:HG21	1:A:529:PHE:HE1	1.84	0.43
1:C:363:THR:OG1	1:C:364:PRO:HD2	2.19	0.43
1:A:430:GLU:O	1:A:434:LYS:HA	2.19	0.42
1:B:342:GLY:O	1:B:346:ALA:HB3	2.19	0.42
1:B:23:ASN:OD1	1:B:24:VAL:HG23	2.19	0.42
1:A:617:VAL:HG11	1:A:627:PRO:CD	2.50	0.42
1:A:482:VAL:HG13	1:A:483:THR:N	2.35	0.42
1:A:319:THR:HG22	1:A:325:ILE:HG13	2.02	0.41
1:A:373:TRP:NE1	1:A:402:ILE:HG13	2.35	0.41
1:C:342:GLY:O	1:C:346:ALA:HB3	2.21	0.41
1:C:413:LEU:HB3	1:C:428:TYR:CZ	2.56	0.41
1:A:420:ILE:O	1:A:420:ILE:HG23	2.21	0.41
1:A:222:ARG:O	1:A:225:ARG:HG2	2.21	0.41
1:B:326:HIS:N	1:B:329:ASP:OD2	2.46	0.40
1:A:489:GLY:O	1:A:536:ARG:NH2	2.45	0.40
1:B:43:ARG:NH1	1:B:410:LEU:O	2.52	0.40
1:B:120:ASN:N	1:B:120:ASN:OD1	2.54	0.40
1:B:363:THR:CG2	1:B:364:PRO:HD2	2.52	0.40
1:B:420:ILE:HG23	1:B:420:ILE: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	A	595/686 (87%)	582 (98%)	12 (2%)	1 (0%)	43	73
1	B	521/686 (76%)	509 (98%)	11 (2%)	1 (0%)	43	73
1	C	530/686 (77%)	514 (97%)	15 (3%)	1 (0%)	43	73
All	All	1646/2058 (80%)	1605 (98%)	38 (2%)	3 (0%)	43	73

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	468	SER
1	B	468	SER
1	C	468	SER

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	492/568 (87%)	492 (100%)	0	100	100
1	B	433/568 (76%)	433 (100%)	0	100	100
1	C	439/568 (77%)	434 (99%)	5 (1%)	65	78
All	All	1364/1704 (80%)	1359 (100%)	5 (0%)	84	86

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	120	ASN
1	C	194	PHE
1	C	257	ILE
1	C	298	THR
1	C	514	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	86	HIS
1	A	95	ASN
1	A	513	HIS
1	C	86	HIS
1	C	95	ASN
1	C	228	ASN
1	C	513	HIS

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](#)

3 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	7RM	A	701	-	28,28,28	0.94	2 (7%)	40,42,42	0.39	0
2	7RM	B	701	-	28,28,28	0.95	2 (7%)	40,42,42	0.43	0
2	7RM	C	701	-	28,28,28	0.91	2 (7%)	40,42,42	0.70	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
2	7RM	A	701	-	-	1/14/31/31	0/3/3/3
2	7RM	B	701	-	-	1/14/31/31	0/3/3/3
2	7RM	C	701	-	-	0/14/31/31	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	701	7RM	C02-N04	-3.74	1.34	1.38
2	A	701	7RM	C02-N04	-3.66	1.34	1.38
2	C	701	7RM	C02-N04	-3.63	1.34	1.38
2	A	701	7RM	S05-N04	3.00	1.64	1.59
2	B	701	7RM	S05-N04	2.96	1.64	1.59
2	C	701	7RM	S05-N04	2.72	1.64	1.59

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	701	7RM	O08-C09-C10-O14
2	B	701	7RM	O08-C09-C10-O14

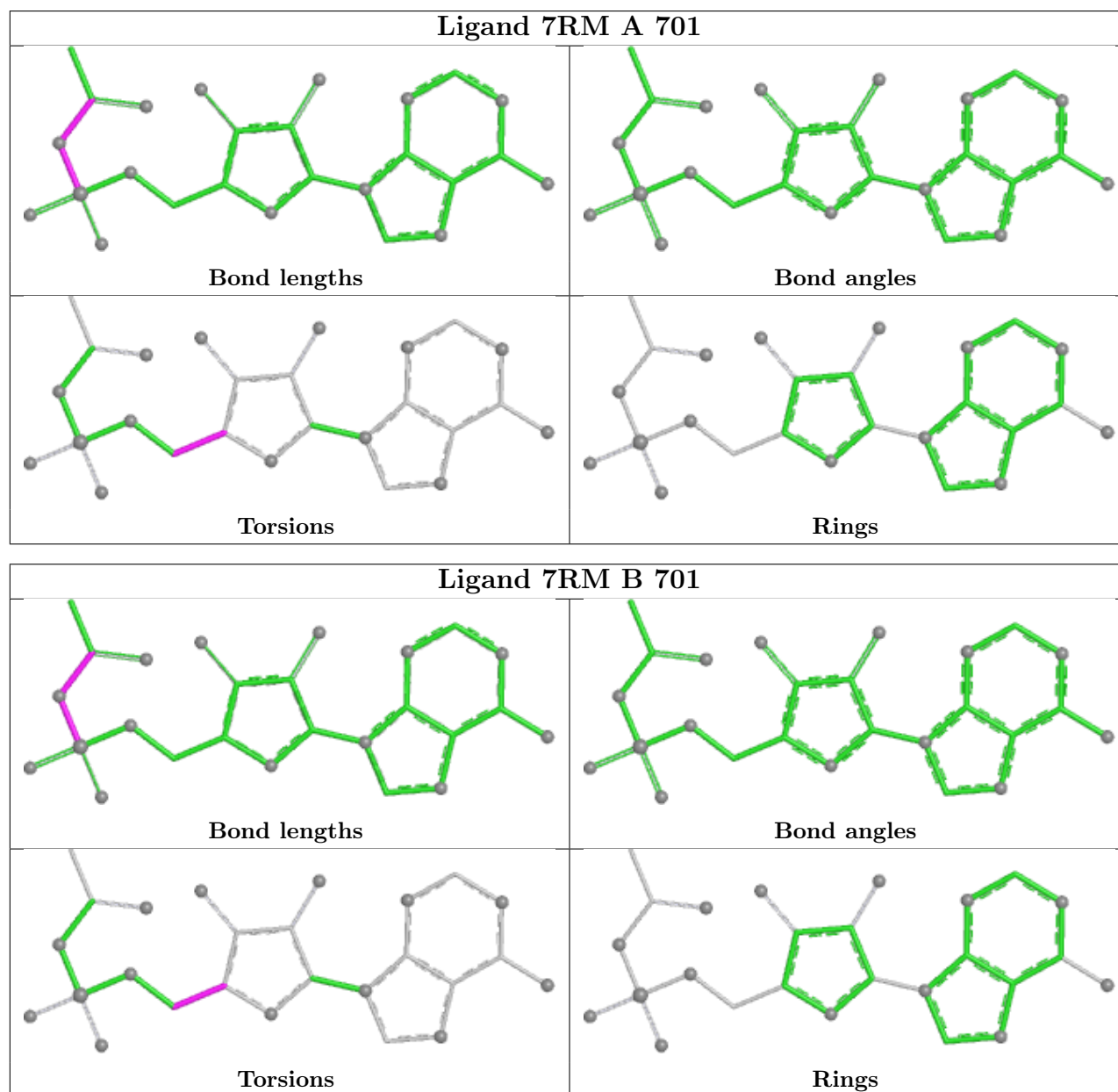
There are no ring outliers.

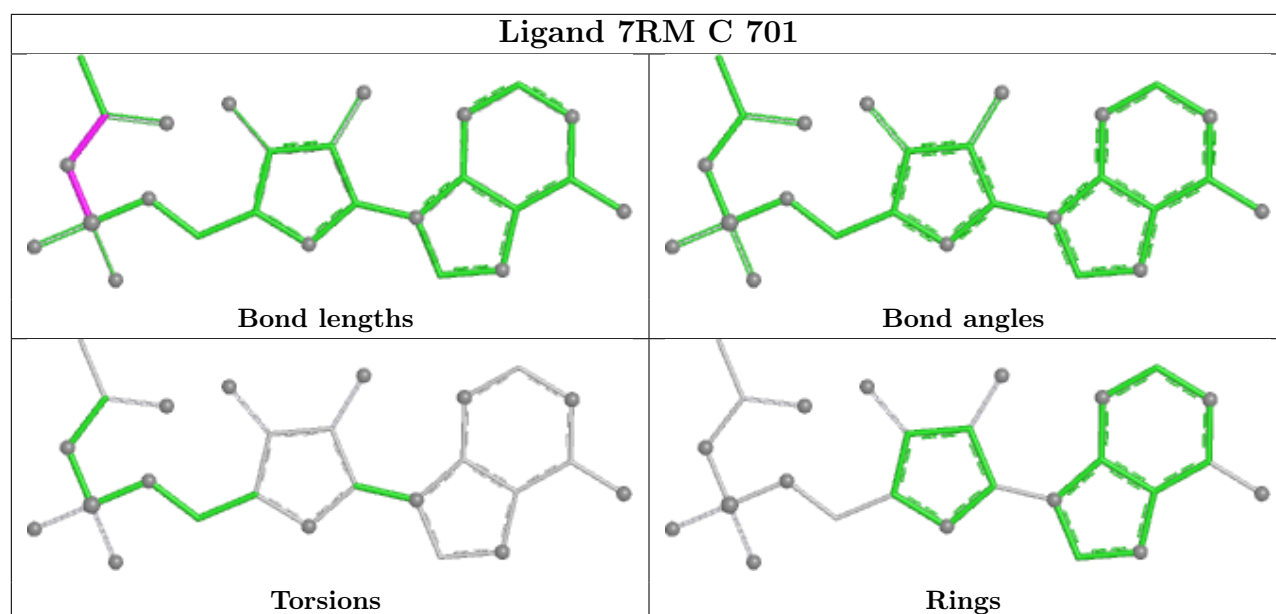
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	701	7RM	1	0
2	B	701	7RM	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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	599/686 (87%)	-0.37	0 100 100	54, 86, 155, 198	0
1	B	525/686 (76%)	-0.39	1 (0%) 91 83	56, 90, 140, 166	0
1	C	532/686 (77%)	-0.45	0 100 100	56, 80, 122, 195	0
All	All	1656/2058 (80%)	-0.40	1 (0%) 92 86	54, 85, 147, 198	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	437	CYS	2.3

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](#)

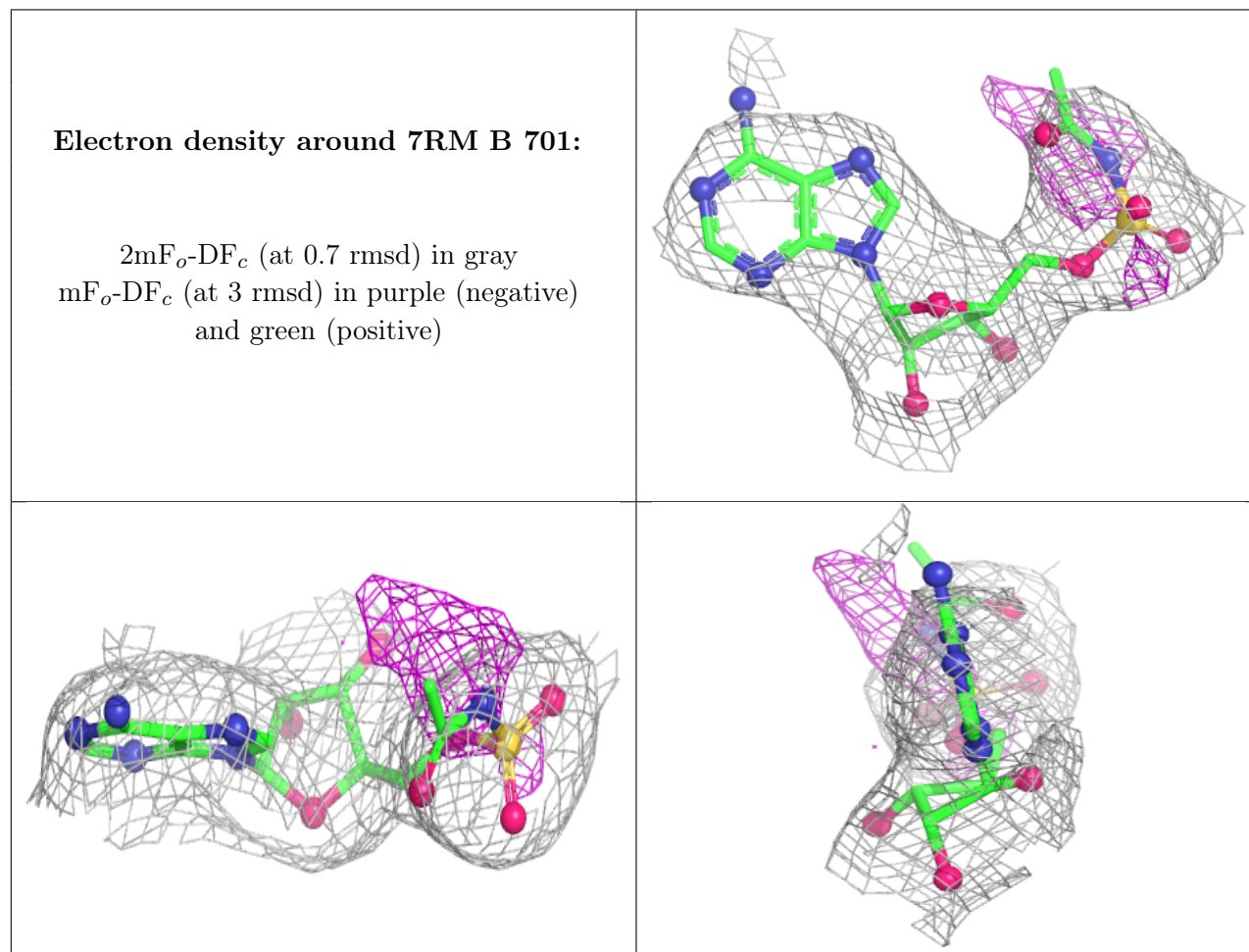
There are no oligosaccharides in this entry.

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.

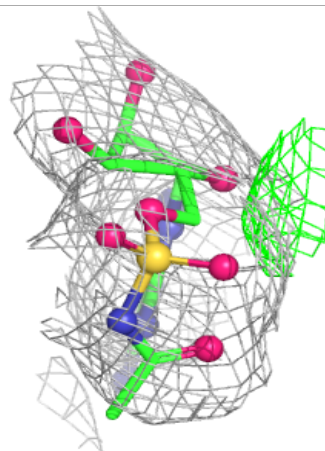
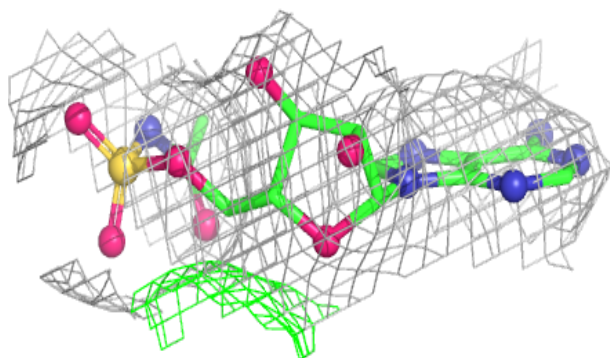
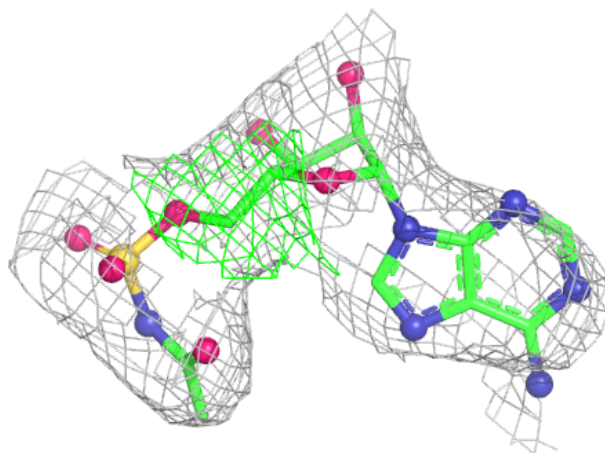
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	7RM	B	701	26/26	0.91	0.09	76,98,107,112	0
2	7RM	A	701	26/26	0.94	0.10	74,91,108,112	0
2	7RM	C	701	26/26	0.95	0.09	61,81,98,171	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



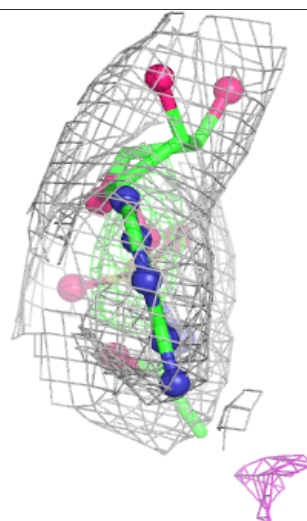
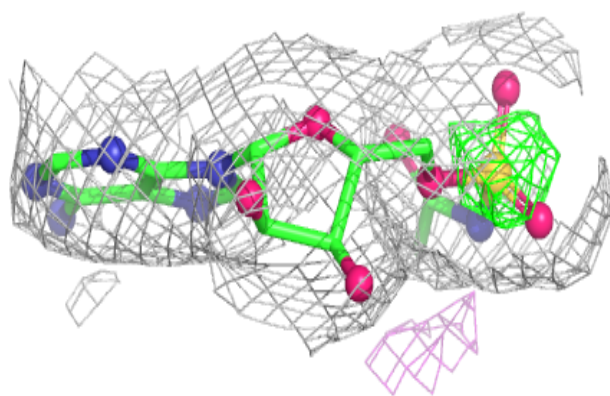
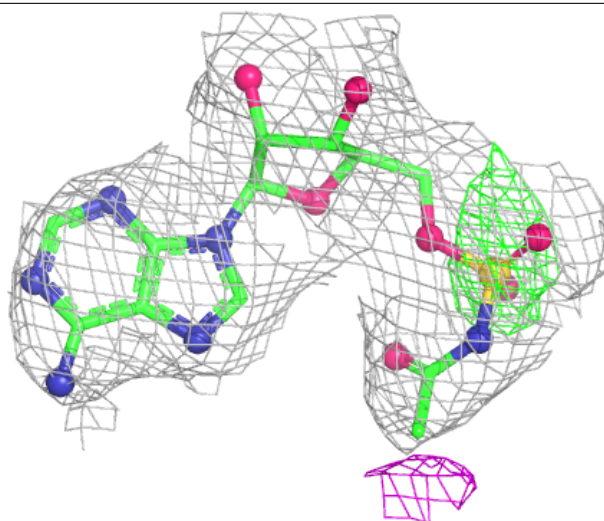
Electron density around 7RM A 701:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around 7RM C 701:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.