



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 31, 2022 – 04:55 PM EDT

PDB ID : 8CSB  
Title : WbbB D232N in complex with CMP-beta-Kdo  
Authors : Forrester, T.J.B.; Kimber, M.S.  
Deposited on : 2022-05-12  
Resolution : 2.25 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

---

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.31.2  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

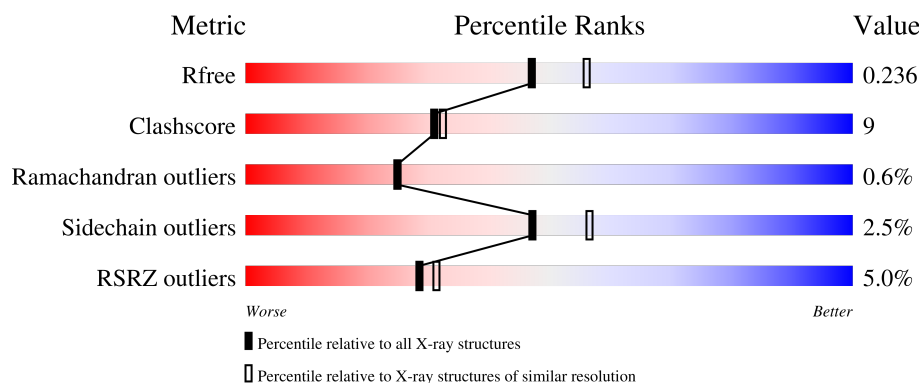
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.25 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))
$R_{free}$	130704	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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  $\geq 3$ , 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	410	
1	B	410	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6518 atoms, of which 72 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 N-acetyl glucosaminyl transferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	394	Total	C	N	O	S	0	0	0
			3127	2004	515	596	12			
1	B	391	Total	C	N	O	S	0	0	0
			3100	1987	510	591	12			

There are 22 discrepancies between the modelled and reference sequences:

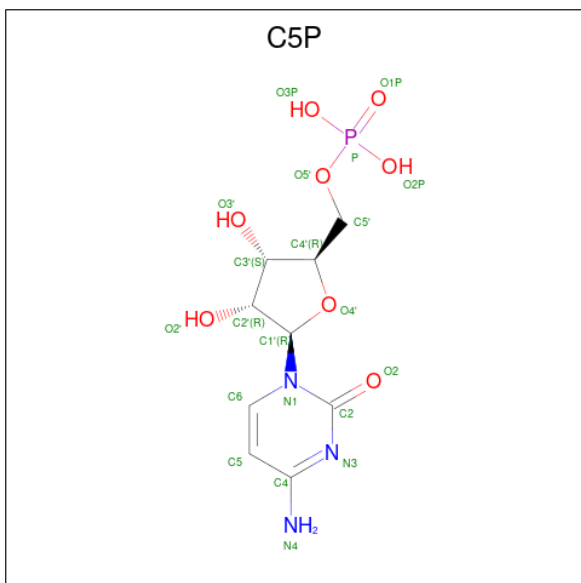
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP Q6U8B0
A	1	GLY	-	expression tag	UNP Q6U8B0
A	232	ASN	ASP	engineered mutation	UNP Q6U8B0
A	402	LEU	-	expression tag	UNP Q6U8B0
A	403	GLU	-	expression tag	UNP Q6U8B0
A	404	HIS	-	expression tag	UNP Q6U8B0
A	405	HIS	-	expression tag	UNP Q6U8B0
A	406	HIS	-	expression tag	UNP Q6U8B0
A	407	HIS	-	expression tag	UNP Q6U8B0
A	408	HIS	-	expression tag	UNP Q6U8B0
A	409	HIS	-	expression tag	UNP Q6U8B0
B	0	MET	-	expression tag	UNP Q6U8B0
B	1	GLY	-	expression tag	UNP Q6U8B0
B	232	ASN	ASP	engineered mutation	UNP Q6U8B0
B	402	LEU	-	expression tag	UNP Q6U8B0
B	403	GLU	-	expression tag	UNP Q6U8B0
B	404	HIS	-	expression tag	UNP Q6U8B0
B	405	HIS	-	expression tag	UNP Q6U8B0
B	406	HIS	-	expression tag	UNP Q6U8B0
B	407	HIS	-	expression tag	UNP Q6U8B0
B	408	HIS	-	expression tag	UNP Q6U8B0
B	409	HIS	-	expression tag	UNP Q6U8B0

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



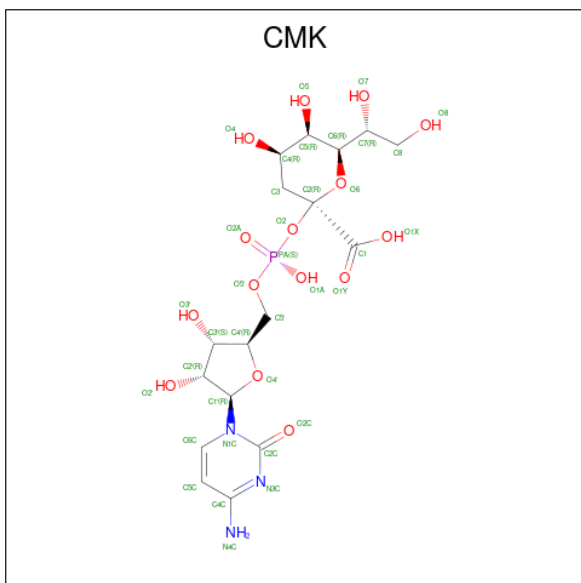
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is CYTIDINE-5'-MONOPHOSPHATE (three-letter code: C5P) (formula:  $C_9H_{14}N_3O_8P$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total 33	C 9	H 12	N 3	O 8	P 1	0	1
3	B	1	Total 33	C 9	H 12	N 3	O 8	P 1	0	1

- Molecule 4 is CYTIDINE 5'-MONOPHOSPHATE 3-DEOXY-BETA-D-GULO-OCT-2-UL O-PYRANOSONIC ACID (three-letter code: CMK) (formula: C<sub>17</sub>H<sub>26</sub>N<sub>3</sub>O<sub>15</sub>P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total 60	C 17	H 24	N 3	O 15	P 1	0	1
4	B	1	Total 60	C 17	H 24	N 3	O 15	P 1	0	1

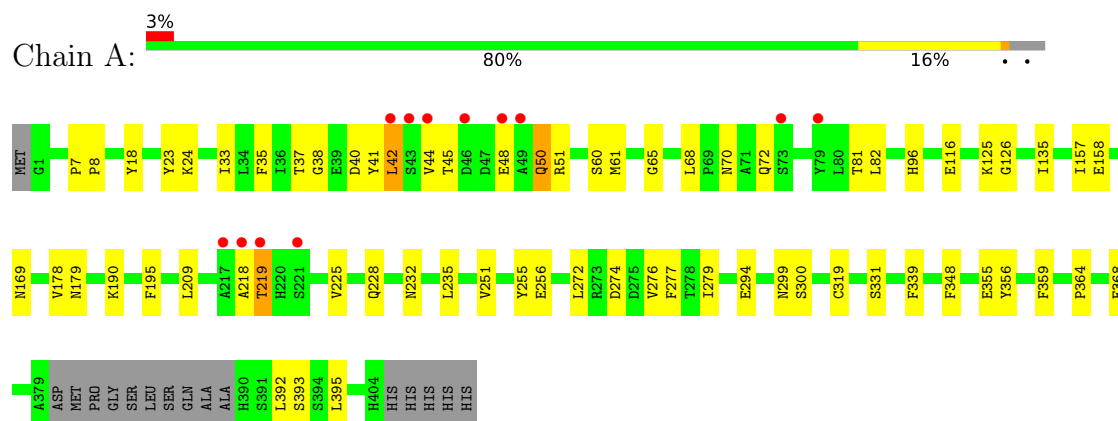
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	44	Total O 44 44	0	0
5	B	41	Total O 41 41	0	0

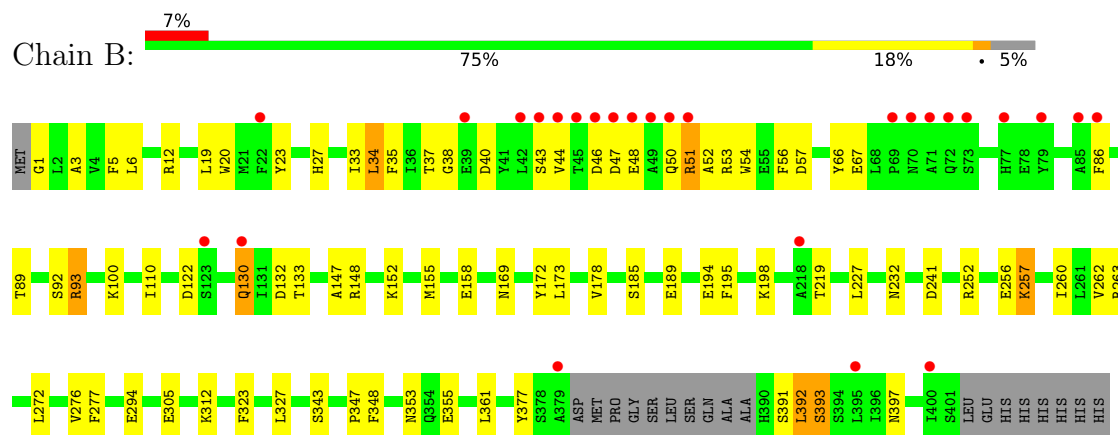
### 3 Residue-property plots [i](#)

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: N-acetyl glucosaminyl transferase



- Molecule 1: N-acetyl glucosaminyl transferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	92.71Å 157.44Å 120.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.99 – 2.25 47.99 – 1.91	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.99-2.25) 95.4 (47.99-1.91)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.24 (at 1.91Å)	Xtriage
Refinement program	PHENIX 1.19_4092	Depositor
R, $R_{free}$	0.203 , 0.244 0.196 , 0.236	Depositor DCC
$R_{free}$ test set	3258 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	62.3	Xtriage
Anisotropy	0.213	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 54.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.004 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	6518	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.17% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CSO, PO4, C5P, CMK

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	0.71	0/3197	0.75	1/4343 (0.0%)
1	B	0.67	1/3169 (0.0%)	0.75	1/4305 (0.0%)
All	All	0.69	1/6366 (0.0%)	0.75	2/8648 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	305	GLU	CB-CG	-5.14	1.42	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	241	ASP	CB-CG-OD1	5.62	123.36	118.30
1	A	209	LEU	CB-CG-CD1	-5.37	101.87	111.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3127	0	3018	53	0
1	B	3100	0	2993	59	0
2	A	15	0	0	2	0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	5	0	0	1	0
3	A	21	12	12	0	0
3	B	21	12	12	1	0
4	A	36	24	24	4	0
4	B	36	24	24	5	0
5	A	44	0	0	1	0
5	B	41	0	0	3	0
All	All	6446	72	6083	113	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 9.

All (113) 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:232:ASN:ND2	2:B:501:PO4:O2	2.01	0.93
1:B:27:HIS:HD2	1:B:66:TYR:HA	1.42	0.83
1:B:27:HIS:CD2	1:B:66:TYR:HA	2.15	0.81
1:A:61:MET:HE1	1:A:68:LEU:HG	1.62	0.80
1:B:257:LYS:HD2	1:B:257:LYS:H	1.47	0.78
1:B:232:ASN:HD21	4:B:502[A]:CMK:H5	1.52	0.75
1:A:48:GLU:HG3	1:A:51:ARG:HH12	1.50	0.74
1:A:232:ASN:ND2	4:A:505[A]:CMK:H3C2	2.09	0.68
1:B:169:ASN:HB3	1:B:348:PHE:HB2	1.76	0.68
1:A:40:ASP:O	1:A:44:VAL:HG13	1.94	0.68
1:A:33:ILE:HD11	1:A:35:PHE:CZ	2.30	0.67
1:A:44:VAL:HG12	1:A:50:GLN:HE22	1.58	0.67
1:A:33:ILE:HD11	1:A:35:PHE:CE1	2.31	0.65
1:B:391:SER:O	1:B:393:SER:N	2.29	0.65
1:B:198:LYS:HD3	1:B:397:ASN:HD21	1.62	0.65
1:B:51:ARG:HA	1:B:56:PHE:CD2	2.32	0.64
1:B:130:GLN:O	1:B:130:GLN:HG3	1.97	0.64
1:A:169:ASN:HB3	1:A:348:PHE:CB	2.27	0.64
1:A:61:MET:CE	1:A:68:LEU:HG	2.29	0.62
1:A:256:GLU:HA	1:A:256:GLU:OE1	2.00	0.62
1:B:252:ARG:HD3	1:B:257:LYS:NZ	2.15	0.61
1:B:198:LYS:HD3	1:B:397:ASN:ND2	2.15	0.61
1:B:169:ASN:HB3	1:B:348:PHE:CB	2.30	0.61
1:A:51:ARG:HB2	1:A:51:ARG:NH1	2.17	0.60
1:B:227:LEU:HD11	1:B:272:LEU:HD11	1.82	0.59
1:B:158:GLU:HB3	1:B:178:VAL:HG21	1.85	0.58

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:225:VAL:HG22	1:A:251:VAL:HG21	1.86	0.57
1:B:37:THR:HG23	1:B:38:GLY:N	2.19	0.57
1:B:155:MET:CE	1:B:361:LEU:HG	2.35	0.56
1:B:173:LEU:C	1:B:173:LEU:HD23	2.26	0.56
1:B:54:TRP:HA	1:B:57:ASP:OD2	2.06	0.56
1:A:23:TYR:OH	1:A:45:THR:HG22	2.05	0.56
1:B:148:ARG:NH1	5:B:602:HOH:O	2.34	0.56
1:A:70:ASN:OD1	1:A:72:GLN:HG3	2.05	0.56
1:B:19:LEU:HD11	1:B:23:TYR:CZ	2.41	0.56
1:A:48:GLU:HA	1:A:51:ARG:HH22	1.71	0.55
1:B:48:GLU:OE1	1:B:48:GLU:HA	2.05	0.55
1:B:5:PHE:O	1:B:6:LEU:HD23	2.06	0.55
1:A:96:HIS:NE2	2:A:502:PO4:O1	2.39	0.55
1:B:155:MET:HE1	1:B:361:LEU:HG	1.89	0.54
1:A:51:ARG:HB2	1:A:51:ARG:CZ	2.38	0.54
1:A:135:ILE:HG23	1:A:157:ILE:HD12	1.90	0.54
1:A:135:ILE:CG2	1:A:157:ILE:HD12	2.39	0.53
1:A:44:VAL:HG12	1:A:50:GLN:NE2	2.23	0.52
1:A:276:VAL:HG13	1:A:277:PHE:CD2	2.45	0.52
1:A:81:THR:HG22	5:A:624:HOH:O	2.10	0.51
1:A:8:PRO:HB3	1:A:38:GLY:HA3	1.92	0.51
1:B:232:ASN:OD1	4:B:502[A]:CMK:H6	2.11	0.51
1:A:169:ASN:HB3	1:A:348:PHE:HB2	1.91	0.50
1:A:48:GLU:HA	1:A:51:ARG:NH2	2.26	0.50
1:A:44:VAL:HA	1:A:50:GLN:HE21	1.77	0.50
1:A:228:GLN:HG2	1:A:300:SER:HB2	1.94	0.50
1:A:190:LYS:NZ	1:B:122:ASP:OD2	2.32	0.49
1:B:48:GLU:HB3	1:B:51:ARG:NE	2.28	0.49
1:A:44:VAL:HA	1:A:50:GLN:NE2	2.27	0.49
1:B:252:ARG:HD3	1:B:257:LYS:HZ3	1.76	0.49
1:B:27:HIS:CE1	1:B:67:GLU:OE1	2.66	0.49
1:B:262:VAL:HG11	1:B:272:LEU:HD11	1.96	0.48
1:B:86:PHE:CZ	1:B:110:ILE:HG21	2.48	0.48
1:B:276:VAL:HG13	1:B:277:PHE:N	2.29	0.48
1:B:347:PRO:HG3	1:B:377:TYR:CZ	2.49	0.47
1:B:3:ALA:HA	1:B:34:LEU:O	2.14	0.47
1:B:89:THR:O	1:B:93:ARG:HG2	2.14	0.47
1:A:274:ASP:OD1	1:A:274:ASP:N	2.41	0.47
1:B:20:TRP:HB3	1:B:54:TRP:CH2	2.49	0.47
1:A:42:LEU:HD23	1:A:42:LEU:N	2.30	0.47
1:B:86:PHE:HZ	1:B:110:ILE:HG21	1.80	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:PHE:CZ	1:A:339:PHE:HB2	2.50	0.47
1:A:125:LYS:HD3	1:A:126:GLY:N	2.29	0.46
1:B:50:GLN:O	1:B:53:ARG:HG2	2.15	0.46
1:A:364:PRO:HB2	1:A:368:GLU:OE1	2.15	0.46
1:B:232:ASN:ND2	4:B:502[A]:CMK:H3C2	2.31	0.46
1:A:82:LEU:HD23	1:A:116:GLU:HG2	1.99	0.45
1:A:279:ILE:O	1:A:279:ILE:HG13	2.15	0.45
1:B:263:ARG:HE	3:B:503[B]:C5P:C2	2.30	0.45
1:B:133:THR:CG2	1:B:361:LEU:HD11	2.46	0.45
1:B:46:ASP:OD1	1:B:47:ASP:N	2.50	0.45
1:B:185:SER:HB3	1:B:323:PHE:HB3	1.99	0.44
1:A:218:ALA:O	1:A:219:THR:CB	2.65	0.44
1:A:24:LYS:NZ	1:A:65:GLY:O	2.47	0.44
1:A:232:ASN:OD1	4:A:505[A]:CMK:H6	2.18	0.43
1:B:1:GLY:N	1:B:132:ASP:OD2	2.51	0.43
1:B:27:HIS:O	1:B:27:HIS:ND1	2.51	0.43
1:A:255:TYR:OH	1:A:294:GLU:OE2	2.37	0.43
1:B:327:LEU:HD23	1:B:327:LEU:HA	1.72	0.43
1:A:48:GLU:CG	1:A:51:ARG:HH12	2.27	0.43
4:B:502[A]:CMK:O5'	4:B:502[A]:CMK:H6C	2.18	0.43
2:A:501:PO4:O1	4:A:505[A]:CMK:H8C1	2.19	0.42
1:B:33:ILE:HG21	1:B:35:PHE:CZ	2.54	0.42
1:B:232:ASN:HD21	4:B:502[A]:CMK:C5	2.27	0.42
1:A:169:ASN:HB3	1:A:348:PHE:HB3	1.98	0.42
1:A:356:TYR:O	1:A:359:PHE:HB3	2.20	0.42
1:B:147:ALA:HB1	1:B:152:LYS:O	2.20	0.42
1:A:37:THR:HG23	1:A:38:GLY:N	2.35	0.42
1:B:12:ARG:HD3	5:B:638:HOH:O	2.19	0.42
1:B:50:GLN:C	1:B:52:ALA:H	2.23	0.41
1:A:178:VAL:O	1:A:179:ASN:HB2	2.20	0.41
1:A:276:VAL:HG13	1:A:277:PHE:N	2.35	0.41
1:A:339:PHE:CD2	1:A:339:PHE:C	2.94	0.41
1:A:392:LEU:O	1:A:392:LEU:HD23	2.21	0.41
1:B:172:TYR:HA	5:B:608:HOH:O	2.20	0.41
1:B:294:GLU:OE1	1:B:312:LYS:HE3	2.20	0.41
1:A:37:THR:OG1	1:A:41:TYR:CD1	2.73	0.41
1:A:392:LEU:HA	1:A:395:LEU:HD12	2.03	0.41
1:A:299:ASN:HB2	1:A:319:CYS:HB3	2.03	0.41
1:B:256:GLU:O	1:B:260:ILE:HG13	2.21	0.41
1:A:7:PRO:HG2	1:A:18:TYR:HE2	1.86	0.40
1:B:155:MET:HE3	1:B:361:LEU:HG	2.03	0.40

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:195:PHE:CE1	1:B:392:LEU:HD21	2.56	0.40
1:B:353:ASN:OD1	1:B:355:GLU:HB2	2.21	0.40
1:A:158:GLU:HG2	4:A:505[A]:CMK:O8	2.21	0.40
1:B:40:ASP:O	1:B:44:VAL:HG13	2.22	0.40
1:B:194:GLU:HB2	1:B:392:LEU:HD23	2.03	0.40

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	389/410 (95%)	372 (96%)	15 (4%)	2 (0%)	29	29
1	B	386/410 (94%)	372 (96%)	11 (3%)	3 (1%)	19	17
All	All	775/820 (94%)	744 (96%)	26 (3%)	5 (1%)	25	25

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	392	LEU
1	A	219	THR
1	B	219	THR
1	A	50	GLN
1	B	51	ARG

### 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	335/348 (96%)	328 (98%)	7 (2%)	53	62
1	B	332/348 (95%)	322 (97%)	10 (3%)	41	50
All	All	667/696 (96%)	650 (98%)	17 (2%)	47	56

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

Mol	Chain	Res	Type
1	A	42	LEU
1	A	60	SER
1	A	235	LEU
1	A	272	LEU
1	A	331	SER
1	A	355	GLU
1	A	393	SER
1	B	34	LEU
1	B	43	SER
1	B	92	SER
1	B	93	ARG
1	B	100	LYS
1	B	130	GLN
1	B	189	GLU
1	B	257	LYS
1	B	343	SER
1	B	393	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	GLN
1	A	290	ASN
1	B	27	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

2 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	$\# Z  > 2$
1	CSO	B	28	1	3,6,7	0.69	0	0,6,8	-	-
1	CSO	A	28	1	3,6,7	0.67	0	0,6,8	-	-

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
1	CSO	B	28	1	-	0/1/5/7	-
1	CSO	A	28	1	-	0/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

8 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	C5P	A	504[B]	-	22,22,22	3.34	12 (54%)	33,33,33	1.50	7 (21%)
2	PO4	B	501	-	4,4,4	0.99	0	6,6,6	0.44	0
2	PO4	A	501	-	4,4,4	1.03	0	6,6,6	0.50	0
4	CMK	A	505[A]	-	35,38,38	3.20	12 (34%)	42,58,58	1.76	12 (28%)
2	PO4	A	502	-	4,4,4	0.76	0	6,6,6	0.66	0
3	C5P	B	503[B]	-	22,22,22	3.29	10 (45%)	33,33,33	1.55	7 (21%)
4	CMK	B	502[A]	-	35,38,38	3.48	12 (34%)	42,58,58	1.99	13 (30%)
2	PO4	A	503	-	4,4,4	0.96	0	6,6,6	0.38	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	C5P	B	503[B]	-	-	0/10/26/26	0/2/2/2
3	C5P	A	504[B]	-	-	2/10/26/26	0/2/2/2
4	CMK	B	502[A]	-	-	12/22/62/62	0/3/3/3
4	CMK	A	505[A]	-	-	10/22/62/62	0/3/3/3

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	502[A]	CMK	O4'-C1'	13.23	1.59	1.41
3	A	504[B]	C5P	P-O5'	11.06	1.95	1.60
4	A	505[A]	CMK	O4'-C1'	10.82	1.56	1.41
3	B	503[B]	C5P	P-O5'	10.51	1.94	1.60
4	B	502[A]	CMK	C3'-C2'	-7.11	1.33	1.53
4	A	505[A]	CMK	C3'-C2'	-7.07	1.34	1.53
4	B	502[A]	CMK	O6-C2	6.42	1.51	1.42
4	A	505[A]	CMK	O4'-C4'	-5.95	1.31	1.45
4	A	505[A]	CMK	O6-C2	5.91	1.50	1.42
4	B	502[A]	CMK	O4'-C4'	-5.68	1.32	1.45

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	503[B]	C5P	C4-N4	5.65	1.47	1.33
3	A	504[B]	C5P	C4-N4	5.15	1.46	1.33
3	B	503[B]	C5P	C2-N3	4.88	1.46	1.36
3	A	504[B]	C5P	C2-N3	4.46	1.45	1.36
4	B	502[A]	CMK	C3'-C4'	4.44	1.64	1.53
4	A	505[A]	CMK	C3'-C4'	4.38	1.64	1.53
4	B	502[A]	CMK	C4C-N4C	3.95	1.46	1.35
4	A	505[A]	CMK	O2'-C2'	3.88	1.52	1.43
4	B	502[A]	CMK	C3-C4	-3.82	1.47	1.53
4	B	502[A]	CMK	O2'-C2'	3.80	1.51	1.43
4	A	505[A]	CMK	C4C-N4C	3.79	1.46	1.35
4	B	502[A]	CMK	PA-O2	3.59	1.69	1.60
3	B	503[B]	C5P	C1'-N1	3.54	1.57	1.47
4	A	505[A]	CMK	C3-C4	-3.48	1.47	1.53
3	A	504[B]	C5P	C5-C4	3.34	1.50	1.42
3	A	504[B]	C5P	C3'-C4'	3.23	1.61	1.53
3	A	504[B]	C5P	C1'-N1	3.23	1.56	1.47
4	A	505[A]	CMK	PA-O2	3.21	1.68	1.60
3	B	503[B]	C5P	C5'-C4'	3.02	1.61	1.51
4	A	505[A]	CMK	PA-O5'	3.00	1.71	1.59
3	B	503[B]	C5P	C3'-C4'	2.96	1.60	1.53
3	B	503[B]	C5P	C5-C4	2.94	1.49	1.42
3	A	504[B]	C5P	C2-N1	2.91	1.46	1.40
3	B	503[B]	C5P	O5'-C5'	-2.76	1.34	1.44
4	A	505[A]	CMK	O6-C6	2.71	1.48	1.44
3	A	504[B]	C5P	O5'-C5'	-2.70	1.34	1.44
4	B	502[A]	CMK	PA-O5'	2.55	1.69	1.59
3	B	503[B]	C5P	C2-N1	2.51	1.45	1.40
4	B	502[A]	CMK	O6-C6	2.42	1.47	1.44
4	A	505[A]	CMK	C4-C5	-2.37	1.49	1.52
3	A	504[B]	C5P	C5'-C4'	2.30	1.58	1.51
4	B	502[A]	CMK	C2-C1	-2.20	1.49	1.54
3	B	503[B]	C5P	C6-C5	2.15	1.40	1.35
3	A	504[B]	C5P	C2'-C1'	2.12	1.60	1.53
3	A	504[B]	C5P	C6-C5	2.10	1.39	1.35
3	A	504[B]	C5P	O2'-C2'	-2.05	1.38	1.43

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	502[A]	CMK	C3-C4-C5	4.39	115.13	110.84
4	B	502[A]	CMK	C3'-C2'-C1'	4.28	107.42	100.98

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	505[A]	CMK	C4C-N3C-C2C	4.19	120.59	116.34
4	A	505[A]	CMK	C3'-C2'-C1'	4.14	107.21	100.98
4	B	502[A]	CMK	O6-C6-C5	4.05	114.27	108.52
4	B	502[A]	CMK	C5'-C4'-C3'	-3.72	101.23	115.18
4	A	505[A]	CMK	O6-C6-C5	3.64	113.69	108.52
4	B	502[A]	CMK	O2'-C2'-C1'	-3.34	98.50	110.85
3	A	504[B]	C5P	O5'-P-O1P	-3.27	97.30	106.47
4	B	502[A]	CMK	C4C-N3C-C2C	3.11	119.50	116.34
4	A	505[A]	CMK	O1Y-C1-C2	-2.97	114.13	123.70
3	B	503[B]	C5P	O3'-C3'-C4'	2.91	119.46	111.05
4	A	505[A]	CMK	O4'-C1'-C2'	-2.89	102.71	106.93
3	B	503[B]	C5P	C4-N3-C2	2.84	124.84	120.25
4	A	505[A]	CMK	C5'-C4'-C3'	-2.83	104.56	115.18
4	B	502[A]	CMK	O4'-C4'-C5'	2.82	118.64	109.37
3	B	503[B]	C5P	O2P-P-O5'	-2.79	99.30	106.73
3	A	504[B]	C5P	C4-N3-C2	2.78	124.74	120.25
4	B	502[A]	CMK	O6-C2-C3	2.75	115.20	111.24
4	B	502[A]	CMK	O4'-C1'-C2'	-2.74	102.92	106.93
4	B	502[A]	CMK	O1A-PA-O2	2.67	117.22	106.43
3	A	504[B]	C5P	O3'-C3'-C4'	2.53	118.37	111.05
3	A	504[B]	C5P	O2P-P-O3P	2.37	116.68	107.64
4	A	505[A]	CMK	O5'-C5'-C4'	2.35	117.10	108.99
3	A	504[B]	C5P	O3P-P-O5'	-2.35	100.47	106.73
3	A	504[B]	C5P	O4'-C4'-C5'	2.29	116.89	109.37
3	B	503[B]	C5P	P-O5'-C5'	2.25	124.50	118.30
3	B	503[B]	C5P	O4'-C4'-C5'	2.23	116.70	109.37
4	A	505[A]	CMK	O4'-C4'-C3'	2.21	109.49	105.11
4	A	505[A]	CMK	O4'-C4'-C5'	2.21	116.63	109.37
4	B	502[A]	CMK	O3'-C3'-C4'	2.18	117.35	111.05
3	A	504[B]	C5P	C5'-C4'-C3'	-2.18	107.03	115.18
4	A	505[A]	CMK	O2'-C2'-C1'	-2.18	102.82	110.85
3	B	503[B]	C5P	C5'-C4'-C3'	-2.17	107.04	115.18
3	B	503[B]	C5P	O2'-C2'-C3'	-2.17	104.80	111.82
4	A	505[A]	CMK	C8-C7-C6	-2.12	107.87	112.17
4	B	502[A]	CMK	C7-C6-C5	-2.11	110.53	114.03
4	B	502[A]	CMK	C4-C5-C6	2.08	114.58	110.41
4	A	505[A]	CMK	O3'-C3'-C2'	2.04	118.43	111.82

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	504[B]	C5P	C5'-O5'-P-O1P
4	A	505[A]	CMK	C5'-O5'-PA-O1A
4	A	505[A]	CMK	O6-C6-C7-C8
4	A	505[A]	CMK	O6-C6-C7-O7
4	B	502[A]	CMK	O1X-C1-C2-O6
4	B	502[A]	CMK	O6-C6-C7-C8
4	B	502[A]	CMK	O6-C6-C7-O7
4	B	502[A]	CMK	C5-C6-C7-C8
4	B	502[A]	CMK	C5-C6-C7-O7
4	B	502[A]	CMK	O7-C7-C8-O8
4	A	505[A]	CMK	C5'-O5'-PA-O2
4	B	502[A]	CMK	C5'-O5'-PA-O2
4	B	502[A]	CMK	C6-C7-C8-O8
4	A	505[A]	CMK	O1Y-C1-C2-O2
4	B	502[A]	CMK	O1Y-C1-C2-O2
4	A	505[A]	CMK	C5'-O5'-PA-O2A
4	B	502[A]	CMK	C5'-O5'-PA-O1A
4	A	505[A]	CMK	O7-C7-C8-O8
3	A	504[B]	C5P	C5'-O5'-P-O3P
4	A	505[A]	CMK	O1X-C1-C2-O6
4	A	505[A]	CMK	C2-O2-PA-O2A
4	B	502[A]	CMK	C2-O2-PA-O2A
4	B	502[A]	CMK	C5'-O5'-PA-O2A
4	A	505[A]	CMK	C5-C6-C7-C8

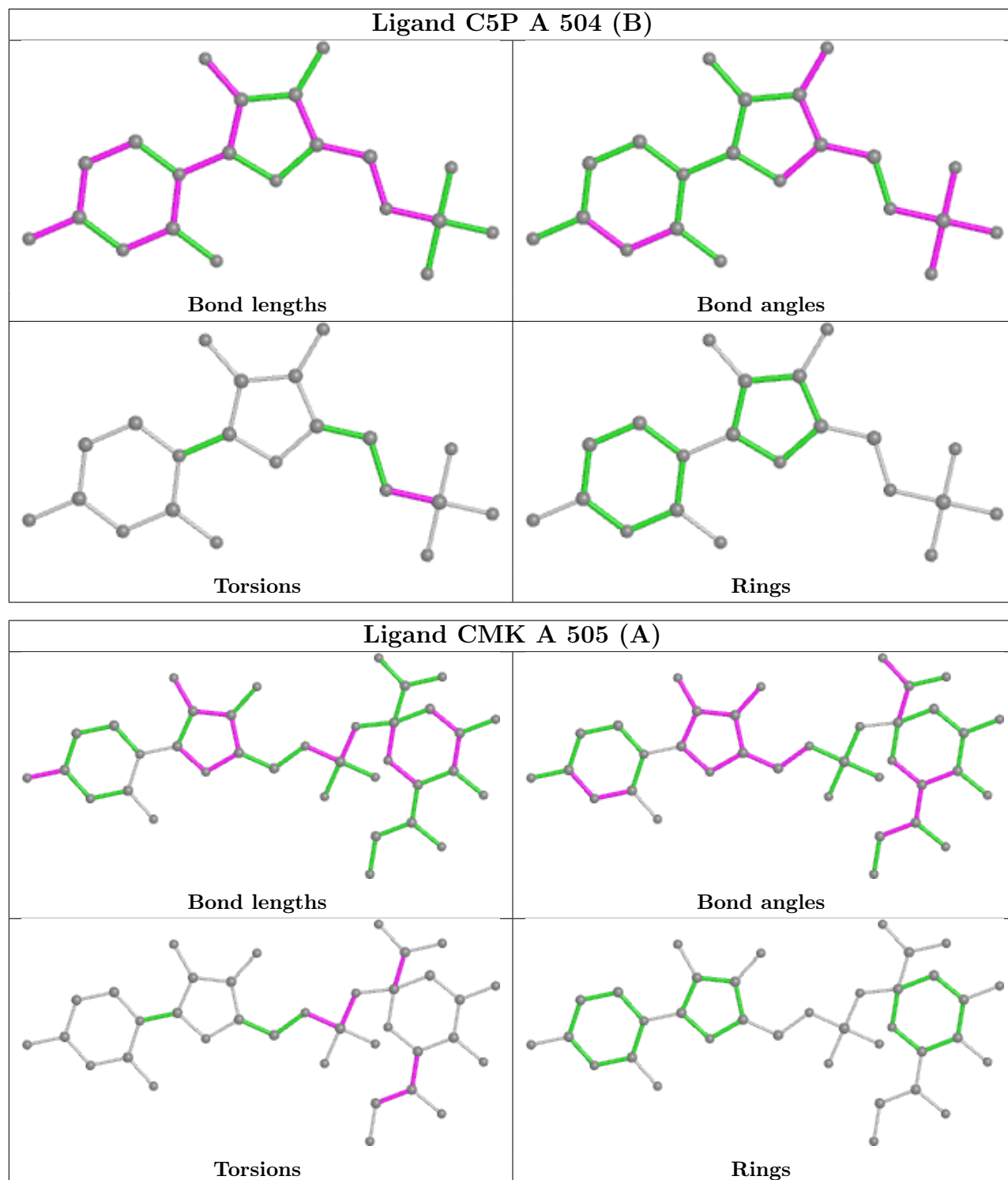
There are no ring outliers.

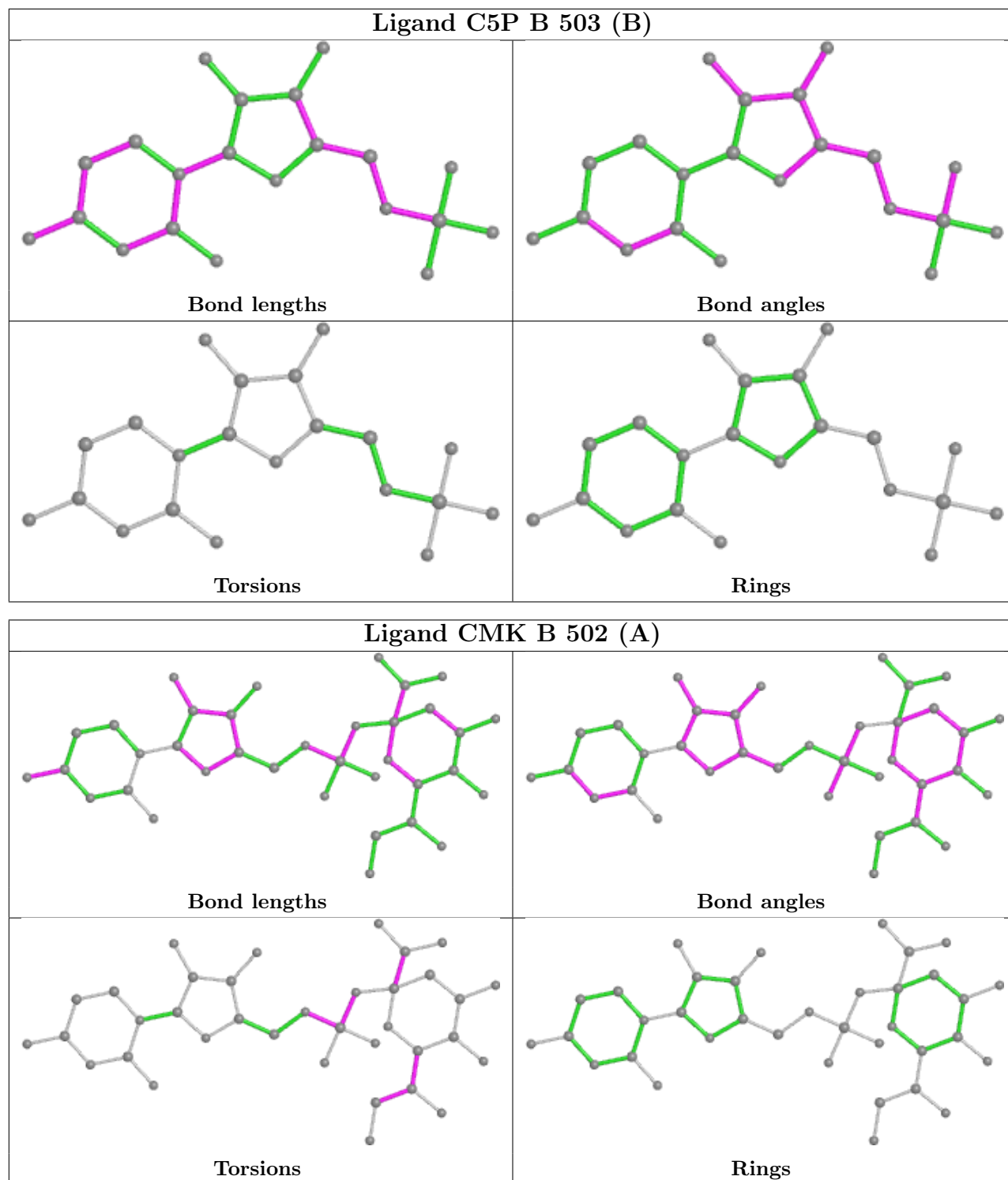
6 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	PO4	1	0
2	A	501	PO4	1	0
4	A	505[A]	CMK	4	0
2	A	502	PO4	1	0
3	B	503[B]	C5P	1	0
4	B	502[A]	CMK	5	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 ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	393/410 (95%)	0.05	12 (3%) 49 52	48, 67, 117, 191	0
1	B	390/410 (95%)	0.38	27 (6%) 16 18	47, 73, 128, 204	0
All	All	783/820 (95%)	0.21	39 (4%) 28 31	47, 69, 125, 204	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	45	THR	10.5
1	A	217	ALA	9.8
1	B	46	ASP	6.9
1	B	22	PHE	5.7
1	B	50	GLN	5.5
1	B	44	VAL	5.3
1	A	49	ALA	4.8
1	B	48	GLU	4.7
1	A	218	ALA	4.5
1	A	48	GLU	4.2
1	A	219	THR	3.9
1	B	86	PHE	3.9
1	B	47	ASP	3.5
1	B	51	ARG	3.5
1	B	39	GLU	3.5
1	B	43	SER	3.4
1	B	85	ALA	3.4
1	B	71	ALA	3.3
1	B	79	TYR	3.3
1	A	43	SER	3.0
1	B	72	GLN	2.9
1	B	379	ALA	2.9
1	B	73	SER	2.9
1	B	77	HIS	2.8

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	69	PRO	2.7
1	A	44	VAL	2.7
1	B	70	ASN	2.7
1	B	218	ALA	2.6
1	A	73	SER	2.6
1	B	49	ALA	2.6
1	B	395	LEU	2.6
1	B	130	GLN	2.5
1	B	42	LEU	2.5
1	B	123	SER	2.4
1	A	221	SER	2.4
1	B	400	ILE	2.3
1	A	42	LEU	2.2
1	A	79	TYR	2.1
1	A	46	ASP	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	CSO	A	28	7/8	0.87	0.12	81,85,95,95	0
1	CSO	B	28	7/8	0.92	0.10	94,98,101,105	0

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	PO4	A	502	5/5	0.82	0.24	122,132,132,133	0

*Continued on next page...*

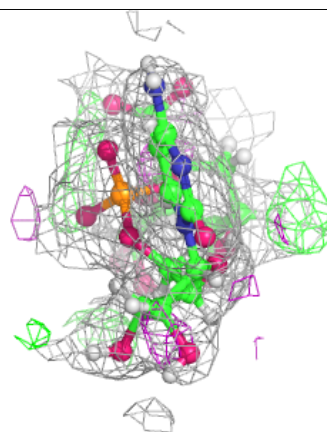
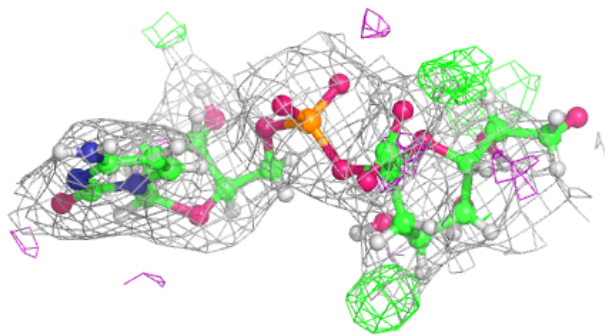
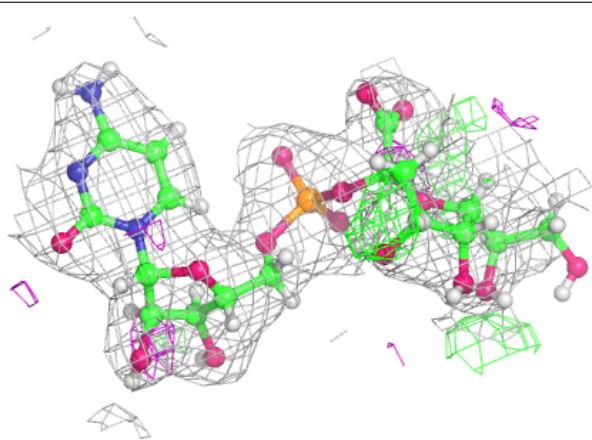
*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PO4	B	501	5/5	0.89	0.20	139,147,150,151	0
2	PO4	A	501	5/5	0.92	0.19	129,129,130,130	0
2	PO4	A	503	5/5	0.93	0.25	154,154,155,157	0
4	CMK	A	505[A]	36/36	0.94	0.15	56,69,94,95	60
4	CMK	B	502[A]	36/36	0.95	0.16	58,71,101,108	60
3	C5P	A	504[B]	21/21	0.96	0.14	55,59,72,72	33
3	C5P	B	503[B]	21/21	0.97	0.14	58,60,73,74	33

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 CMK A 505 (A):**

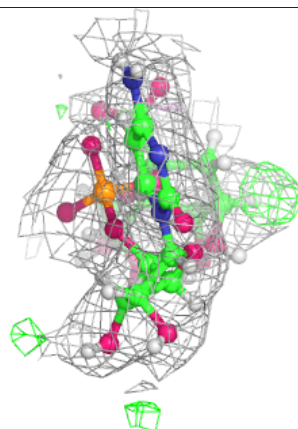
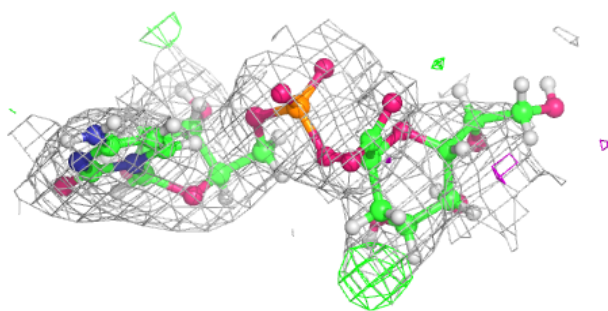
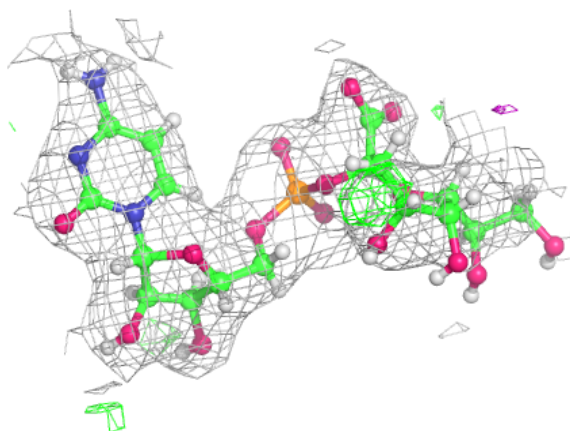
2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)





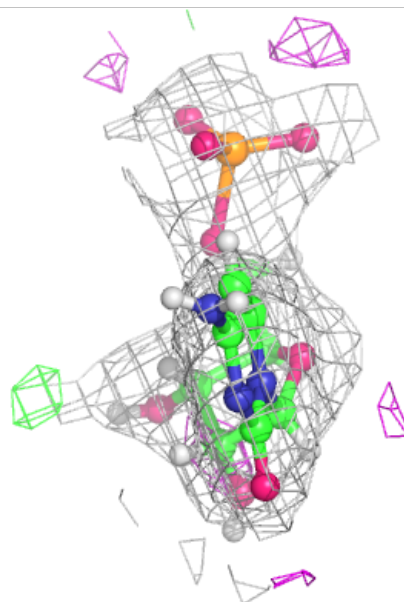
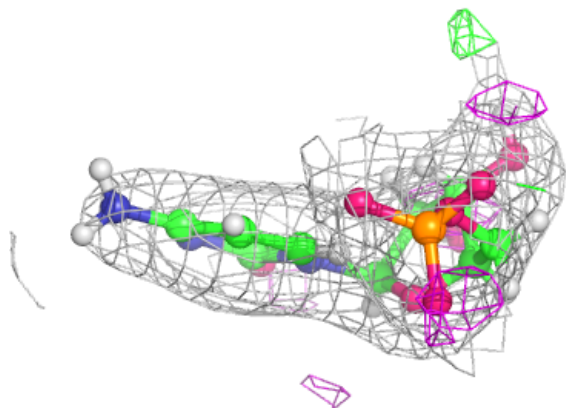
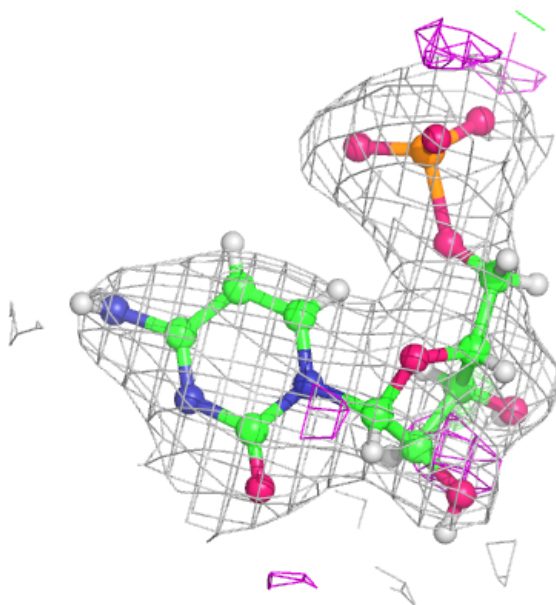
**Electron density around CMK B 502 (A):**

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



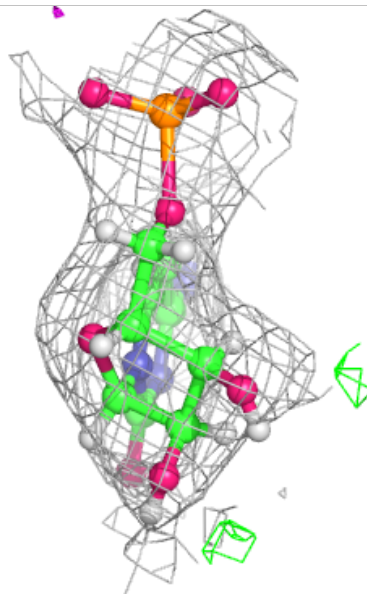
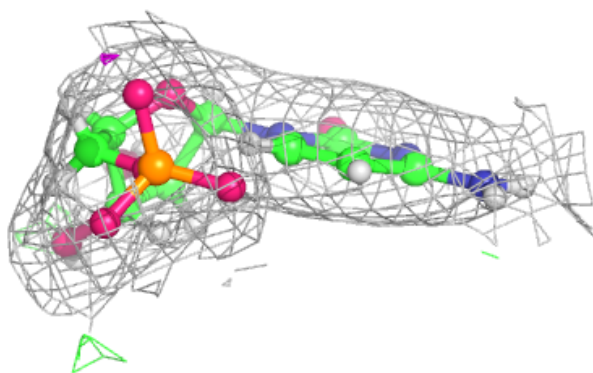
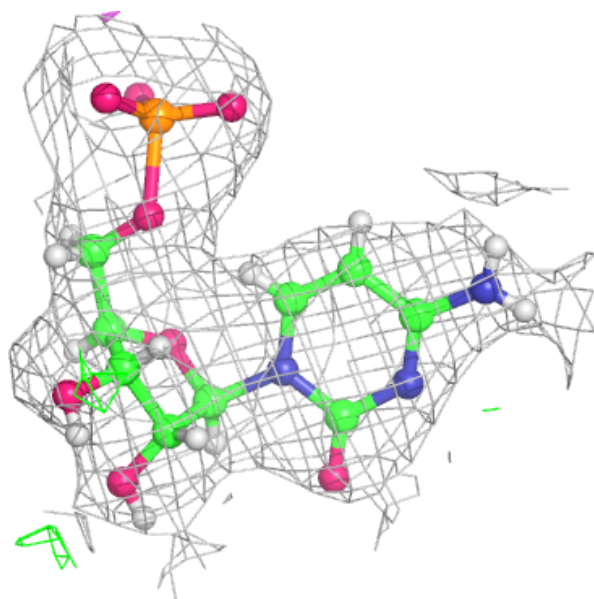
**Electron density around C5P A 504 (B):**

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



**Electron density around C5P B 503 (B):**

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



## 6.5 Other polymers ⓘ

There are no such residues in this entry.