wwPDB X-ray Structure Validation Summary Report (i)

Sep 14, 2023 – 07:42 AM EDT

PDB ID	:	1XPK
Title	:	CRYSTAL STRUCTURE OF STAPHYLOCOCCUS AUREUS HMG-COA SYNTHASE WITH HMG-CoA AND WITH ACETOACETYL-COA AND ACETYLATED CYSTEINE
Authors	:	Theisen, M.J.; Misra, I.; Saadat, D.; Campobasso, N.; Miziorko, H.M.; Harrison, D.H.T.
Deposited on	:	2004-10-08
Resolution	:	2.00 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 (i) 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 (i)) were used in the production of this report:

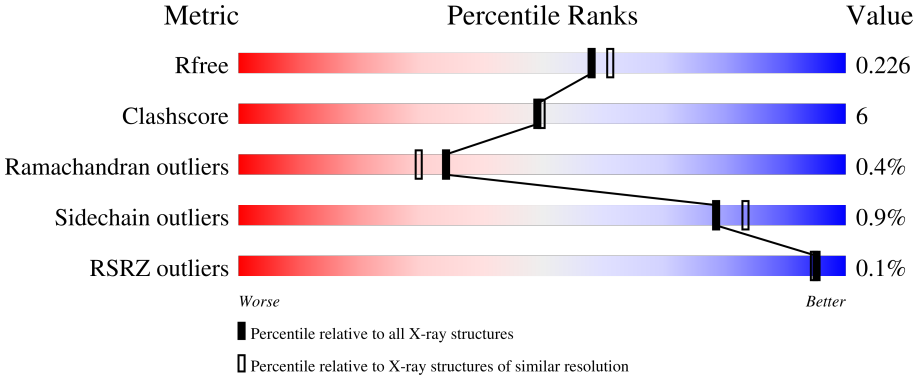
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 <=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	389	85% 14% •
1	B	389	86% 13% •
1	D	389	85% 14%
2	C	388	88% 12%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	SCY	A	111[A]	-	-	X	-
1	SCY	D	111[A]	-	-	X	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 12897 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 3-hydroxy-3-methylglutaryl CoA synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	387	2998	1910	498	579	11	0	2	0
1	B	387	2978	1892	495	581	10	0	1	0
1	D	387	2991	1897	498	585	11	0	2	0

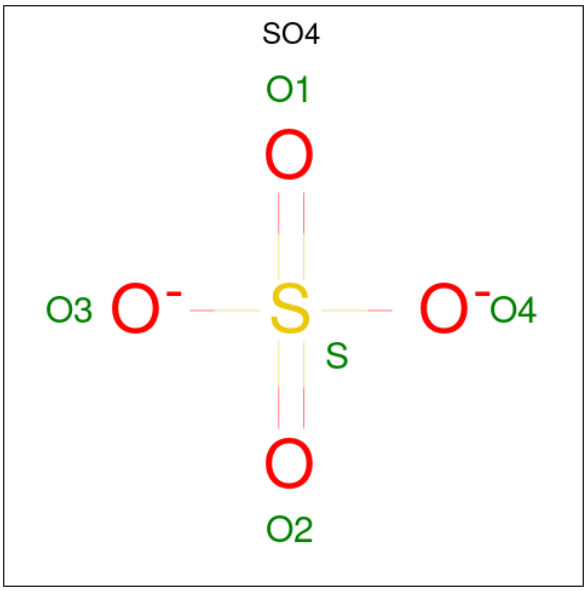
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	111	SCY	CYS	microheterogeneity	UNP Q79ZY6
D	111	SCY	CYS	microheterogeneity	UNP Q79ZY6

- Molecule 2 is a protein called 3-hydroxy-3-methylglutaryl CoA synthase.

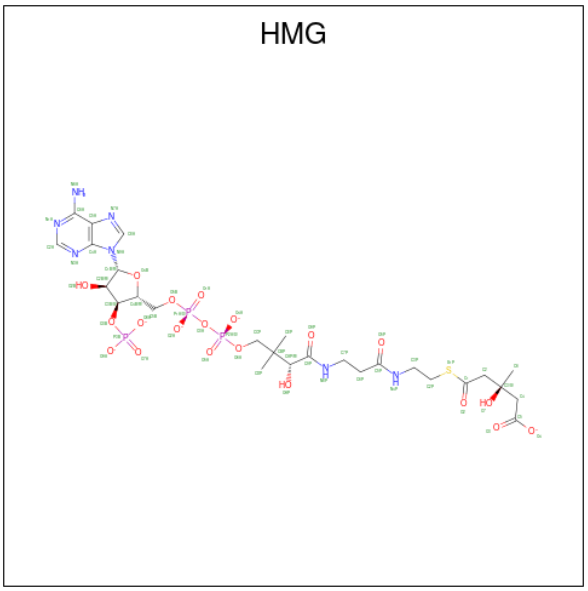
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	387	2977	1895	497	575	10	0	1	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



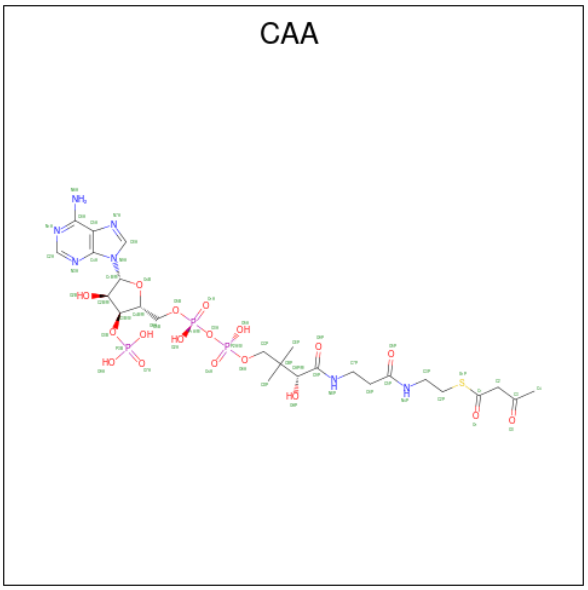
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0

- Molecule 4 is 3-HYDROXY-3-METHYLGLUTARYL-COENZYME A (three-letter code: HMG) (formula: $C_{27}H_{39}N_7O_{20}P_3S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
4	A	1	58	27	7	20	3	1	0	1
4	C	1	58	27	7	20	3	1	0	0
4	D	1	58	27	7	20	3	1	0	1

- Molecule 5 is ACETOACETYL-COENZYME A (three-letter code: CAA) (formula: $C_{25}H_{40}N_7O_{18}P_3S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
5	A	1	54	25	7	18	3	1	0	1

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
5	B	1	54	25	7	18	3	1	0	0
5	D	1	54	25	7	18	3	1	0	1

- Molecule 6 is water.

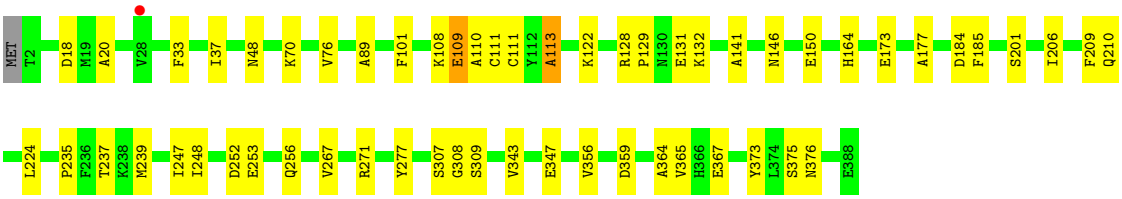
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	154	154	154	0	0
6	B	137	137	137	0	0
6	C	141	141	141	0	0
6	D	145	145	145	0	0

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.

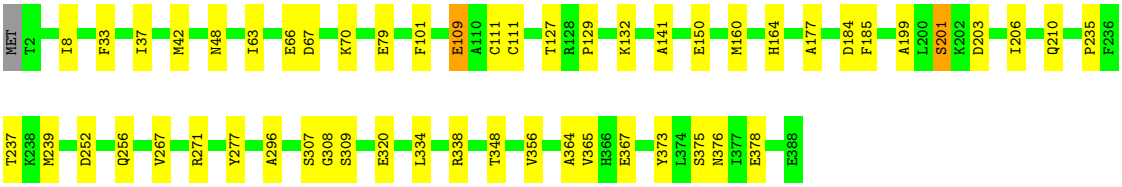
• Molecule 1: 3-hydroxy-3-methylglutaryl CoA synthase

Chain A: 85% 14%



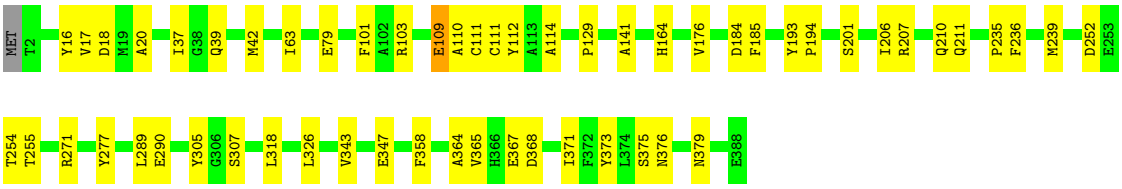
• Molecule 1: 3-hydroxy-3-methylglutaryl CoA synthase

Chain B: 86% 13%



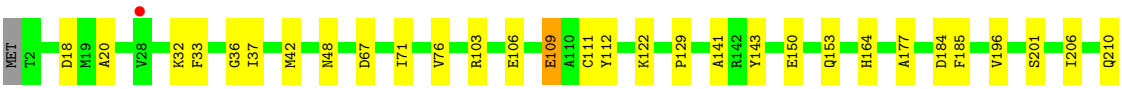
• Molecule 1: 3-hydroxy-3-methylglutaryl CoA synthase

Chain D: 85% 14%



• Molecule 2: 3-hydroxy-3-methylglutaryl CoA synthase

Chain C: 88% 12%



T237
V267
R271
Y277
S307
A329
V343
Y346
E347
F358
V365
Y373
L374
S375
N376
I377
E378
H385
E388

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	64.27Å 84.61Å 94.63Å 84.25° 72.52° 70.44°	Depositor
Resolution (Å)	35.00 – 2.00 79.73 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (35.00-2.00) 76.7 (79.73-2.00)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	0.03	Depositor
$< I/\sigma(I) >$ [1]	5.47 (at 2.00Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.198 , 0.234 0.191 , 0.226	Depositor DCC
R_{free} test set	4609 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	25.4	Xtriage
Anisotropy	0.366	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 43.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.006 for -h,-k,-h+l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	12897	wwPDB-VP
Average B, all atoms (Å^2)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.27% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: SCY, HMG, SO4, CAA

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	0.34	0/3050	0.60	1/4139 (0.0%)
1	B	0.33	0/3029	0.59	0/4111
1	D	0.33	0/3043	0.59	0/4132
2	C	0.33	0/3039	0.59	0/4127
All	All	0.33	0/12161	0.59	1/16509 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	113	ALA	N-CA-C	5.08	124.72	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	2998	0	2843	34	0
1	B	2978	0	2793	34	0
1	D	2991	0	2814	42	0
2	C	2977	0	2813	30	0
3	A	10	0	0	0	0
3	B	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	10	0	0	0	0
3	D	10	0	0	0	0
4	A	58	0	39	0	0
4	C	58	0	39	2	0
4	D	58	0	39	0	0
5	A	54	0	36	2	0
5	B	54	0	36	0	0
5	D	54	0	36	2	0
6	A	154	0	0	2	0
6	B	137	0	0	2	0
6	C	141	0	0	2	0
6	D	145	0	0	2	0
All	All	12897	0	11488	135	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 6.

The worst 5 of 135 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:376:ASN:HD21	1:B:378:GLU:HG3	1.38	0.87
1:B:376:ASN:ND2	1:B:378:GLU:HG3	1.98	0.79
1:B:79:GLU:OE2	1:B:111:SCY:HE2	1.87	0.74
1:A:111[A]:SCY:HE3	5:A:1402[A]:CAA:H4'3	1.68	0.73
1:A:237:THR:HG22	1:A:267:VAL:HB	1.70	0.71

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	385/389 (99%)	361 (94%)	21 (6%)	3 (1%)	19	13
1	B	385/389 (99%)	365 (95%)	19 (5%)	1 (0%)	41	37
1	D	385/389 (99%)	365 (95%)	19 (5%)	1 (0%)	41	37
2	C	386/388 (100%)	366 (95%)	19 (5%)	1 (0%)	41	37
All	All	1541/1555 (99%)	1457 (94%)	78 (5%)	6 (0%)	34	30

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	109	GLU
1	B	109	GLU
2	C	109	GLU
1	A	113	ALA
1	D	109	GLU

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	294/319 (92%)	291 (99%)	3 (1%)	76	81
1	B	291/319 (91%)	288 (99%)	3 (1%)	76	81
1	D	296/319 (93%)	295 (100%)	1 (0%)	92	95
2	C	291/319 (91%)	288 (99%)	3 (1%)	76	81
All	All	1172/1276 (92%)	1162 (99%)	10 (1%)	78	83

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	346	TYR
2	C	385	HIS
1	D	109	GLU
1	B	109	GLU
1	B	127	THR

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

Mol	Chain	Res	Type
2	C	325	HIS
2	C	336	ASN
1	D	191	HIS
2	C	376	ASN
1	B	376	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)

3 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	SCY	A	111[A]	1	7,8,9	0.63	0	3,9,11	0.73	0
1	SCY	D	111[A]	1	7,8,9	0.55	0	3,9,11	0.72	0
1	SCY	B	111	1	7,8,9	0.75	0	3,9,11	0.79	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
1	SCY	A	111[A]	1	-	2/5/7/9	-
1	SCY	D	111[A]	1	-	2/5/7/9	-
1	SCY	B	111	1	-	2/5/7/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	111[A]	SCY	OCD-CD-SG-CB
1	D	111[A]	SCY	OCD-CD-SG-CB
1	A	111[A]	SCY	CE-CD-SG-CB
1	B	111	SCY	OCD-CD-SG-CB
1	D	111[A]	SCY	CE-CD-SG-CB

There are no ring outliers.

3 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	111[A]	SCY	5	0
1	D	111[A]	SCY	8	0
1	B	111	SCY	2	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

14 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	$\#\|Z\| > 2$
4	HMG	A	1401[B]	-	52,60,60	0.79	0	62,90,90	1.33	5 (8%)
4	HMG	C	3401	-	52,60,60	0.80	1 (1%)	62,90,90	1.31	4 (6%)
4	HMG	D	4401[B]	-	52,60,60	0.77	0	62,90,90	1.32	4 (6%)
5	CAA	D	4402[A]	-	47,56,56	0.72	0	60,83,83	1.34	4 (6%)
5	CAA	B	2402	-	47,56,56	0.74	1 (2%)	60,83,83	1.31	4 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	SO4	B	2502	-	4,4,4	0.25	0	6,6,6	0.05	0
3	SO4	C	3501	-	4,4,4	0.27	0	6,6,6	0.10	0
3	SO4	C	3502	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	A	1502	-	4,4,4	0.26	0	6,6,6	0.07	0
3	SO4	B	2501	-	4,4,4	0.25	0	6,6,6	0.11	0
3	SO4	D	4501	-	4,4,4	0.24	0	6,6,6	0.06	0
3	SO4	A	1501	-	4,4,4	0.26	0	6,6,6	0.08	0
5	CAA	A	1402[A]	-	47,56,56	0.73	1 (2%)	60,83,83	1.33	4 (6%)
3	SO4	D	4502	-	4,4,4	0.26	0	6,6,6	0.05	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	HMG	A	1401[B]	-	-	15/56/77/77	0/3/3/3
4	HMG	D	4401[B]	-	-	11/56/77/77	0/3/3/3
5	CAA	D	4402[A]	-	-	12/50/71/71	0/3/3/3
5	CAA	B	2402	-	-	9/50/71/71	0/3/3/3
4	HMG	C	3401	-	-	11/56/77/77	0/3/3/3
5	CAA	A	1402[A]	-	-	13/50/71/71	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	3401	HMG	C1-S1P	2.38	1.81	1.76
5	B	2402	CAA	C1-S1P	2.16	1.81	1.76
5	A	1402[A]	CAA	C1-S1P	2.04	1.81	1.76

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	C	3401	HMG	P1A-O3A-P2A	-6.80	109.48	132.83
5	B	2402	CAA	P2A-O3A-P1A	-6.75	109.68	132.83
5	D	4402[A]	CAA	P2A-O3A-P1A	-6.56	110.31	132.83
4	D	4401[B]	HMG	P1A-O3A-P2A	-6.56	110.31	132.83
4	A	1401[B]	HMG	P1A-O3A-P2A	-6.41	110.84	132.83

There are no chirality outliers.

5 of 71 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1401[B]	HMG	CCP-O6A-P2A-O3A
4	A	1401[B]	HMG	C5B-O5B-P1A-O3A
4	A	1401[B]	HMG	O9P-C9P-CAP-OAP
4	A	1401[B]	HMG	N8P-C9P-CAP-OAP
4	C	3401	HMG	C5B-O5B-P1A-O3A

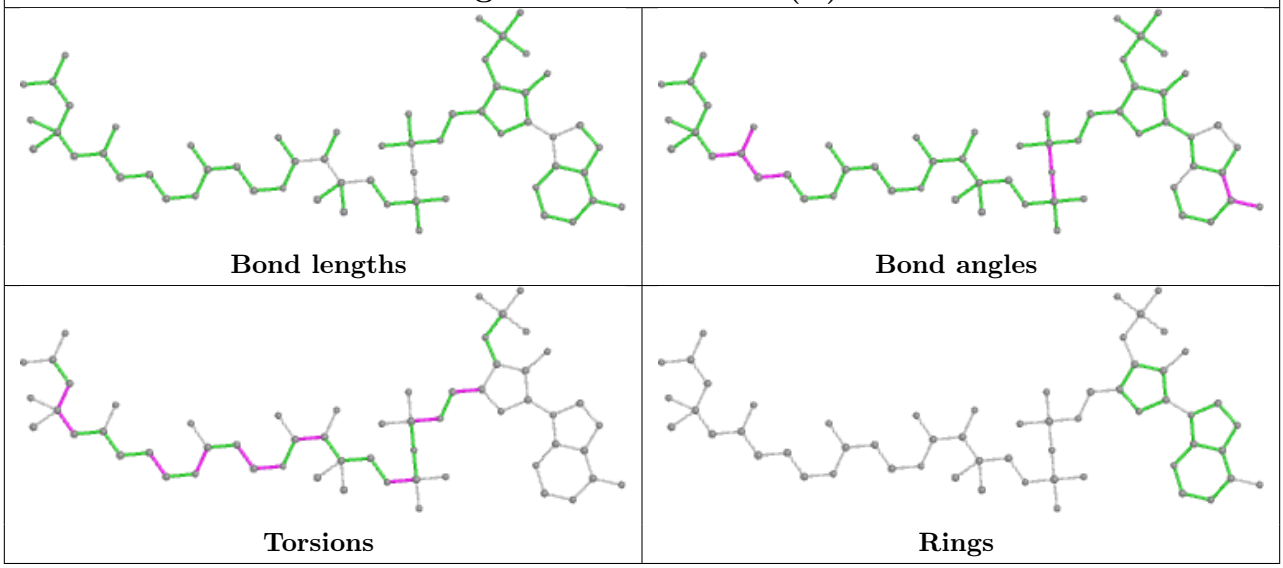
There are no ring outliers.

3 monomers are involved in 6 short contacts:

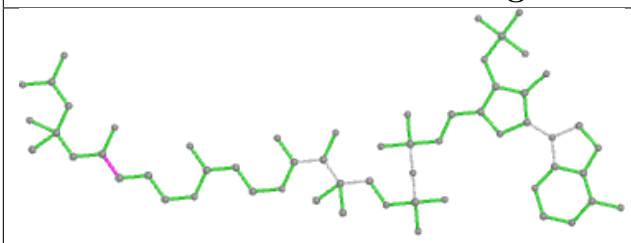
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	3401	HMG	2	0
5	D	4402[A]	CAA	2	0
5	A	1402[A]	CAA	2	0

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 then 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.

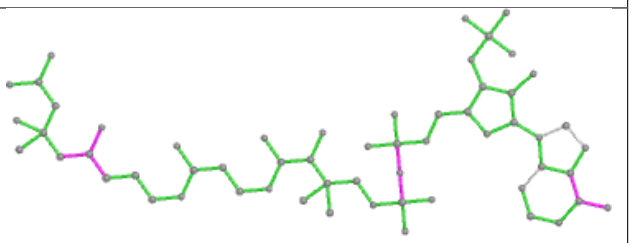
Ligand HMG A 1401 (B)



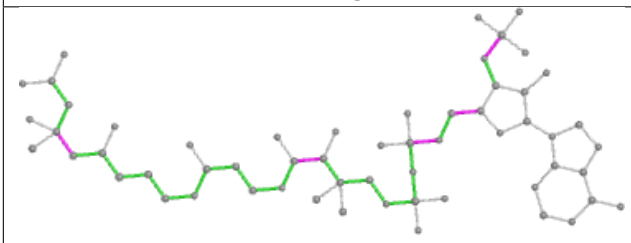
Ligand HMG C 3401



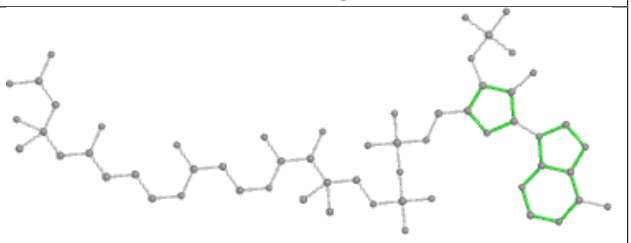
Bond lengths



Bond angles

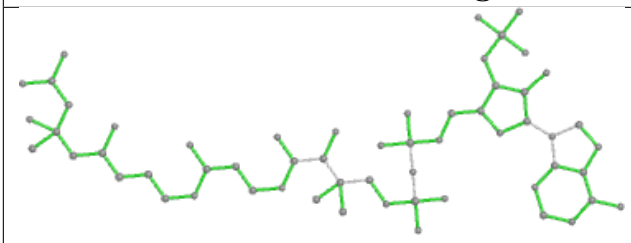


Torsions

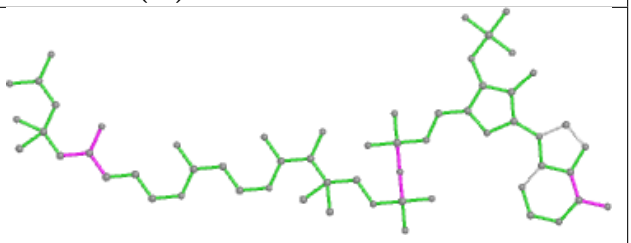


Rings

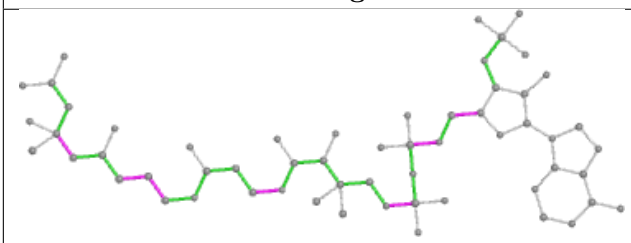
Ligand HMG D 4401 (B)



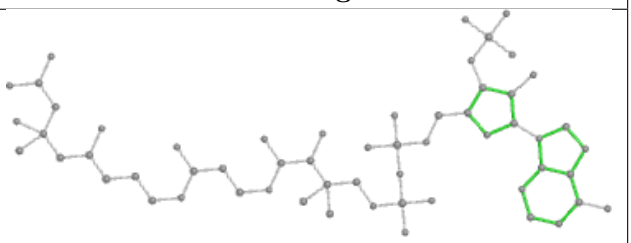
Bond lengths



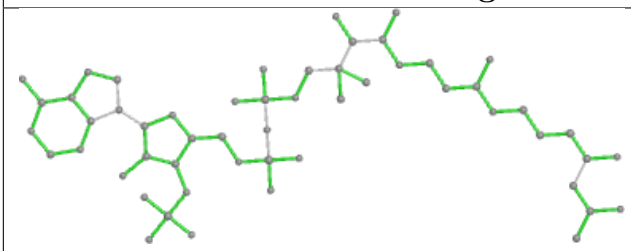
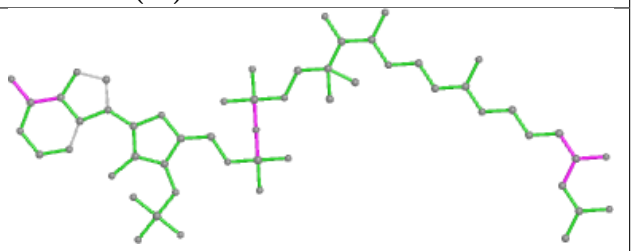
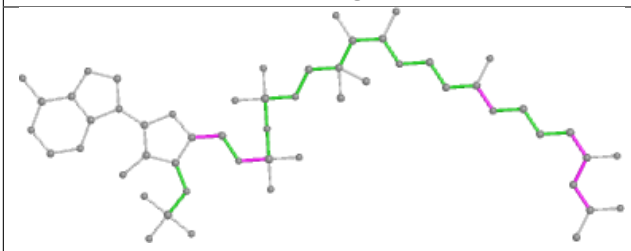
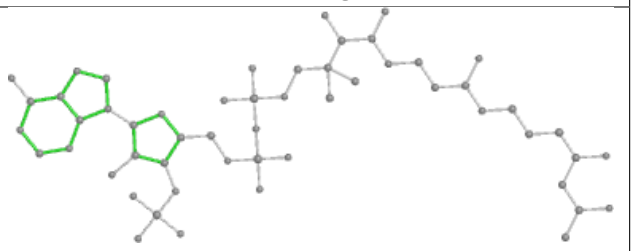
Bond angles

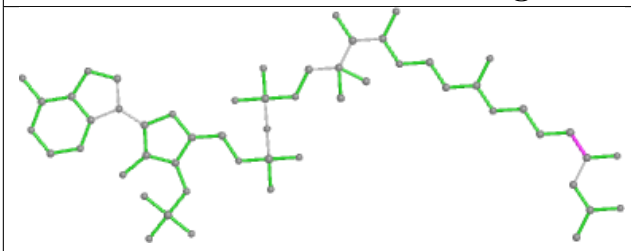
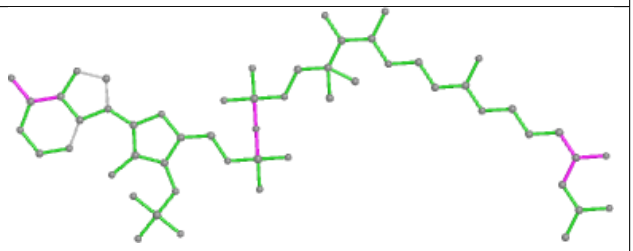
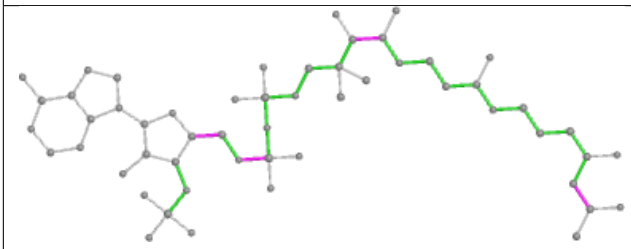
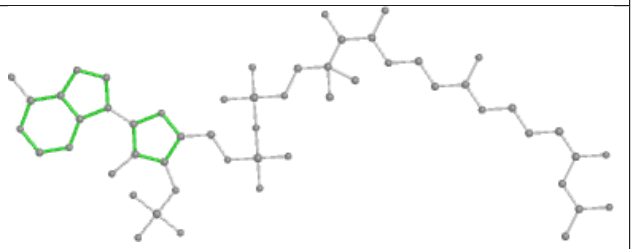


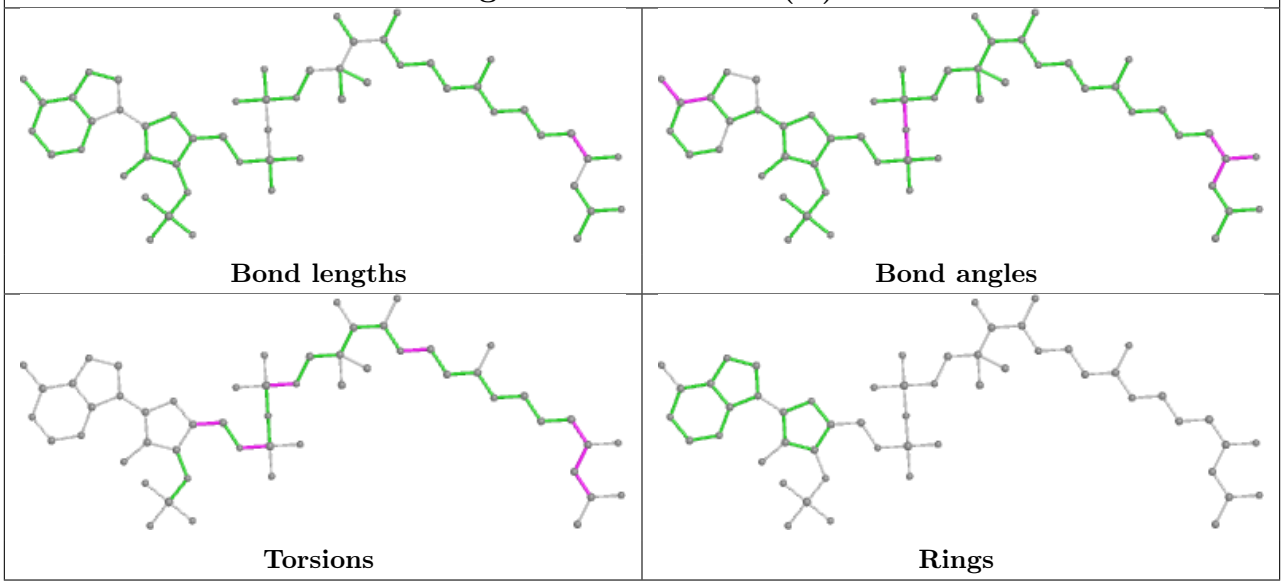
Torsions



Rings

Ligand CAA D 4402 (A)	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CAA B 2402	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CAA A 1402 (A)	
 Bond lengths	Bond angles
Torsions	Rings

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	386/389 (99%)	-0.25	1 (0%)	94	93	15, 25, 42, 47	0
1	B	386/389 (99%)	-0.17	0	100	100	15, 26, 43, 49	0
1	D	386/389 (99%)	-0.22	0	100	100	15, 26, 42, 46	0
2	C	387/388 (99%)	-0.19	1 (0%)	94	93	14, 26, 42, 48	0
All	All	1545/1555 (99%)	-0.21	2 (0%)	95	95	14, 26, 42, 49	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	28	VAL	3.0
1	A	28	VAL	2.7

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, 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
1	SCY	B	111	9/10	0.92	0.12	22,24,35,35	0
1	SCY	D	111[A]	9/10	0.93	0.12	24,25,32,33	9
1	SCY	A	111[A]	9/10	0.95	0.11	20,21,30,32	9

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

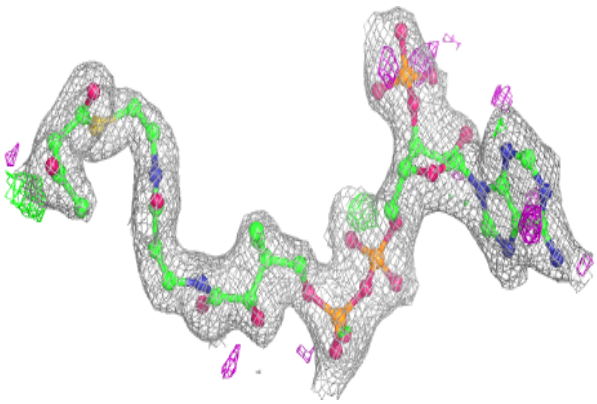
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

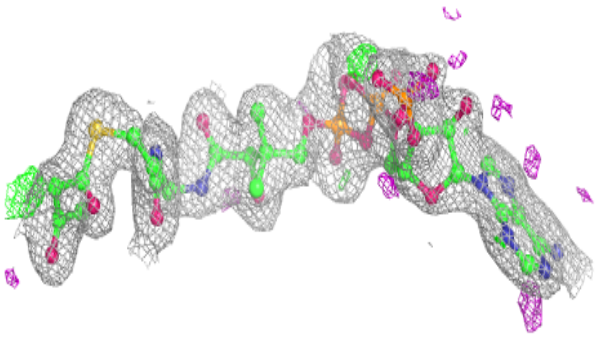
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	SO4	C	3502	5/5	0.84	0.21	82,83,83,83	0
5	CAA	B	2402	54/54	0.92	0.12	30,42,56,57	0
3	SO4	A	1502	5/5	0.93	0.20	78,79,79,79	0
4	HMG	C	3401	58/58	0.93	0.12	27,38,54,56	0
3	SO4	B	2502	5/5	0.93	0.18	88,88,88,88	0
3	SO4	D	4502	5/5	0.94	0.17	75,75,75,76	0
4	HMG	D	4401[B]	58/58	0.94	0.12	20,42,55,55	58
5	CAA	A	1402[A]	54/54	0.94	0.14	23,39,50,50	54
4	HMG	A	1401[B]	58/58	0.94	0.13	27,43,52,53	58
5	CAA	D	4402[A]	54/54	0.94	0.12	20,39,54,54	54
3	SO4	B	2501	5/5	0.95	0.15	47,47,48,49	0
3	SO4	A	1501	5/5	0.97	0.14	52,52,53,54	0
3	SO4	D	4501	5/5	0.97	0.09	45,46,47,47	0
3	SO4	C	3501	5/5	0.97	0.11	43,45,45,46	0

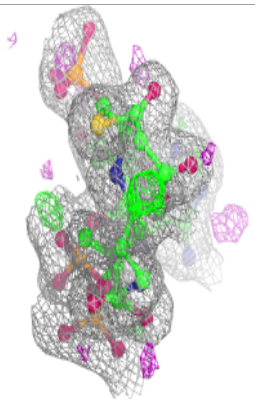
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around CAA B 2402:

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







Electron density around HMG C 3401:

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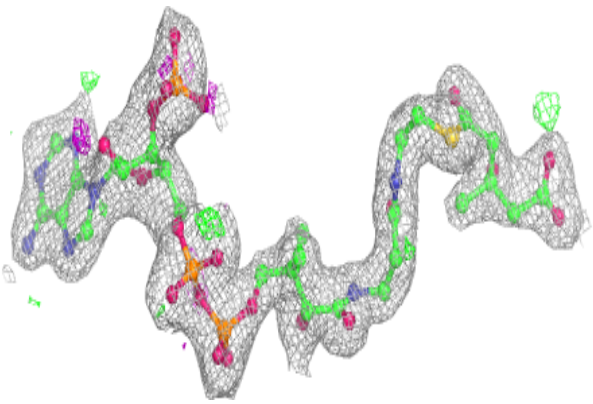
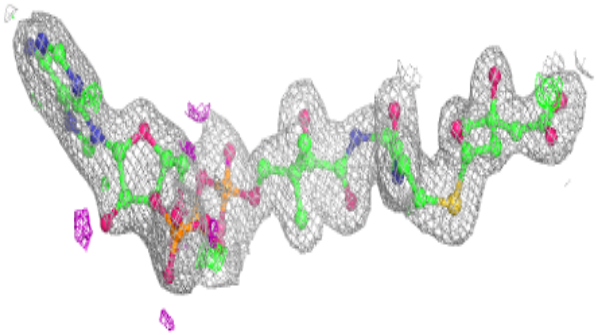
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





Electron density around HMG D 4401 (B):

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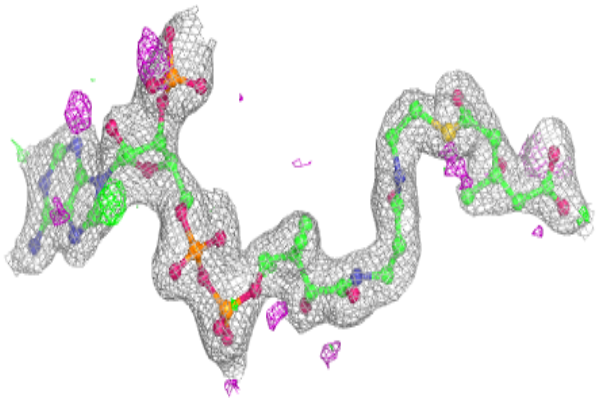
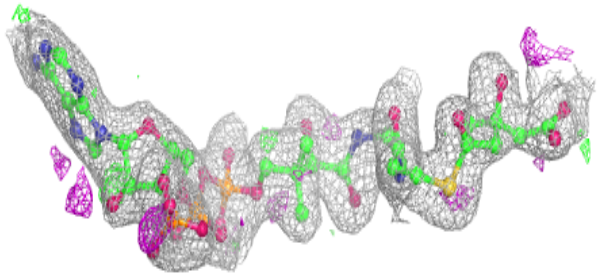
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





Electron density around CAA A 1402 (A):

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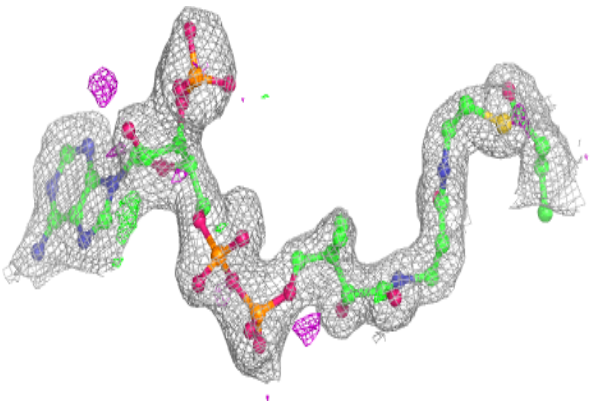
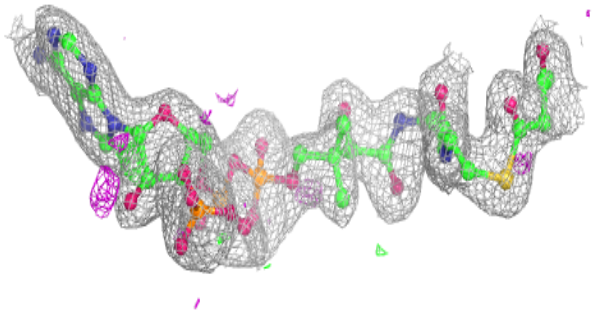
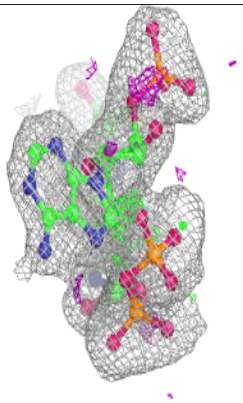
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







Electron density around HMG A 1401 (B):

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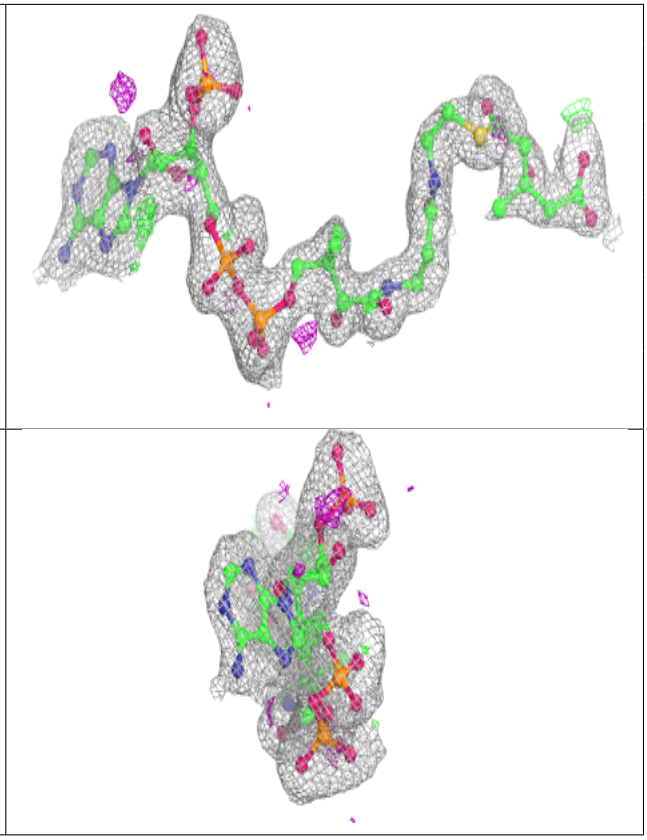
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around CAA D 4402 (A):

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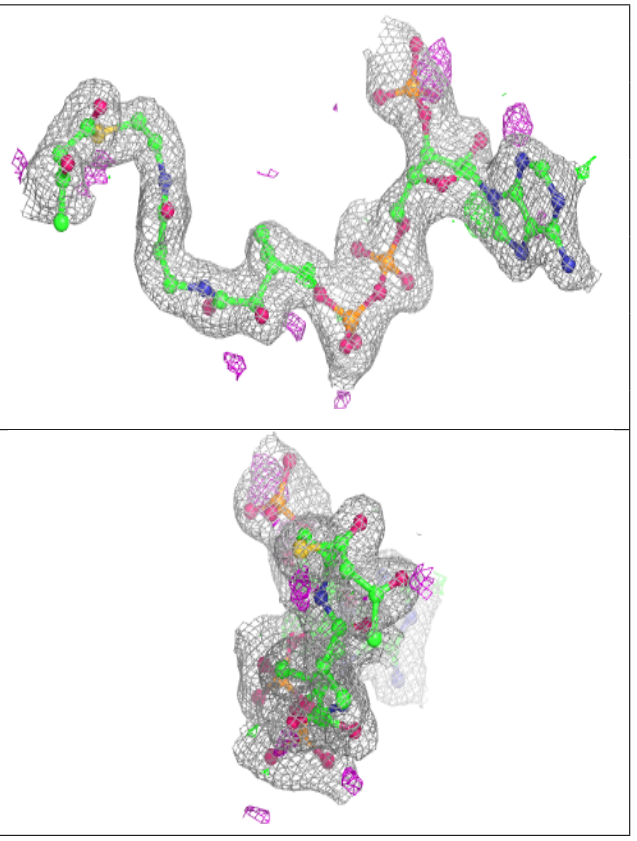
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.