wwPDB X-ray Structure Validation Summary Report (i)

Oct 10, 2023 – 10:28 AM EDT

PDB ID	:	7LDV
Title	:	Zoogloea ramigera biosynthetic thiolase Q183Y/Y218E/delH221/S227K mutant
Authors	:	Marshall, A.C.; Bruning, J.B.
Deposited on	:	2021-01-14
Resolution	:	2.90 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:

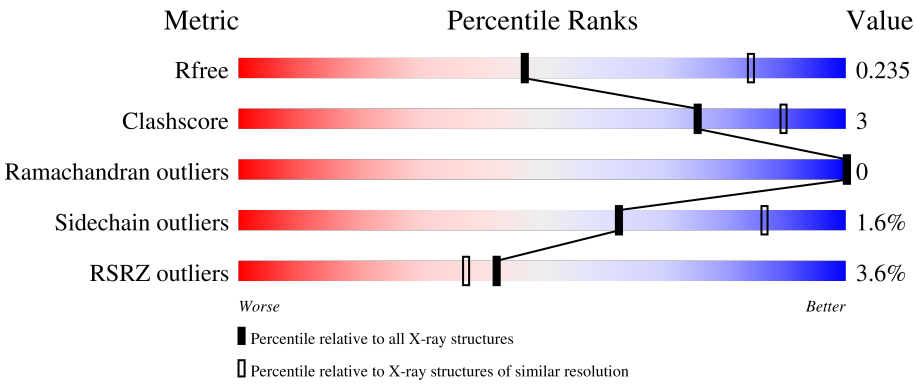
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & 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 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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	398	3% 93% 5% •
1	B	398	3% 93% 5% •
1	C	398	4% 86% 10% ••
1	D	398	5% 88% 9% ••

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 11828 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-CoA acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	389	2787	1734	498	534	21	0	0	0
1	B	389	2794	1736	502	535	21	0	0	0
1	C	389	2809	1746	504	538	21	0	0	0
1	D	389	2795	1736	500	538	21	0	0	0

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MET	-	initiating methionine	UNP P07097
A	-5	HIS	-	expression tag	UNP P07097
A	-4	HIS	-	expression tag	UNP P07097
A	-3	HIS	-	expression tag	UNP P07097
A	-2	HIS	-	expression tag	UNP P07097
A	-1	HIS	-	expression tag	UNP P07097
A	0	HIS	-	expression tag	UNP P07097
A	11	ALA	-	insertion	UNP P07097
A	129	ARG	ALA	conflict	UNP P07097
A	183	TYR	GLN	engineered mutation	UNP P07097
A	218	GLU	TYR	engineered mutation	UNP P07097
A	?	-	HIS	deletion	UNP P07097
A	226	LYS	SER	engineered mutation	UNP P07097
B	-6	MET	-	initiating methionine	UNP P07097
B	-5	HIS	-	expression tag	UNP P07097
B	-4	HIS	-	expression tag	UNP P07097
B	-3	HIS	-	expression tag	UNP P07097
B	-2	HIS	-	expression tag	UNP P07097
B	-1	HIS	-	expression tag	UNP P07097
B	0	HIS	-	expression tag	UNP P07097
B	11	ALA	-	insertion	UNP P07097

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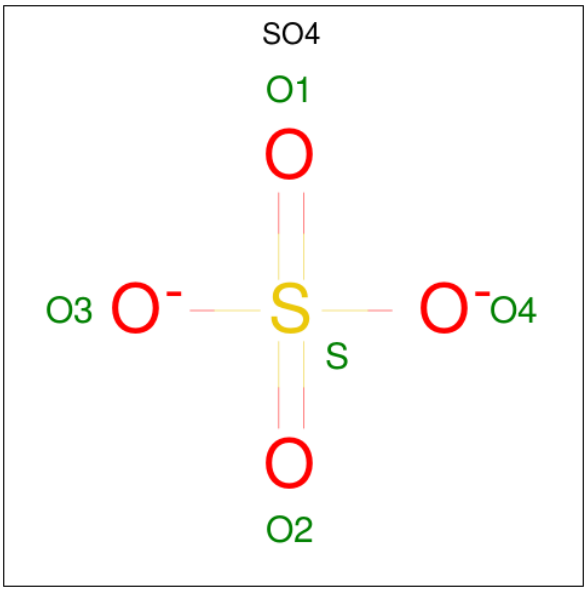
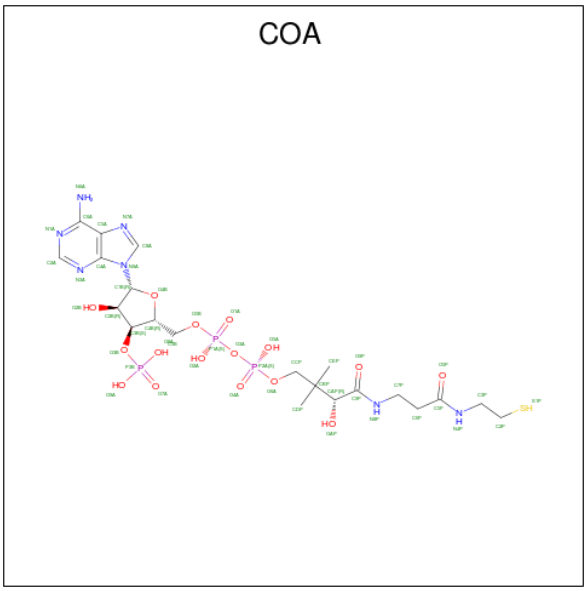
Chain	Residue	Modelled	Actual	Comment	Reference
B	129	ARG	ALA	conflict	UNP P07097
B	183	TYR	GLN	engineered mutation	UNP P07097
B	218	GLU	TYR	engineered mutation	UNP P07097
B	?	-	HIS	deletion	UNP P07097
B	226	LYS	SER	engineered mutation	UNP P07097
C	-6	MET	-	initiating methionine	UNP P07097
C	-5	HIS	-	expression tag	UNP P07097
C	-4	HIS	-	expression tag	UNP P07097
C	-3	HIS	-	expression tag	UNP P07097
C	-2	HIS	-	expression tag	UNP P07097
C	-1	HIS	-	expression tag	UNP P07097
C	0	HIS	-	expression tag	UNP P07097
C	11	ALA	-	insertion	UNP P07097
C	129	ARG	ALA	conflict	UNP P07097
C	183	TYR	GLN	engineered mutation	UNP P07097
C	218	GLU	TYR	engineered mutation	UNP P07097
C	?	-	HIS	deletion	UNP P07097
C	226	LYS	SER	engineered mutation	UNP P07097
D	-6	MET	-	initiating methionine	UNP P07097
D	-5	HIS	-	expression tag	UNP P07097
D	-4	HIS	-	expression tag	UNP P07097
D	-3	HIS	-	expression tag	UNP P07097
D	-2	HIS	-	expression tag	UNP P07097
D	-1	HIS	-	expression tag	UNP P07097
D	0	HIS	-	expression tag	UNP P07097
D	11	ALA	-	insertion	UNP P07097
D	129	ARG	ALA	conflict	UNP P07097
D	183	TYR	GLN	engineered mutation	UNP P07097
D	218	GLU	TYR	engineered mutation	UNP P07097
D	?	-	HIS	deletion	UNP P07097
D	226	LYS	SER	engineered mutation	UNP P07097

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



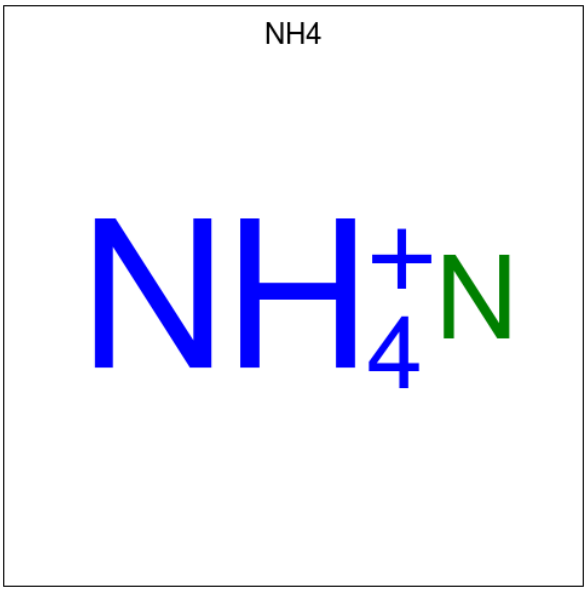
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	O	S			
2	A	1	5	4	1		0	0
2	A	1	5	4	1		0	0
2	A	1	5	4	1		0	0
2	B	1	5	4	1		0	0
2	B	1	5	4	1		0	0
2	B	1	5	4	1		0	0
2	C	1	5	4	1		0	0
2	D	1	5	4	1		0	0
2	D	1	5	4	1		0	0
2	D	1	5	4	1		0	0

- Molecule 3 is COENZYME A (three-letter code: COA) (formula: $C_{21}H_{36}N_7O_{16}P_3S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
3	A	1	48	21	7	16	3	1	0	0
3	B	1	48	21	7	16	3	1	0	0
3	C	1	48	21	7	16	3	1	0	0
3	D	1	48	21	7	16	3	1	0	0

- Molecule 4 is AMMONIUM ION (three-letter code: NH4) (formula: H_4N) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total N 1 1	0	0
4	B	1	Total N 1 1	0	0
4	C	1	Total N 1 1	0	0
4	D	1	Total N 1 1	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Cl 1 1	0	0
5	C	4	Total Cl 4 4	0	0
5	D	1	Total Cl 1 1	0	0

- Molecule 6 is water.

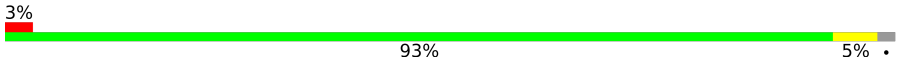
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	116	Total O 116 116	0	0
6	B	120	Total O 120 120	0	0
6	C	88	Total O 88 88	0	0
6	D	67	Total O 67 67	0	0

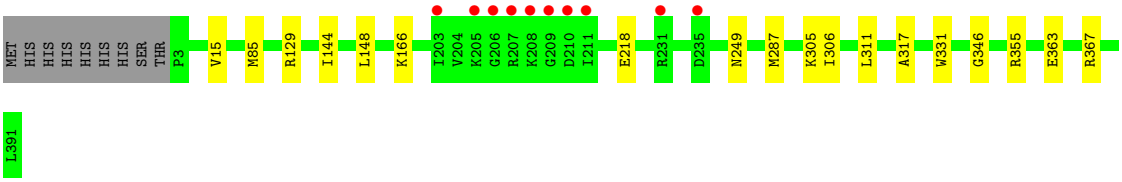
3 Residue-property plots (i)

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: Acetyl-CoA acetyltransferase

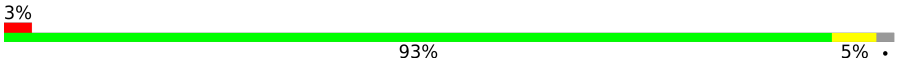
Chain A:

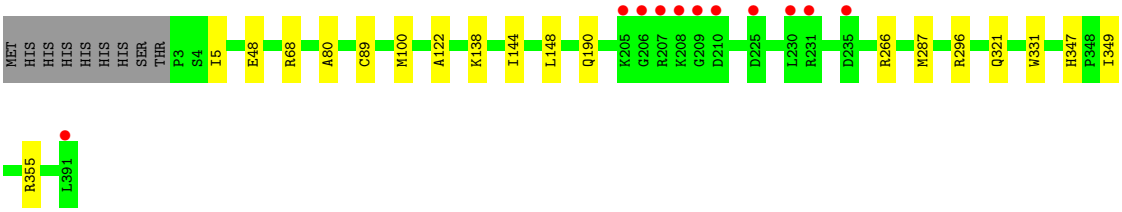




- Molecule 1: Acetyl-CoA acetyltransferase

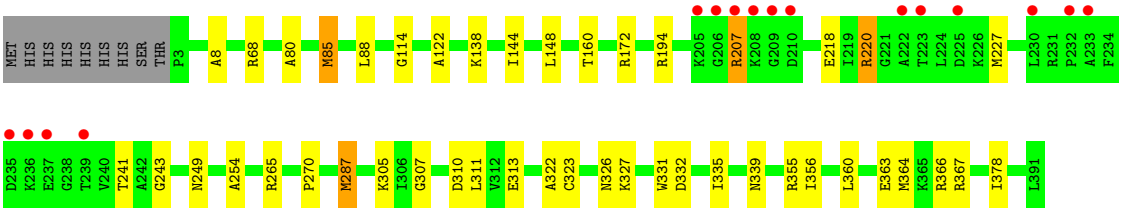
Chain B:





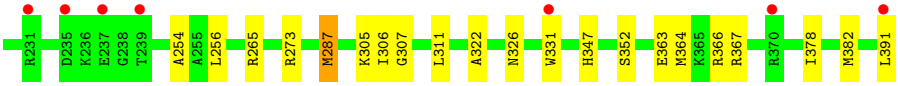
- Molecule 1: Acetyl-CoA acetyltransferase

Chain C:



- Molecule 1: Acetyl-CoA acetyltransferase

Chain D:


R231
D235
K236
E237
G238
T239
A254
A255
L256
R265
R273
M287
K305
I306
G307
L311
A322
N326
W331
H347
S352
E363
M364
K365
R366
R367
R370
I378
M382
L391

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	84.76Å 78.97Å 152.88Å 90.00° 94.49° 90.00°	Depositor
Resolution (Å)	47.23 – 2.90 47.23 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.7 (47.23-2.90) 99.7 (47.23-2.90)	Depositor EDS
R_{merge}	0.45	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.32 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.15_3459	Depositor
R, R_{free}	0.196 , 0.234 0.198 , 0.235	Depositor DCC
R_{free} test set	2262 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	40.1	Xtriage
Anisotropy	0.385	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 67.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	11828	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.76% 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: CL, NH4, COA, SCY, SO4

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	0.24	0/2818	0.43	0/3807
1	B	0.24	0/2825	0.43	0/3816
1	C	0.25	0/2840	0.44	0/3832
1	D	0.25	0/2826	0.44	0/3819
All	All	0.25	0/11309	0.44	0/15274

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 (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	2787	0	2768	10	0
1	B	2794	0	2779	10	0
1	C	2809	0	2812	31	0
1	D	2795	0	2775	23	0
2	A	15	0	0	0	0
2	B	15	0	0	0	0
2	C	5	0	0	1	0
2	D	15	0	0	1	0
3	A	48	0	32	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	48	0	32	1	0
3	C	48	0	32	0	0
3	D	48	0	32	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	1	0	0	0	0
5	C	4	0	0	0	0
5	D	1	0	0	0	0
6	A	116	0	0	1	0
6	B	120	0	0	2	0
6	C	88	0	0	4	0
6	D	67	0	0	1	0
All	All	11828	0	11262	70	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.

The worst 5 of 70 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:C:160:THR:HG21	1:C:287:MET:HG3	1.59	0.82
1:D:160:THR:HG21	1:D:287:MET:HG3	1.63	0.79
1:C:311:LEU:HD23	1:C:363:GLU:HG3	1.70	0.73
1:A:218:GLU:HG3	1:A:249:ASN:HD21	1.55	0.71
1:C:218:GLU:HG3	1:C:249:ASN:HD21	1.55	0.70

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	386/398 (97%)	376 (97%)	10 (3%)	0	100	100
1	B	386/398 (97%)	376 (97%)	10 (3%)	0	100	100
1	C	386/398 (97%)	378 (98%)	8 (2%)	0	100	100
1	D	386/398 (97%)	377 (98%)	9 (2%)	0	100	100
All	All	1544/1592 (97%)	1507 (98%)	37 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	267/284 (94%)	263 (98%)	4 (2%)	65	87
1	B	269/284 (95%)	265 (98%)	4 (2%)	65	87
1	C	273/284 (96%)	268 (98%)	5 (2%)	59	85
1	D	270/284 (95%)	266 (98%)	4 (2%)	65	87
All	All	1079/1136 (95%)	1062 (98%)	17 (2%)	62	86

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	220	ARG
1	D	331	TRP
1	B	355	ARG
1	C	85	MET
1	C	207	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

4 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	89	1	7,8,9	0.92	0	3,9,11	0.82	0
1	SCY	C	89	1	7,8,9	0.91	0	3,9,11	0.83	0
1	SCY	B	89	1	7,8,9	0.90	0	3,9,11	0.80	0
1	SCY	D	89	1	7,8,9	0.91	0	3,9,11	0.82	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	89	1	-	0/5/7/9	-
1	SCY	C	89	1	-	0/5/7/9	-
1	SCY	B	89	1	-	0/5/7/9	-
1	SCY	D	89	1	-	0/5/7/9	-

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	89	SCY	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 24 ligands modelled in this entry, 4 are modelled with single atom and 6 are monoatomic - leaving 14 for Mogul analysis.

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	SO4	C	401	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	A	402	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	D	403	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	B	402	-	4,4,4	0.14	0	6,6,6	0.04	0
3	COA	A	404	-	41,50,50	1.33	3 (7%)	52,75,75	1.46	9 (17%)
2	SO4	D	401	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	B	403	-	4,4,4	0.14	0	6,6,6	0.04	0
3	COA	C	402	-	41,50,50	1.37	3 (7%)	52,75,75	1.42	8 (15%)
3	COA	D	402	-	41,50,50	1.38	4 (9%)	52,75,75	1.45	11 (21%)
2	SO4	B	401	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	A	401	-	4,4,4	0.14	0	6,6,6	0.05	0
3	COA	B	404	-	41,50,50	1.32	3 (7%)	52,75,75	1.46	9 (17%)
2	SO4	A	403	-	4,4,4	0.13	0	6,6,6	0.05	0
2	SO4	D	404	-	4,4,4	0.14	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
3	COA	B	404	-	-	19/44/64/64	0/3/3/3
3	COA	A	404	-	-	9/44/64/64	0/3/3/3
3	COA	D	402	-	-	9/44/64/64	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	COA	C	402	-	-	18/44/64/64	0/3/3/3

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	402	COA	O4B-C1B	5.01	1.48	1.41
3	D	402	COA	O4B-C1B	4.89	1.47	1.41
3	B	404	COA	O4B-C1B	4.54	1.47	1.41
3	A	404	COA	O4B-C1B	4.49	1.47	1.41
3	A	404	COA	C8A-N7A	-3.92	1.27	1.34

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	404	COA	P2A-O3A-P1A	-5.30	114.65	132.83
3	C	402	COA	P2A-O3A-P1A	-5.28	114.72	132.83
3	B	404	COA	P2A-O3A-P1A	-5.25	114.81	132.83
3	D	402	COA	P2A-O3A-P1A	-5.14	115.19	132.83
3	B	404	COA	N3A-C2A-N1A	-3.70	122.90	128.68

There are no chirality outliers.

5 of 55 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	404	COA	C3B-O3B-P3B-O8A
3	A	404	COA	C5B-O5B-P1A-O1A
3	A	404	COA	C5B-O5B-P1A-O2A
3	A	404	COA	CCP-O6A-P2A-O4A
3	B	404	COA	C3B-O3B-P3B-O9A

There are no ring outliers.

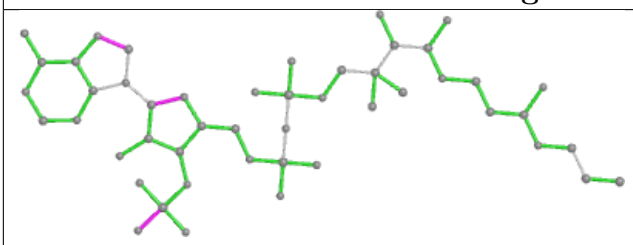
4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	401	SO4	1	0
3	A	404	COA	1	0
2	D	401	SO4	1	0
3	B	404	COA	1	0

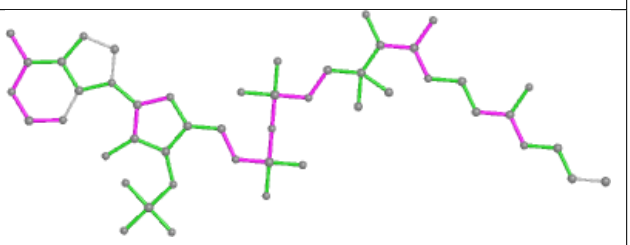
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

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.

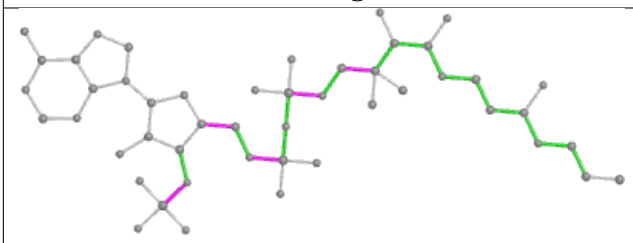
Ligand COA A 404



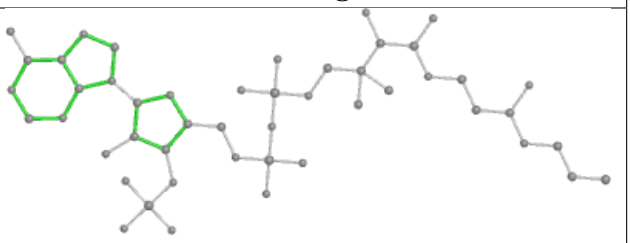
Bond lengths



Bond angles

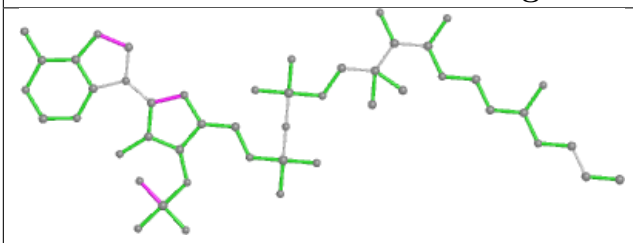


Torsions

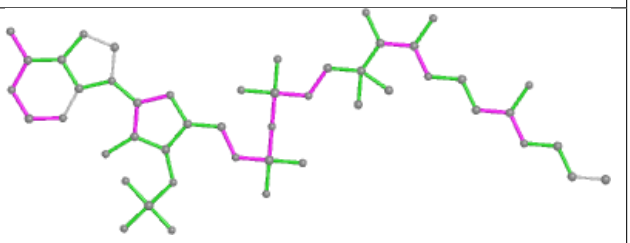


Rings

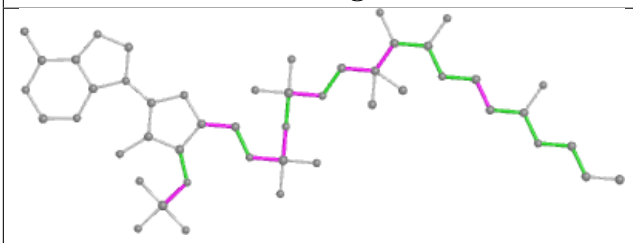
Ligand COA C 402



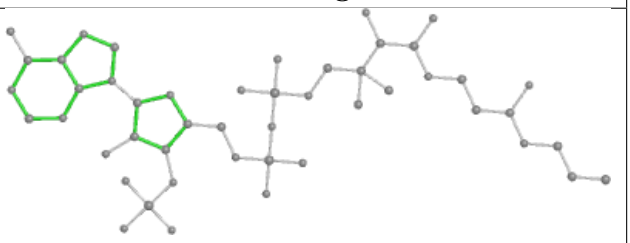
Bond lengths



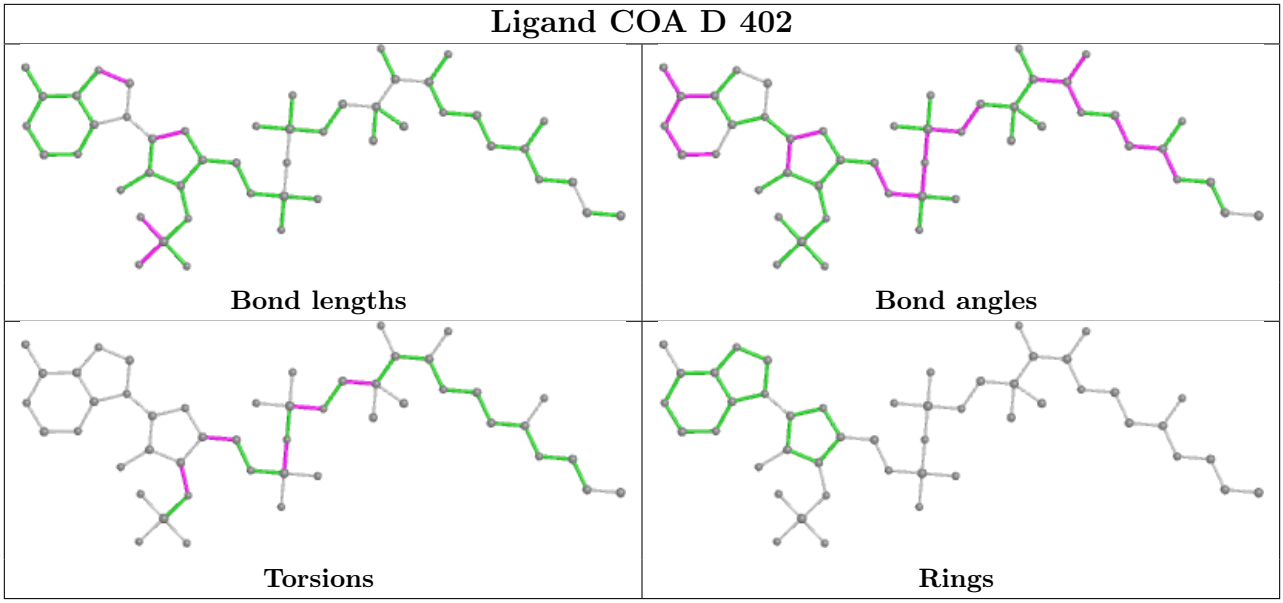
Bond angles

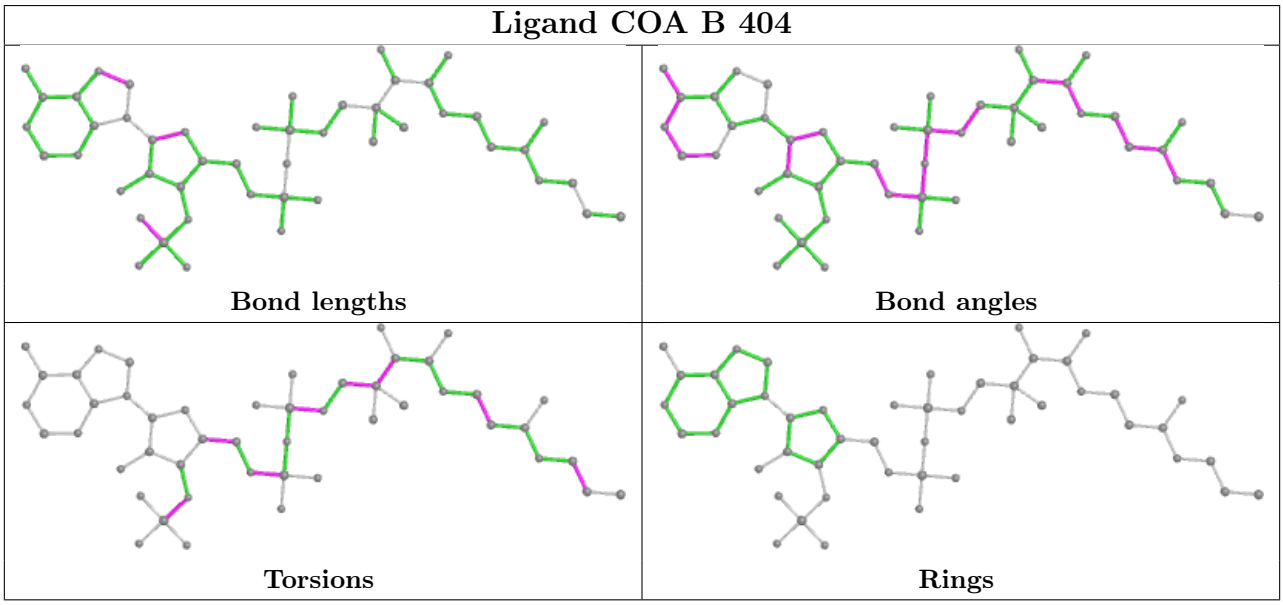


Torsions



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	388/398 (97%)	-0.29	10 (2%)	56	52	19, 36, 60, 97	0
1	B	388/398 (97%)	-0.23	11 (2%)	53	49	20, 37, 60, 103	0
1	C	388/398 (97%)	-0.02	16 (4%)	37	32	27, 43, 70, 110	0
1	D	388/398 (97%)	0.23	19 (4%)	29	26	28, 49, 81, 133	0
All	All	1552/1592 (97%)	-0.08	56 (3%)	42	37	19, 41, 71, 133	0

The worst 5 of 56 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	235	ASP	5.0
1	C	210	ASP	4.7
1	B	208	LYS	4.6
1	B	210	ASP	4.6
1	C	206	GLY	4.1

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	D	89	9/10	0.95	0.14	44,52,57,59	0
1	SCY	B	89	9/10	0.97	0.16	26,37,49,56	0
1	SCY	C	89	9/10	0.97	0.19	33,42,50,52	0
1	SCY	A	89	9/10	0.97	0.14	35,42,55,55	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

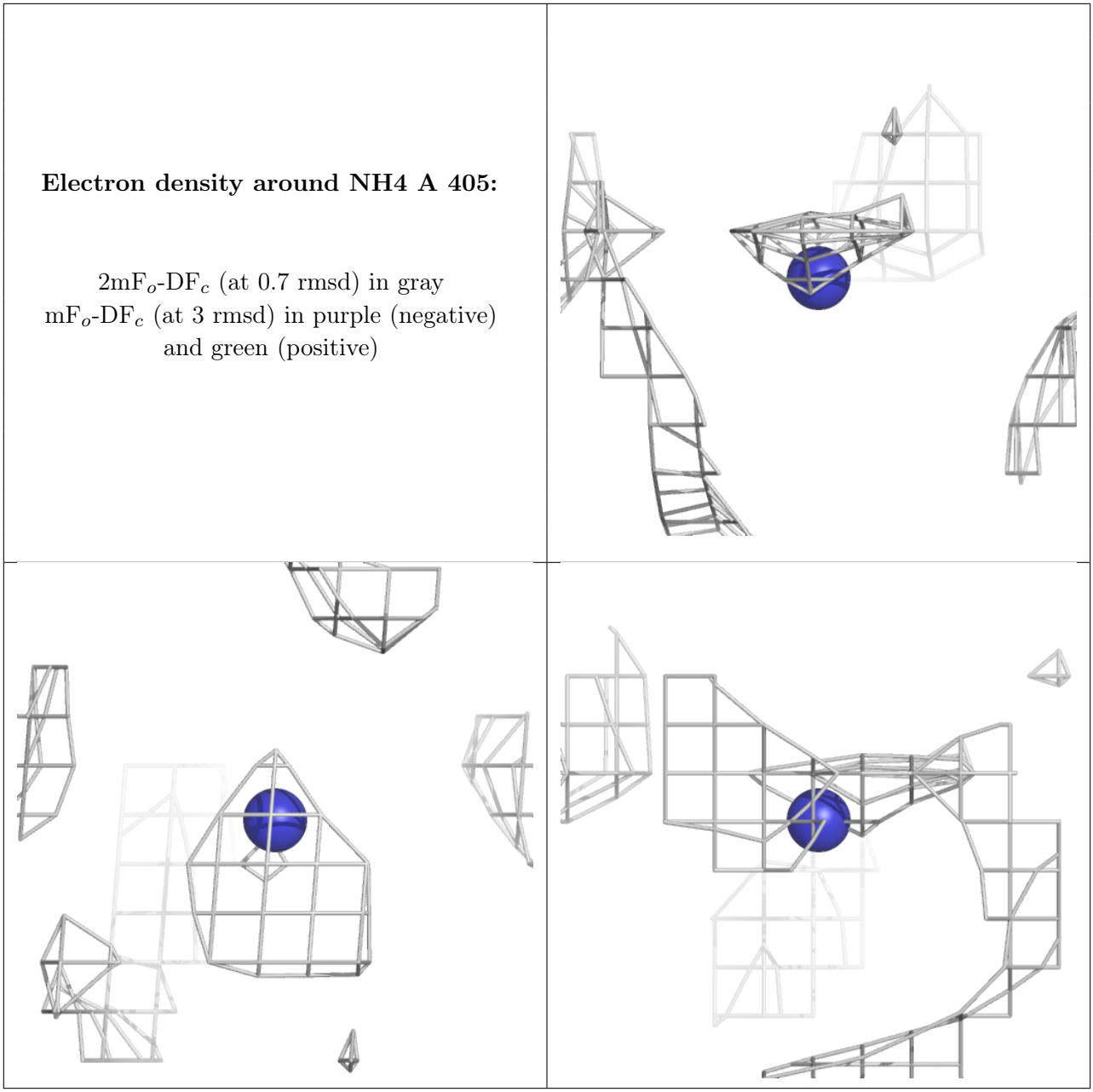
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	NH4	A	405	1/1	0.70	0.36	33,33,33,33	0
4	NH4	B	405	1/1	0.83	0.30	5,5,5,5	0
3	COA	C	402	48/48	0.85	0.26	44,75,83,85	0
3	COA	D	402	48/48	0.85	0.26	52,86,95,99	0
5	CL	C	406	1/1	0.86	0.11	67,67,67,67	0
4	NH4	D	405	1/1	0.87	0.19	32,32,32,32	0
2	SO4	A	403	5/5	0.89	0.29	101,102,102,103	0
2	SO4	D	403	5/5	0.89	0.27	117,118,118,118	0
2	SO4	A	402	5/5	0.91	0.19	93,95,95,95	0
2	SO4	D	404	5/5	0.91	0.17	110,110,111,112	0
3	COA	A	404	48/48	0.91	0.20	24,44,70,73	48
3	COA	B	404	48/48	0.91	0.22	42,61,72,74	0
2	SO4	B	403	5/5	0.91	0.30	107,107,108,109	0
4	NH4	C	403	1/1	0.92	0.24	25,25,25,25	0
2	SO4	A	401	5/5	0.92	0.16	81,81,82,82	0
2	SO4	C	401	5/5	0.92	0.22	107,107,107,108	0
2	SO4	D	401	5/5	0.93	0.18	90,90,91,91	0
5	CL	D	406	1/1	0.93	0.15	67,67,67,67	0
5	CL	C	404	1/1	0.94	0.15	81,81,81,81	0
5	CL	C	405	1/1	0.95	0.20	62,62,62,62	0
2	SO4	B	402	5/5	0.96	0.18	84,84,84,85	0
5	CL	C	407	1/1	0.96	0.19	60,60,60,60	0
2	SO4	B	401	5/5	0.96	0.12	107,107,107,108	0
5	CL	A	406	1/1	0.97	0.19	58,58,58,58	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.

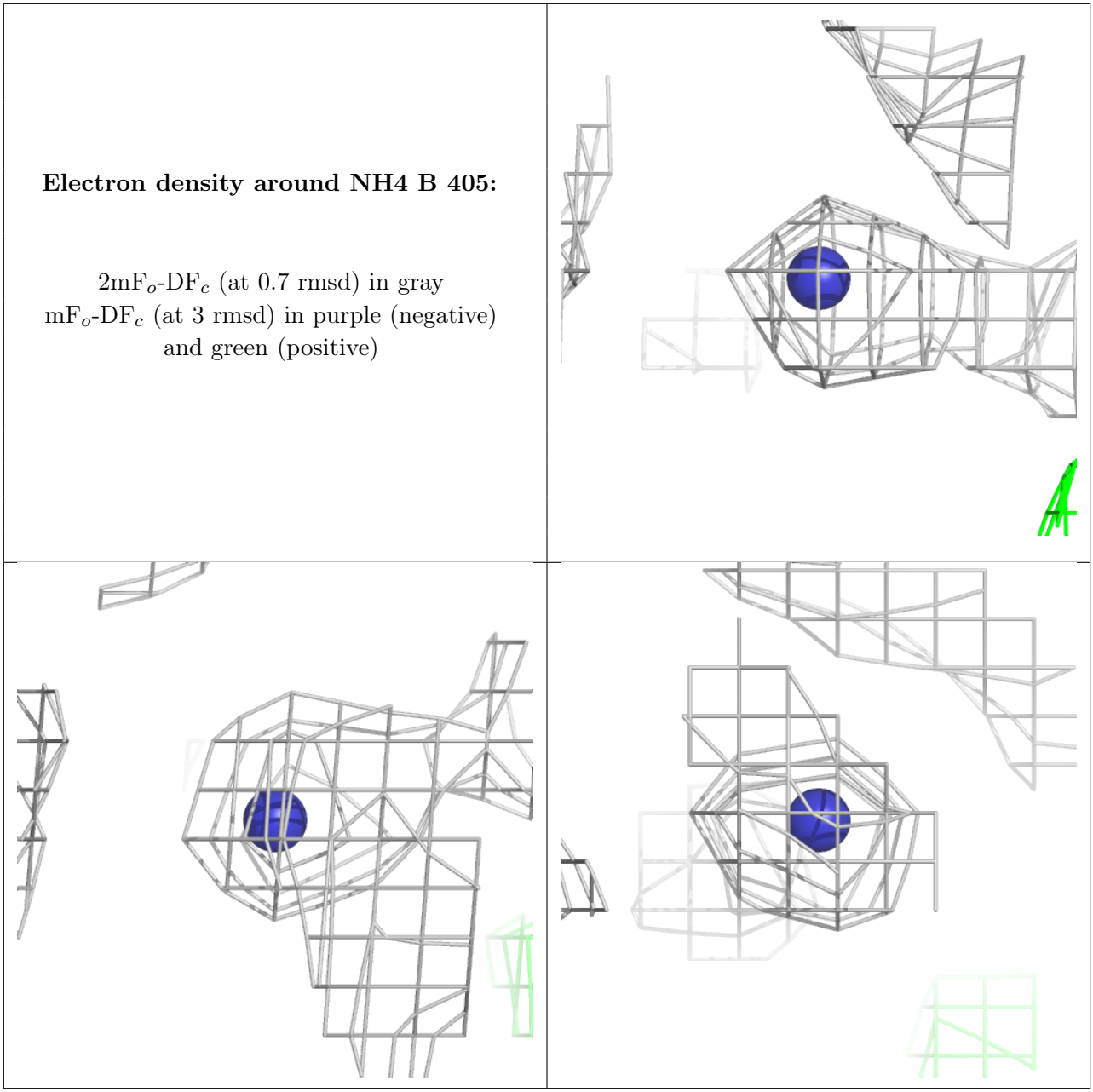
Electron density around NH4 A 405:

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



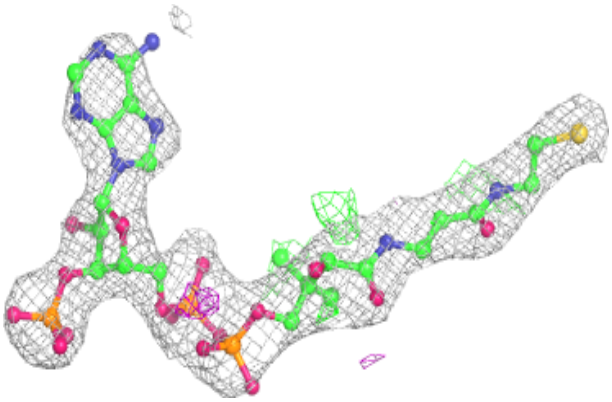
Electron density around NH4 B 405:

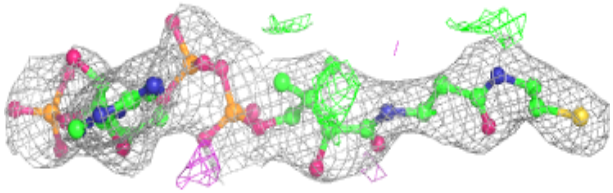
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

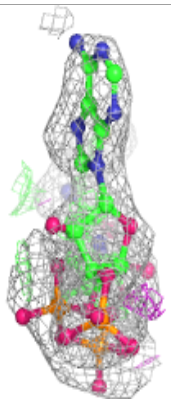


Electron density around COA C 402:

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







Electron density around COA D 402:

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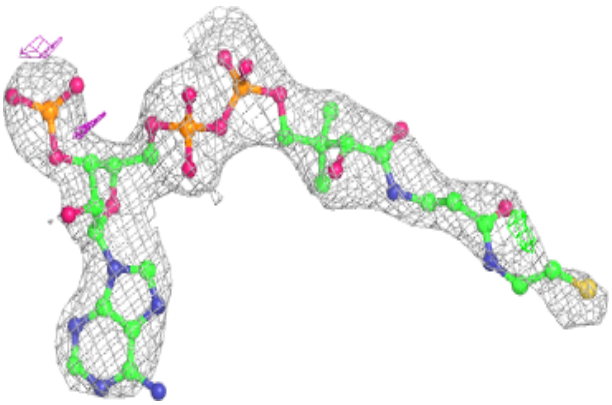
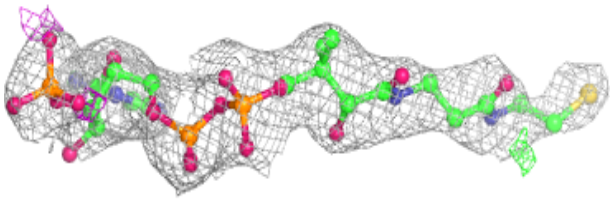
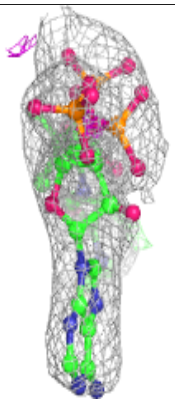
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







Electron density around NH4 D 405:

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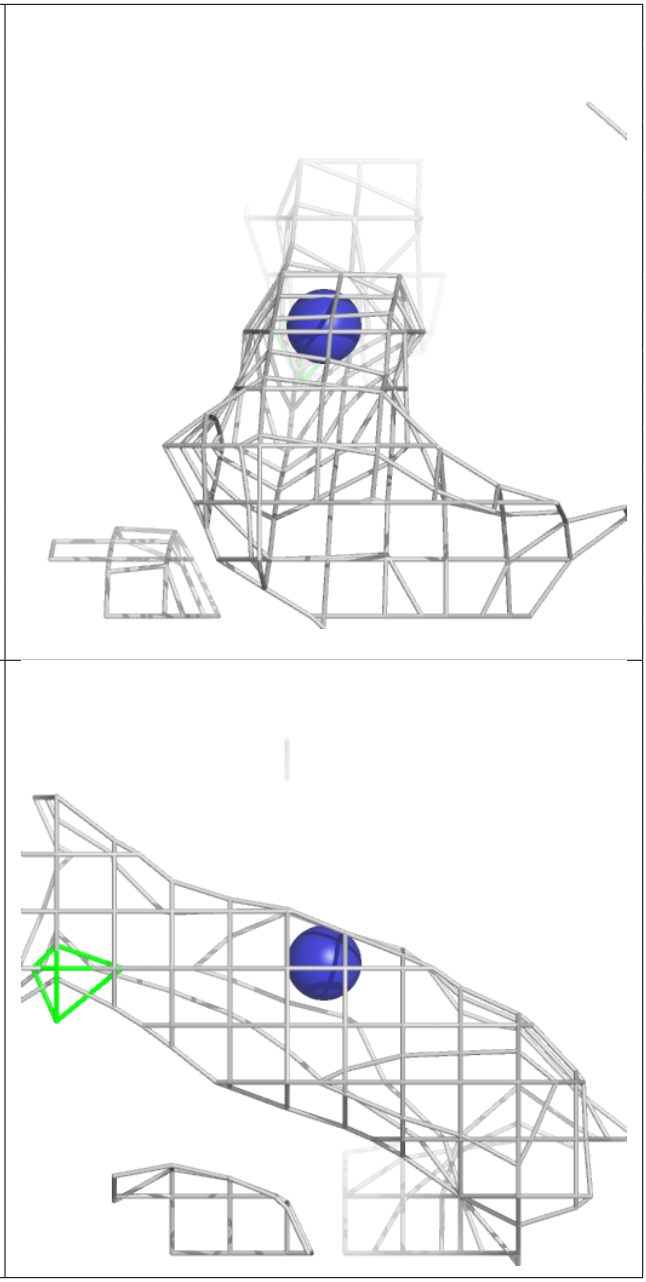
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around COA A 404:

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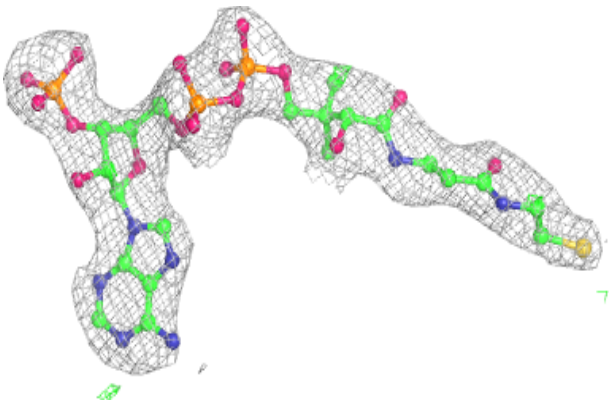
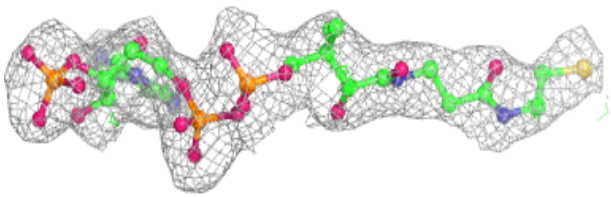
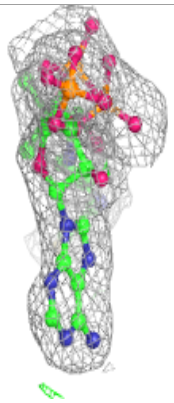
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







Electron density around COA B 404:

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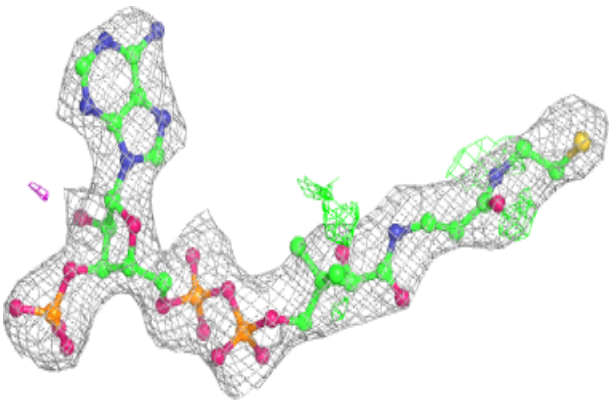
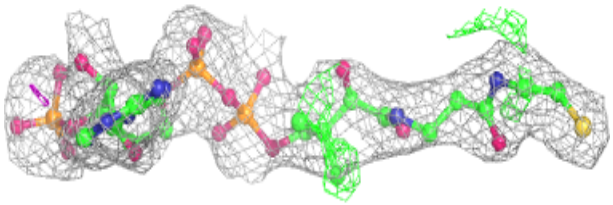
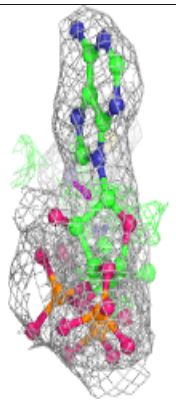
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







Electron density around NH4 C 403:

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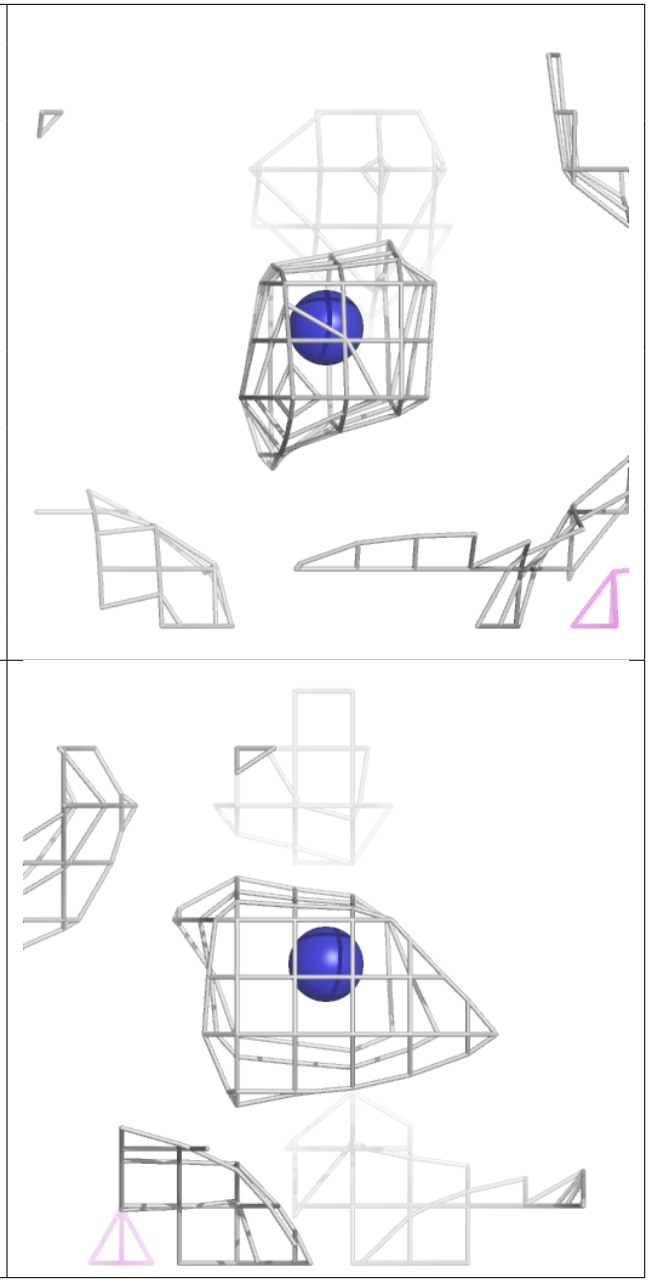
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.