Full wwPDB X-ray Structure Validation Report (i)

May 13, 2020 – 12:37 pm BST

PDB ID	:	6VO5
Title	:	Crystal structure of Human histone acetytransferas 1 (HAT1) in complex with isobutryl-COA and K12A mutant variant of histone H4
Authors	:	Halabelian, L.; Zeng, H.; Dong, A.; Loppnau, P.; Bountra, C.; Edwards, A.M.; Arrowsmith, C.H.; Structural Genomics Consortium (SGC)
Deposited on	:	2020-01-30
Resolution	:	1.60 Å(reported)

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

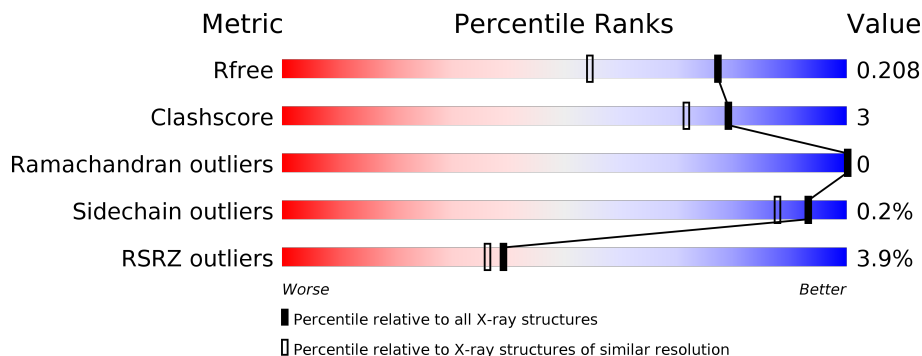|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 1.60 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	Percentile Ranks	Value
Rfree		0.208
Clashscore		3
Ramachandran outliers		0
Sidechain outliers		0.2%
RSRZ outliers		3.9%

Worse ← → Better

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria 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	324	6% / 96%
1	B	324	% / 93% / 5%
2	C	20	15% / 75% / 25%
2	D	20	10% / 70% / 30%

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	UNX	B	406	-	-	-	X

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 6547 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 Histone acetyltransferase type B catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	322	Total 2725	C 1764	N 440	O 505	S 16	0	11	0
1	B	318	Total 2727	C 1765	N 450	O 497	S 15	0	12	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	18	GLY	-	expression tag	UNP O14929
A	19	SER	-	expression tag	UNP O14929
B	18	GLY	-	expression tag	UNP O14929
B	19	SER	-	expression tag	UNP O14929

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	15	Total 97	C 57	N 25	O 15	0	0	0
2	D	14	Total 92	C 54	N 24	O 14	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	12	ALA	LYS	engineered mutation	UNP P62805
D	12	ALA	LYS	engineered mutation	UNP P62805

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).

ACT

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is ISOBUTYRYL-COENZYME A (three-letter code: CO6) (formula: $C_{25}H_{42}N_7O_{17}P_3S$).
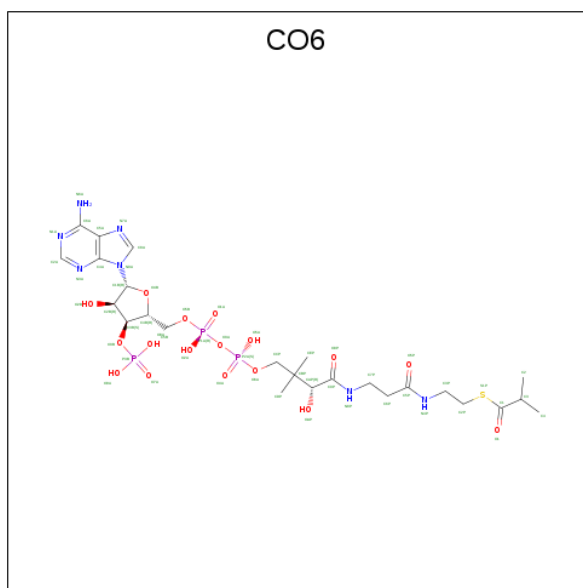
CO6

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	S	0	0
			53	25	7	17	3	1		
4	B	1	Total	C	N	O	P	S	0	1
			59	29	7	18	3	2		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

GOL

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 6	C 3	O 3	0	0
5	B	1	Total 6	C 3	O 3	0	0
5	B	1	Total 6	C 3	O 3	0	0

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O_4S).

SO4
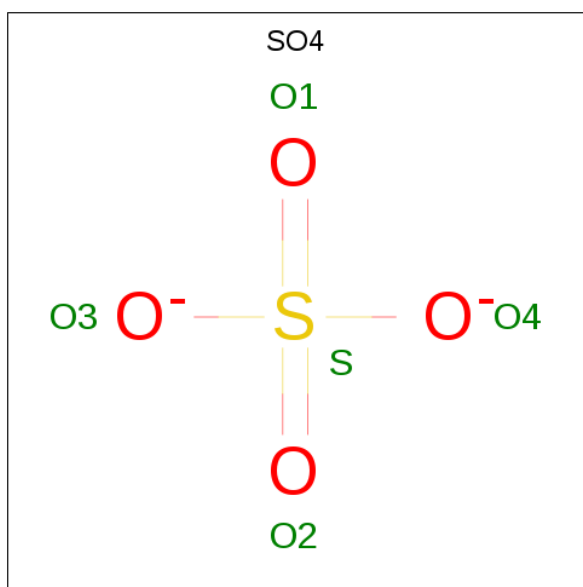
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total 5	O 4	S 1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total 5	O 4	S 1	0	0

- Molecule 7 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	7	Total 7	X 7	0	0
7	A	9	Total 9	X 9	0	0

- Molecule 8 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	373	Total 378	O 378	0	5
8	B	330	Total 334	O 334	0	4
8	C	18	Total 20	O 20	0	2
8	D	14	Total 14	O 14	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.
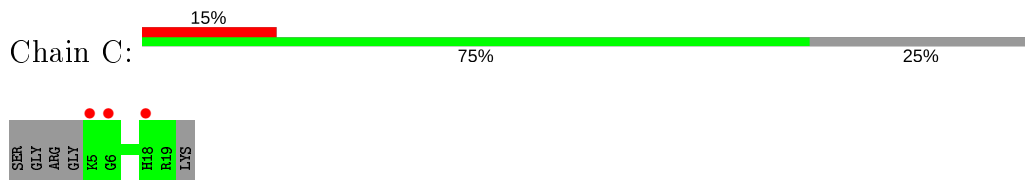
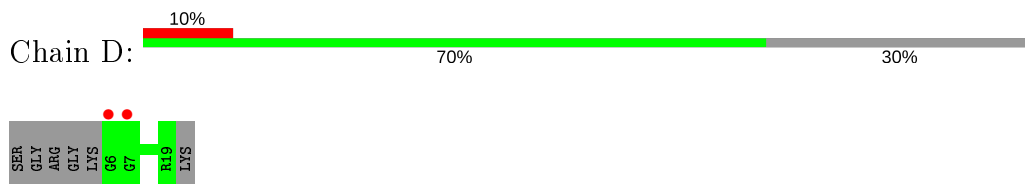• Molecule 1: Histone acetyltransferase type B catalytic subunit
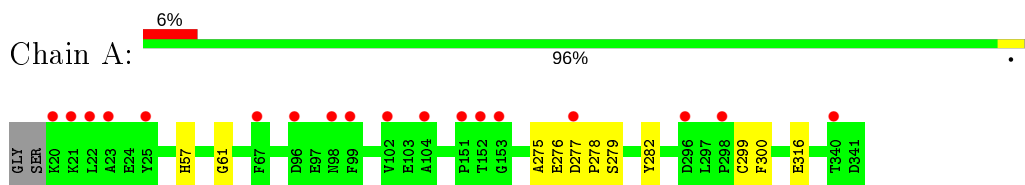
Chain A:

• Molecule 1: Histone acetyltransferase type B catalytic subunit

Chain B:

• Molecule 2: Histone H4

Chain C:

• Molecule 2: Histone H4

Chain D:
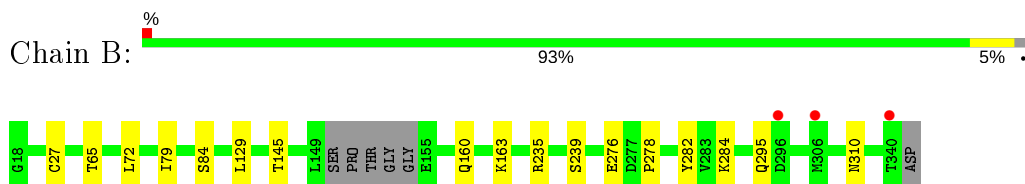
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	116.73Å 155.64Å 53.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.45 – 1.60 47.41 – 1.60	Depositor EDS
% Data completeness (in resolution range)	99.4 (47.45-1.60) 99.4 (47.41-1.60)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	1.95 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.171 , 0.198 0.183 , 0.208	Depositor DCC
R_{free} test set	6413 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	22.7	Xtriage
Anisotropy	0.443	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 45.2	EDS
L-test for twinning[2]	$<|L|> = 0.49$, $<L^2> = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	6547	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 10.62% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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: GOL, CO6, UNX, SO4, YCM, ACT

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	0.64	0/2757	0.74	0/3730
1	B	0.63	0/2753	0.74	0/3716
2	C	0.71	0/97	0.72	0/124
2	D	0.73	0/92	0.70	0/117
All	All	0.64	0/5699	0.74	0/7687

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	2725	0	2583	9	0
1	B	2727	0	2634	15	0
2	C	97	0	99	0	0
2	D	92	0	97	0	0
3	A	4	0	3	0	0
4	A	53	0	38	7	0
4	B	59	0	18	8	0
5	A	6	0	8	1	0
5	B	12	0	16	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	5	0	0	1	0
6	B	5	0	0	0	0
7	A	9	0	0	0	0
7	B	7	0	0	0	0
8	A	378	0	0	1	0
8	B	334	0	0	2	0
8	C	20	0	0	0	0
8	D	14	0	0	0	0
All	All	6547	0	5496	30	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (30) 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:A:278:PRO:HA	4:A:502:CO6:H41	1.41	0.99
1:B:278:PRO:HA	4:B:401[B]:CO6:H41	1.54	0.89
4:A:502:CO6:H21	4:A:502:CO6:H43	1.61	0.80
1:B:276:GLU:O	4:B:401[B]:CO6:H11	1.89	0.72
1:B:145[B]:THR:HG22	1:B:160:GLN:HG2	1.72	0.71
1:B:235[B]:ARG:HG2	8:B:737:HOH:O	1.94	0.67
4:A:502:CO6:C4	4:A:502:CO6:H21	2.31	0.61
1:B:27[B]:YCM:HZ21	1:B:72:LEU:H	1.48	0.59
1:B:295:GLN:NE2	8:B:502:HOH:O	2.34	0.58
4:A:502:CO6:O9A	4:A:502:CO6:H5'1	2.03	0.58
1:A:299[A]:CYS:SG	1:A:300:PHE:CD2	2.98	0.56
1:B:239[B]:SER:O	4:B:401[B]:CO6:H12	2.07	0.55
1:B:163:LYS:O	5:B:403:GOL:H32	2.07	0.54
4:B:401[A]:CO6:H12	4:B:401[A]:CO6:H21	1.91	0.53
1:A:275:ALA:HB1	4:A:502:CO6:H11	1.92	0.52
5:A:503:GOL:H32	8:A:634:HOH:O	2.09	0.50
1:A:299[A]:CYS:SG	1:A:316:GLU:OE1	2.71	0.48
1:B:27[B]:YCM:O	1:B:65:THR:HA	2.14	0.48
1:B:282:TYR:CB	4:B:401[B]:CO6:H43	2.45	0.47
1:A:276[B]:GLU:O	1:A:277[B]:ASP:C	2.54	0.47
1:B:79[B]:ILE:HD12	1:B:84:SER:HB2	1.96	0.47
1:A:279:SER:H	4:A:502:CO6:C4	2.30	0.45
1:B:278:PRO:CA	4:B:401[B]:CO6:H41	2.38	0.43
1:A:282:TYR:CB	4:A:502:CO6:H42	2.48	0.43
1:B:278:PRO:HA	4:B:401[A]:CO6:H11	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:HIS:HA	1:A:61:GLY:O	2.19	0.43
1:B:129:LEU:HA	1:B:129:LEU:HD23	1.92	0.42
1:A:278:PRO:HG3	6:A:504:SO4:O1	2.20	0.41

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	327/324 (101%)	322 (98%)	5 (2%)	0	100	100
1	B	322/324 (99%)	319 (99%)	3 (1%)	0	100	100
2	C	13/20 (65%)	13 (100%)	0	0	100	100
2	D	12/20 (60%)	12 (100%)	0	0	100	100
All	All	674/688 (98%)	666 (99%)	8 (1%)	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	281/289 (97%)	281 (100%)	0	100	100
1	B	284/289 (98%)	283 (100%)	1 (0%)	91	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	6/10 (60%)	6 (100%)	0	100	100
2	D	6/10 (60%)	6 (100%)	0	100	100
All	All	577/598 (96%)	576 (100%)	1 (0%)	93	88

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	310	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	98	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)

8 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	YCM	A	101	1	7,9,10	0.50	0	4,10,12	0.25	0
1	YCM	A	27[B]	1	7,9,10	0.42	0	4,10,12	0.66	0
1	YCM	B	168	1	7,9,10	0.61	0	4,10,12	0.53	0
1	YCM	B	101	1	7,9,10	0.42	0	4,10,12	0.36	0
1	YCM	A	168	1	7,9,10	0.69	0	4,10,12	0.62	0
1	YCM	B	27[B]	1	7,9,10	0.56	0	4,10,12	0.40	0
1	YCM	A	27[A]	1	7,5,10	10.40	1 (14%)	4,5,12	1.88	2 (50%)
1	YCM	B	27[A]	1	7,9,10	0.54	0	4,10,12	0.59	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	YCM	A	101	1	-	1/6/8/10	-
1	YCM	A	27[B]	1	-	2/6/8/10	-
1	YCM	B	168	1	-	1/6/8/10	-
1	YCM	B	101	1	-	0/6/8/10	-
1	YCM	A	168	1	-	1/6/8/10	-
1	YCM	B	27[B]	1	-	3/6/8/10	-
1	YCM	A	27[A]	1	-	2/6/4/10	-
1	YCM	B	27[A]	1	-	0/6/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	27[A]	YCM	CD-SG	27.47	2.52	1.81

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	27[A]	YCM	CE-CD-SG	-3.08	104.52	113.59
1	A	27[A]	YCM	CB-SG-CD	-2.03	85.54	104.44

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	27[B]	YCM	SG-CD-CE-NZ2
1	B	27[B]	YCM	C-CA-CB-SG
1	B	27[B]	YCM	SG-CD-CE-NZ2
1	B	27[B]	YCM	N-CA-CB-SG
1	A	27[B]	YCM	SG-CD-CE-OZ1
1	A	101	YCM	SG-CD-CE-NZ2
1	B	168	YCM	CE-CD-SG-CB
1	A	168	YCM	CE-CD-SG-CB
1	A	27[A]	YCM	CE-CD-SG-CB
1	A	27[A]	YCM	N-CA-CB-SG

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	27[B]	YCM	2	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 25 ligands modelled in this entry, 16 are unknown - leaving 9 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
4	CO6	B	401[A]	-	46,55,55	0.65	1 (2%)	55,82,82	0.76	1 (1%)
4	CO6	B	401[B]	-	46,55,55	0.65	1 (2%)	55,82,82	0.75	1 (1%)
5	GOL	A	503	-	5,5,5	0.09	0	5,5,5	0.29	0
5	GOL	B	403	-	5,5,5	0.14	0	5,5,5	0.47	0
6	SO4	A	504	-	4,4,4	0.59	0	6,6,6	0.07	0
6	SO4	B	404	-	4,4,4	0.43	0	6,6,6	0.06	0
3	ACT	A	501	-	1,3,3	3.90	1 (100%)	0,3,3	0.00	-
5	GOL	B	402	-	5,5,5	0.10	0	5,5,5	0.23	0
4	CO6	A	502	-	46,55,55	0.73	1 (2%)	55,82,82	0.77	1 (1%)

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	CO6	B	401[A]	-	-	5/51/71/71	0/3/3/3
4	CO6	B	401[B]	-	-	3/51/71/71	0/3/3/3
5	GOL	A	503	-	-	0/4/4/4	-
5	GOL	B	403	-	-	0/4/4/4	-
5	GOL	B	402	-	-	2/4/4/4	-

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![Worldwide PDB Protein Data Bank logo]

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	CO6	A	502	-	-	6/51/71/71	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	ACT	CH3-C	3.90	1.53	1.48
4	A	502	CO6	P3B-O3B	3.46	1.65	1.59
4	B	401[A]	CO6	P3B-O3B	2.61	1.64	1.59
4	B	401[B]	CO6	P3B-O3B	2.61	1.64	1.59

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	401[A]	CO6	C5A-C6A-N6A	2.20	123.70	120.35
4	B	401[B]	CO6	C5A-C6A-N6A	2.20	123.70	120.35
4	A	502	CO6	C5A-C6A-N6A	2.15	123.61	120.35

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	402	GOL	C1-C2-C3-O3
4	A	502	CO6	C4B-C3B-O3B-P3B
4	A	502	CO6	O1-C1-S1P-C2P
4	A	502	CO6	C3-C1-S1P-C2P
4	A	502	CO6	S1P-C1-C3-C2
4	A	502	CO6	S1P-C1-C3-C4
4	B	401[A]	CO6	C4B-C3B-O3B-P3B
4	B	401[A]	CO6	O1-C1-S1P-C2P
4	B	401[A]	CO6	C3-C1-S1P-C2P
4	B	401[A]	CO6	S1P-C1-C3-C2
4	B	401[A]	CO6	O1-C1-C3-C2
4	B	401[B]	CO6	C4B-C3B-O3B-P3B
4	B	401[B]	CO6	O1-C1-S1P-C2P
4	B	401[B]	CO6	C3-C1-S1P-C2P
5	B	402	GOL	O2-C2-C3-O3
4	A	502	CO6	O1-C1-C3-C4

There are no ring outliers.

6 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	401[A]	CO6	3	0
4	B	401[B]	CO6	5	0
5	A	503	GOL	1	0
5	B	403	GOL	1	0
6	A	504	SO4	1	0
4	A	502	CO6	7	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 CO6 B 401 (A)

Bond lengths

Bond angles

Torsions

Rings

Ligand CO6 B 401 (B)	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CO6 A 502	
 Bond lengths	 Bond angles
 Torsions	 Rings
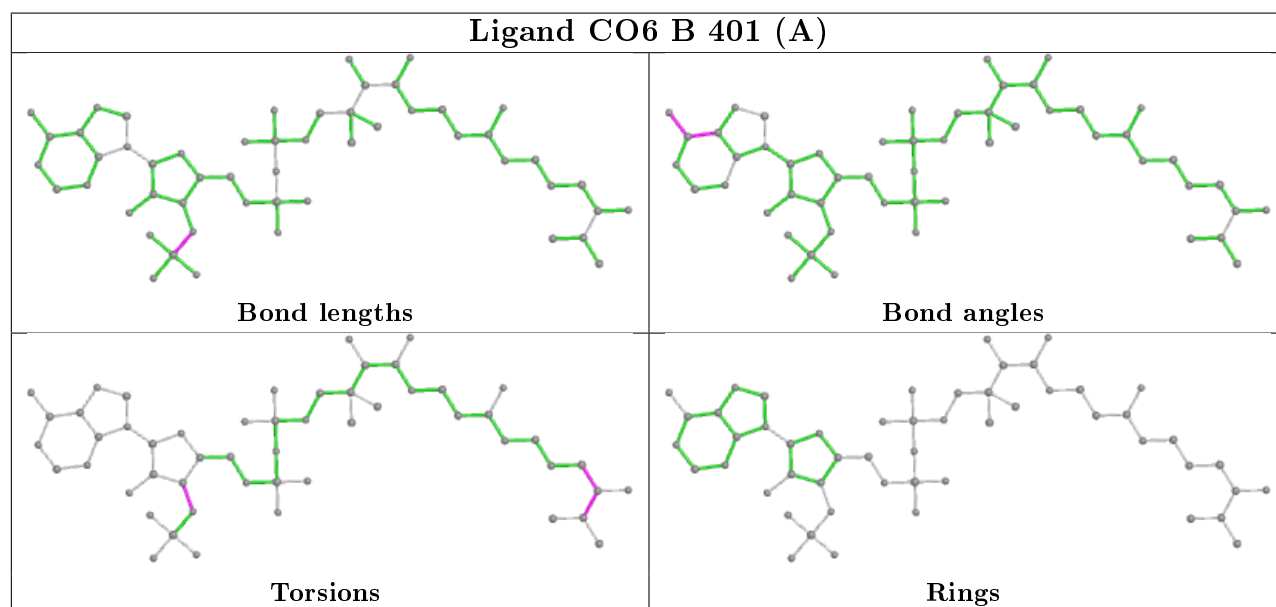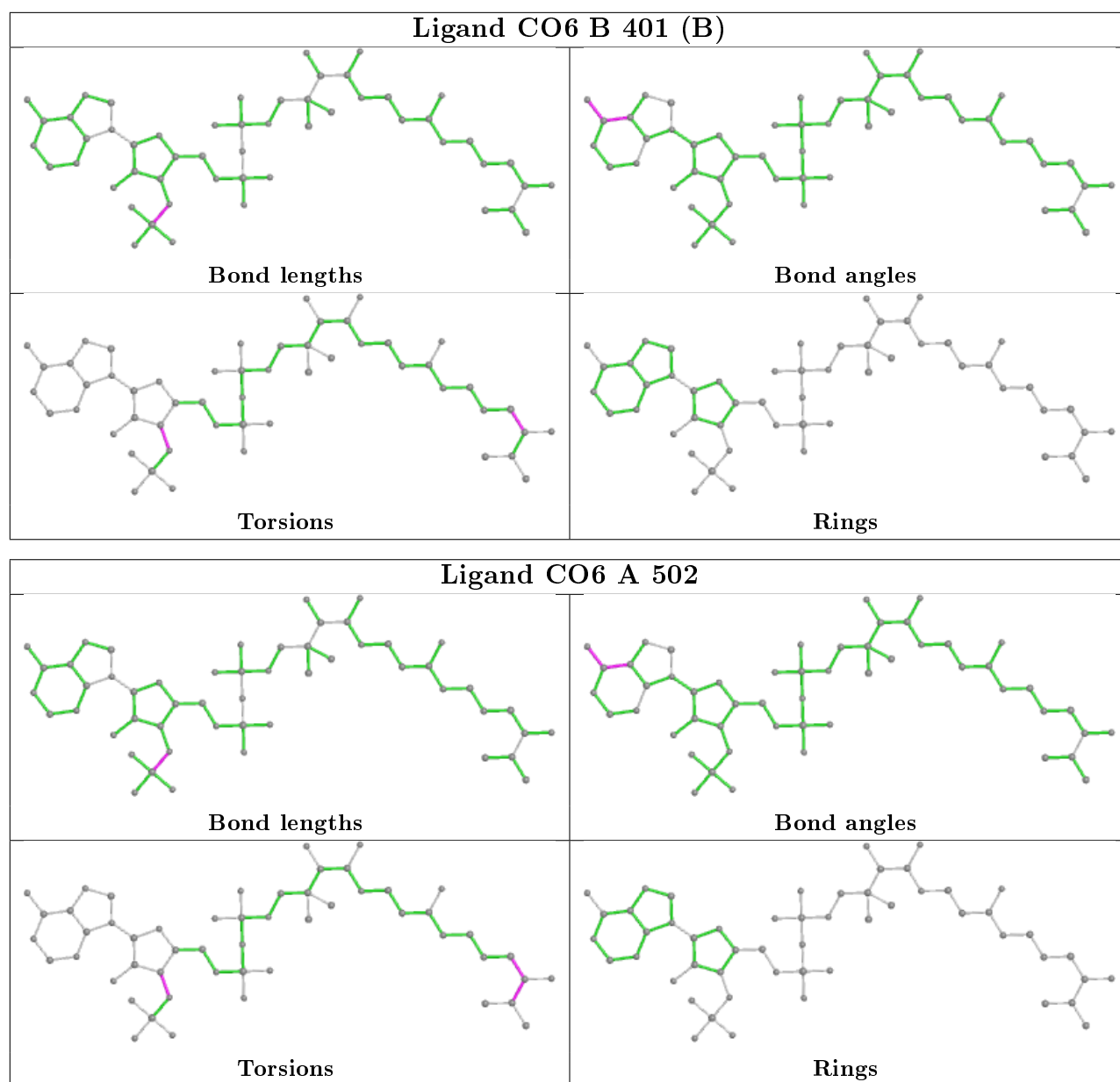
5.7 Other polymers (i)

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	319/324 (98%)	0.01	18 (5%)	24	22	16, 24, 45, 69	0
1	B	315/324 (97%)	-0.16	3 (0%)	82	82	17, 25, 44, 68	0
2	C	15/20 (75%)	0.57	3 (20%)	1	1	21, 27, 54, 68	0
2	D	14/20 (70%)	0.48	2 (14%)	2	2	22, 30, 50, 50	0
All	All	663/688 (96%)	-0.05	26 (3%)	39	36	16, 25, 46, 69	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	22	LEU	6.3
1	A	23	ALA	5.3
2	C	5	LYS	4.8
1	A	25	TYR	4.6
2	C	6	GLY	4.3
2	D	7	GLY	4.0
1	A	21	LYS	3.8
1	A	99	PHE	3.5
1	A	102	VAL	3.4
1	A	151	PRO	3.4
1	A	152	THR	3.2
1	A	67	PHE	3.1
1	B	340	THR	2.8
1	A	340	THR	2.8
1	B	306	MET	2.5
1	A	277[A]	ASP	2.4
1	A	104	ALA	2.4
1	A	153	GLY	2.3
1	A	20	LYS	2.3
1	A	298	PRO	2.3
1	A	98	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	96	ASP	2.2
2	D	6	GLY	2.2
2	C	18	HIS	2.1
1	B	296	ASP	2.0
1	A	296	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, 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(Å²)	Q<0.9
1	YCM	A	27[B]	10/11	0.89	0.12	31,35,46,46	10
1	YCM	A	27[A]	6/11	0.89	0.12	31,32,33,35	6
1	YCM	A	101	10/11	0.92	0.10	31,32,35,36	0
1	YCM	B	168	10/11	0.93	0.12	21,24,40,44	0
1	YCM	A	168	10/11	0.94	0.09	25,29,40,44	0
1	YCM	B	27[B]	10/11	0.96	0.11	25,26,29,29	10
1	YCM	B	27[A]	10/11	0.96	0.11	25,29,34,34	10
1	YCM	B	101	10/11	0.97	0.07	21,23,27,29	0

6.3 Carbohydrates (i)

There are no carbohydrates 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(Å²)	Q<0.9
5	GOL	B	402	6/6	0.74	0.18	38,48,53,54	0
7	UNX	A	511	1/1	0.76	0.23	36,36,36,36	0
7	UNX	A	513	1/1	0.78	0.28	40,40,40,40	0
7	UNX	B	406	1/1	0.78	0.43	43,43,43,43	0
5	GOL	A	503	6/6	0.80	0.29	39,43,44,47	0

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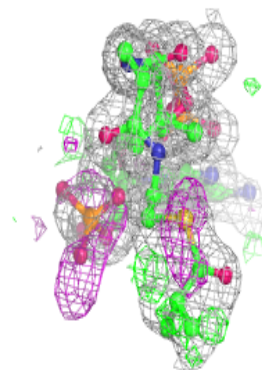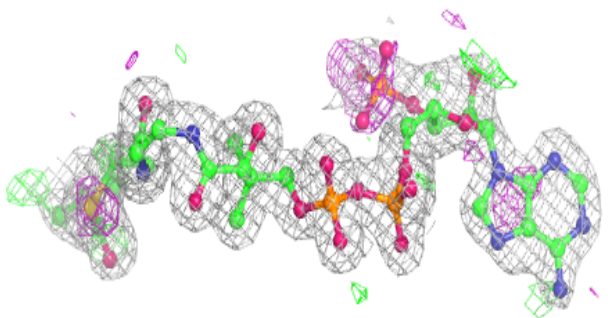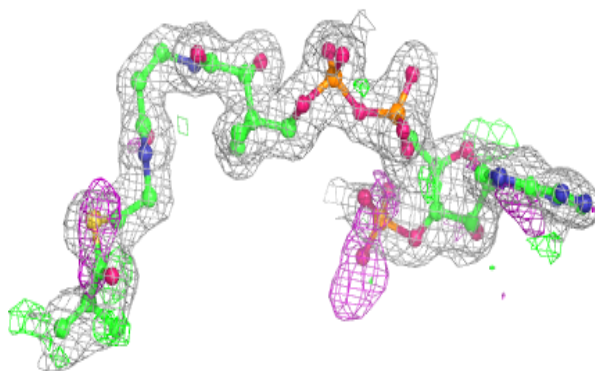| Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
7	UNX	A	507	1/1	0.82	0.22	34,34,34,34	0
7	UNX	A	510	1/1	0.85	0.28	32,32,32,32	0
3	ACT	A	501	4/4	0.85	0.19	56,57,58,58	0
5	GOL	B	403	6/6	0.85	0.10	40,46,47,47	0
7	UNX	A	512	1/1	0.86	0.14	41,41,41,41	0
7	UNX	B	407	1/1	0.87	0.11	33,33,33,33	0
7	UNX	A	506	1/1	0.89	0.18	31,31,31,31	0
7	UNX	A	509	1/1	0.89	0.17	37,37,37,37	0
7	UNX	B	411	1/1	0.90	0.19	38,38,38,38	0
7	UNX	B	410	1/1	0.91	0.19	29,29,29,29	0
7	UNX	B	408	1/1	0.91	0.08	29,29,29,29	0
7	UNX	B	405	1/1	0.92	0.07	36,36,36,36	0
7	UNX	A	505	1/1	0.92	0.18	26,26,26,26	0
4	CO6	A	502	53/53	0.94	0.13	19,31,60,77	0
4	CO6	B	401[B]	53/53	0.94	0.13	20,33,70,81	6
6	SO4	A	504	5/5	0.94	0.14	33,33,37,47	5
6	SO4	B	404	5/5	0.94	0.17	42,43,48,48	5
4	CO6	B	401[A]	53/53	0.94	0.13	20,31,70,81	6
7	UNX	A	508	1/1	0.96	0.23	29,29,29,29	0
7	UNX	B	409	1/1	0.97	0.18	27,27,27,27	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.
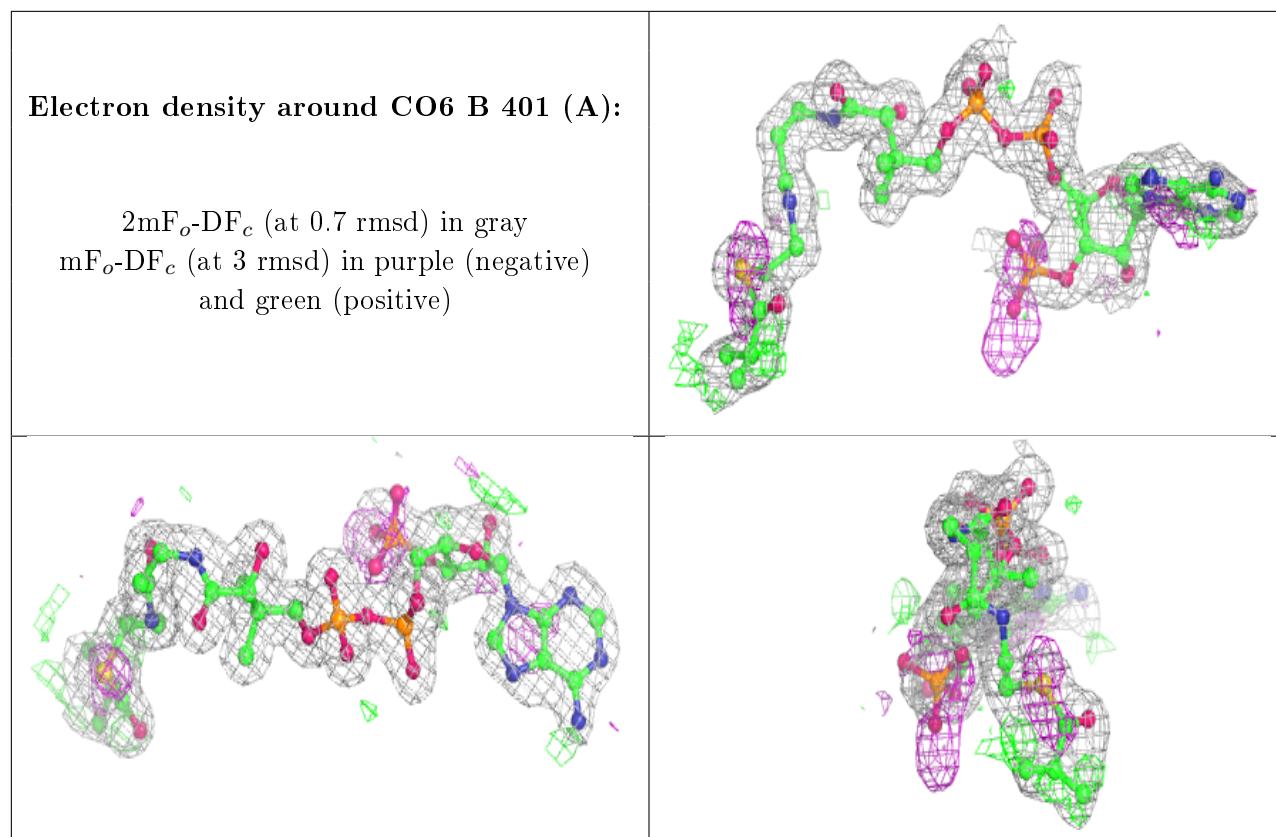
Electron density around CO6 A 502:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
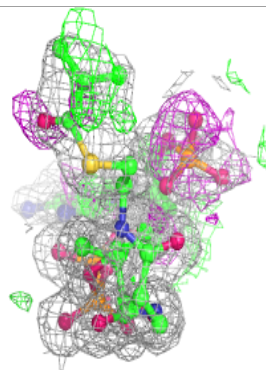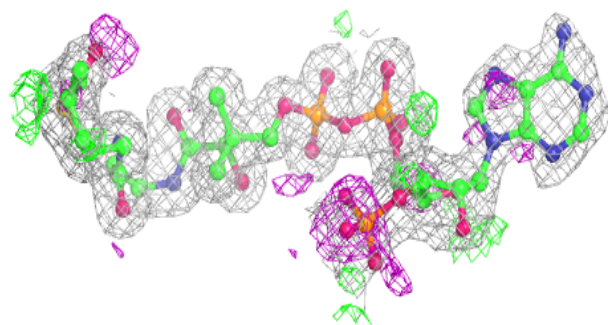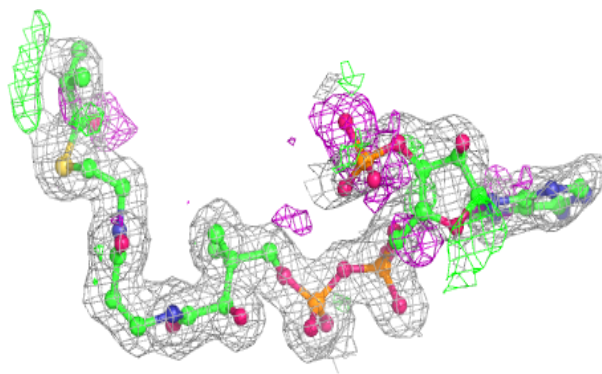
Electron density around CO6 B 401 (B):

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

Electron density around CO6 B 401 (A):

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

6.5 Other polymers (i)

There are no such residues in this entry.