Full wwPDB X-ray Structure Validation Report (i)

May 24, 2020 – 09:20 am BST

PDB ID	:	4PSW
Title	:	Crystal structure of histone acetyltransferase complex
Authors	:	Yang, M.; Li, Y.
Deposited on	:	2014-03-08
Resolution	:	2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

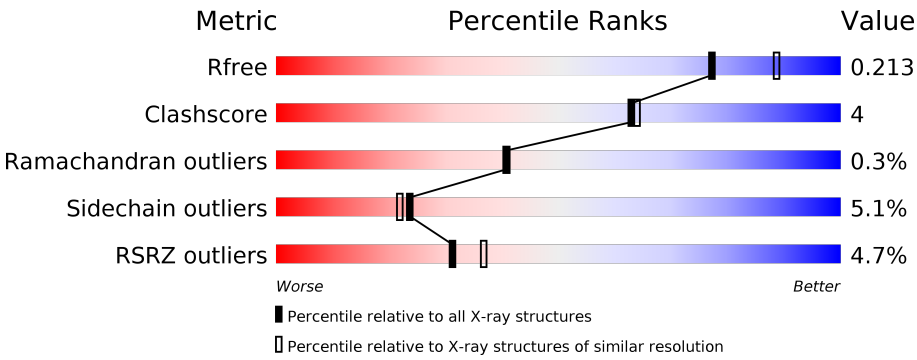
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 2.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	317	6% 86% 11% •
2	B	401	% 81% 9% • 9%
3	C	38	26% 74% 21% • •

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 6398 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
			Total	C	N	O	S			
1	A	316	2628	1695	429	500	4	0	0	0

- Molecule 2 is a protein called Histone acetyltransferase type B subunit 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
2	B	366	2907	1829	492	575	1	10	0	0	0

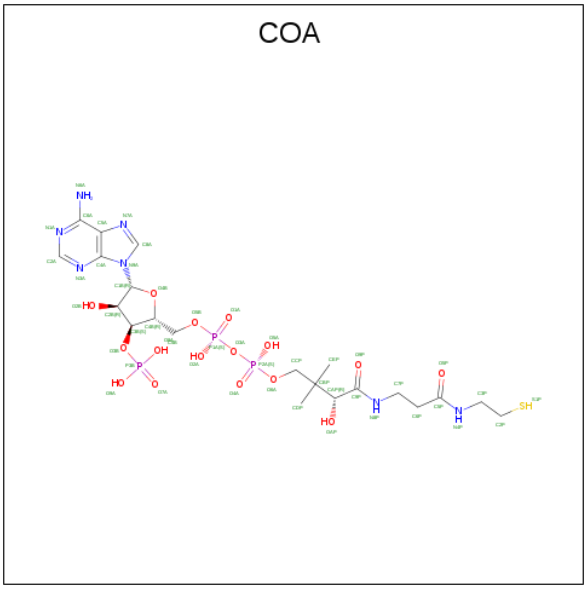
There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	EXPRESSION TAG	UNP P39984
B	2	GLU	-	EXPRESSION TAG	UNP P39984
B	3	ASN	-	EXPRESSION TAG	UNP P39984
B	4	GLN	-	EXPRESSION TAG	UNP P39984
B	5	GLU	-	EXPRESSION TAG	UNP P39984
B	6	LYS	-	EXPRESSION TAG	UNP P39984
B	143	THR	VAL	ENGINEERED MUTATION	UNP P39984
B	391	GLY	-	EXPRESSION TAG	UNP P39984
B	392	PRO	-	EXPRESSION TAG	UNP P39984
B	393	PRO	-	EXPRESSION TAG	UNP P39984
B	394	LYS	-	EXPRESSION TAG	UNP P39984
B	395	VAL	-	EXPRESSION TAG	UNP P39984
B	396	ASN	-	EXPRESSION TAG	UNP P39984
B	397	LYS	-	EXPRESSION TAG	UNP P39984
B	398	ASP	-	EXPRESSION TAG	UNP P39984
B	399	ILE	-	EXPRESSION TAG	UNP P39984
B	400	ILE	-	EXPRESSION TAG	UNP P39984
B	401	SER	-	EXPRESSION TAG	UNP P39984

- Molecule 3 is a protein called Histone H4 type VIII.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	38	289	177	69	43	0	0	0

- Molecule 4 is COENZYME A (three-letter code: COA) (formula: $C_{21}H_{36}N_7O_{16}P_3S$).



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

- Molecule 5 is water.

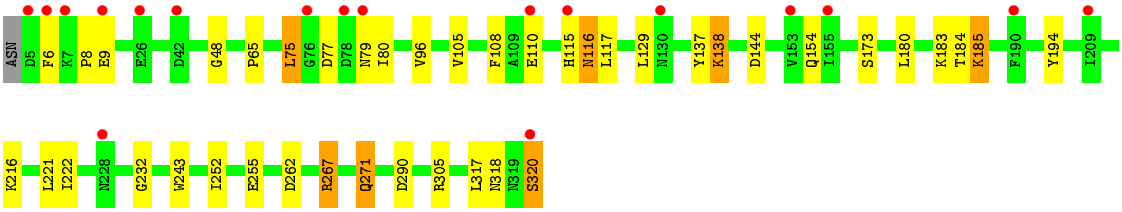
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	174	174	174	0	0
5	B	334	334	334	0	0
5	C	18	18	18	0	0

3 Residue-property plots (i)

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.

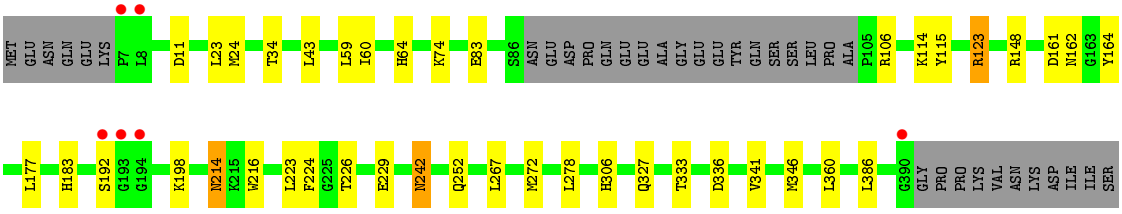
- Molecule 1: Histone acetyltransferase type B catalytic subunit

Chain A:



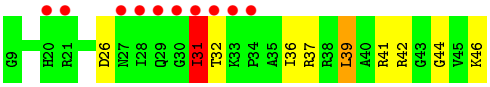
- Molecule 2: Histone acetyltransferase type B subunit 2

Chain B:



- Molecule 3: Histone H4 type VIII

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	77.99Å 98.44Å 124.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.70 – 2.10 29.73 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.70-2.10) 93.8 (29.73-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.85 (at 2.10Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.171 , 0.212 0.172 , 0.213	Depositor DCC
R_{free} test set	2869 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	24.3	Xtriage
Anisotropy	0.423	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 56.3	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	0.95	EDS
Total number of atoms	6398	wwPDB-VP
Average B, all atoms (Å^2)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.75% 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: TPO, COA

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	0.39	0/2691	0.51	0/3637
2	B	0.47	0/2967	0.61	1/4037 (0.0%)
3	C	0.36	0/290	0.50	0/379
All	All	0.43	0/5948	0.56	1/8053 (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})
2	B	278	LEU	CA-CB-CG	-5.94	101.64	115.30

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	2628	0	2568	26	0
2	B	2907	0	2780	19	0
3	C	289	0	330	8	0
4	A	48	0	32	4	0
5	A	174	0	0	7	1
5	B	334	0	0	8	2
5	C	18	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6398	0	5710	50	2

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 4.

All (50) 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)
3:C:46:LYS:O	5:C:108:HOH:O	1.95	0.84
1:A:154:GLN:NE2	5:A:506:HOH:O	2.10	0.83
1:A:271:GLN:HG2	5:A:662:HOH:O	1.77	0.83
1:A:117:LEU:HD12	1:A:180:LEU:HD11	1.66	0.76
2:B:11:ASP:OD1	5:B:624:HOH:O	2.05	0.75
2:B:115:TYR:OH	2:B:148:ARG:O	2.06	0.73
1:A:137:TYR:OH	5:A:610:HOH:O	2.07	0.71
1:A:262:ASP:OD1	5:A:539:HOH:O	2.15	0.64
2:B:341:VAL:O	3:C:41:ARG:NH2	2.34	0.61
3:C:42:ARG:HD3	3:C:46:LYS:HD2	1.82	0.61
1:A:290:ASP:O	5:A:622:HOH:O	2.17	0.58
1:A:116:ASN:N	1:A:116:ASN:OD1	2.20	0.58
2:B:306:HIS:HD2	5:B:677:HOH:O	1.87	0.57
2:B:242:ASN:ND2	5:B:802:HOH:O	2.36	0.57
2:B:229:GLU:OE1	5:B:791:HOH:O	2.17	0.56
2:B:74:LYS:HG2	2:B:114:LYS:HG2	1.88	0.56
1:A:318:ASN:HB2	5:A:587:HOH:O	2.08	0.54
2:B:23:LEU:HD21	3:C:31:ILE:HD13	1.89	0.54
1:A:138:LYS:HE2	5:A:571:HOH:O	2.09	0.52
1:A:267:ARG:NH2	4:A:401:COA:H52A	2.24	0.52
1:A:183:LYS:HG3	1:A:184:THR:HG23	1.92	0.51
1:A:77:ASP:HB3	1:A:80:ILE:HB	1.92	0.51
3:C:39:LEU:HD22	3:C:44:GLY:HA2	1.94	0.50
1:A:48:GLY:HA2	1:A:75:LEU:HD22	1.94	0.49
1:A:173:SER:HB2	1:A:194:TYR:CE1	2.47	0.49
2:B:34:TPO:O2P	2:B:74:LYS:NZ	2.47	0.48
1:A:243:TRP:HE3	1:A:252:ILE:HD12	1.79	0.48
1:A:216:LYS:HD3	5:B:701:HOH:O	2.15	0.46
2:B:177:LEU:HG	2:B:216:TRP:CZ2	2.50	0.46
1:A:232:GLY:HA3	4:A:401:COA:H143	1.97	0.45
3:C:32:THR:O	3:C:36:ILE:HG12	2.17	0.45
2:B:43:LEU:HD21	2:B:60:ILE:HD11	2.00	0.44
1:A:65:PRO:HG2	1:A:96:VAL:HG22	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:24:MET:HG3	3:C:39:LEU:HD13	1.99	0.44
2:B:242:ASN:HB3	5:B:802:HOH:O	2.17	0.44
2:B:327:GLN:NE2	5:B:671:HOH:O	2.46	0.44
2:B:123:ARG:HD3	2:B:164:TYR:O	2.17	0.43
5:B:680:HOH:O	3:C:37:ARG:HG3	2.19	0.43
2:B:177:LEU:HD11	2:B:224:PHE:CG	2.54	0.43
2:B:214:ASN:HB3	2:B:226:THR:HG22	1.99	0.43
1:A:320:SER:OG	1:A:320:SER:O	2.34	0.42
1:A:105:VAL:HA	1:A:108:PHE:CE2	2.54	0.42
1:A:222:ILE:HG13	4:A:401:COA:H142	2.02	0.42
1:A:216:LYS:HD2	1:A:255:GLU:HB2	2.01	0.42
2:B:333:THR:OG1	2:B:336:ASP:HB2	2.20	0.41
1:A:116:ASN:HD22	1:A:185:LYS:HE2	1.85	0.41
1:A:221:LEU:HD12	4:A:401:COA:H61	2.01	0.41
1:A:6:PHE:C	1:A:8:PRO:HD3	2.41	0.41
2:B:252:GLN:NE2	2:B:272:MET:SD	2.92	0.41
1:A:9:GLU:H	1:A:9:GLU:CD	2.24	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:693:HOH:O	5:B:694:HOH:O[4_446]	1.96	0.24
5:A:602:HOH:O	5:B:736:HOH:O[2_444]	2.01	0.19

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	314/317 (99%)	307 (98%)	7 (2%)	0	100 100
2	B	361/401 (90%)	346 (96%)	14 (4%)	1 (0%)	41 41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	C	36/38 (95%)	32 (89%)	3 (8%)	1 (3%)	5 1
All	All	711/756 (94%)	685 (96%)	24 (3%)	2 (0%)	41 41

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	162	ASN
3	C	31	ILE

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	291/292 (100%)	277 (95%)	14 (5%)	25 24
2	B	326/357 (91%)	310 (95%)	16 (5%)	25 23
3	C	27/27 (100%)	24 (89%)	3 (11%)	6 3
All	All	644/676 (95%)	611 (95%)	33 (5%)	24 22

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	75	LEU
1	A	79	ASN
1	A	110	GLU
1	A	115	HIS
1	A	116	ASN
1	A	129	LEU
1	A	138	LYS
1	A	144	ASP
1	A	185	LYS
1	A	267	ARG
1	A	271	GLN
1	A	305	ARG
1	A	317	LEU

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Mol	Chain	Res	Type
1	A	320	SER
2	B	59	LEU
2	B	64	HIS
2	B	83	GLU
2	B	106	ARG
2	B	123	ARG
2	B	161	ASP
2	B	183	HIS
2	B	192	SER
2	B	198	LYS
2	B	214	ASN
2	B	223	LEU
2	B	242	ASN
2	B	267	LEU
2	B	346	MET
2	B	360	LEU
2	B	386	LEU
3	C	26	ASP
3	C	31	ILE
3	C	39	LEU

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

Mol	Chain	Res	Type
2	B	299	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)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	TPO	B	34	2	8,10,11	1.38	1 (12%)	10,14,16	1.20	1 (10%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	TPO	B	34	2	-	3/9/11/13	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	34	TPO	P-OG1	2.62	1.64	1.59

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	34	TPO	CG2-CB-CA	-2.23	108.76	113.16

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	34	TPO	O-C-CA-CB
2	B	34	TPO	CG2-CB-OG1-P
2	B	34	TPO	N-CA-CB-CG2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	34	TPO	1	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

1 ligand is 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	COA	A	401	-	41,50,50	1.81	6 (14%)	52,75,75	1.47	4 (7%)

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	COA	A	401	-	-	19/44/64/64	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	401	COA	C5P-N4P	6.19	1.47	1.33
4	A	401	COA	C9P-N8P	5.70	1.46	1.33
4	A	401	COA	C6A-N6A	3.57	1.47	1.34
4	A	401	COA	C2A-N3A	2.85	1.36	1.32
4	A	401	COA	C2B-C3B	-2.80	1.46	1.52
4	A	401	COA	C2B-C1B	-2.65	1.49	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	401	COA	N3A-C2A-N1A	-5.89	119.47	128.68
4	A	401	COA	C7P-N8P-C9P	3.90	129.55	122.59
4	A	401	COA	C6P-C7P-N8P	2.52	116.98	111.90
4	A	401	COA	C4A-C5A-N7A	-2.24	107.06	109.40

There are no chirality outliers.

All (19) torsion outliers are listed below:

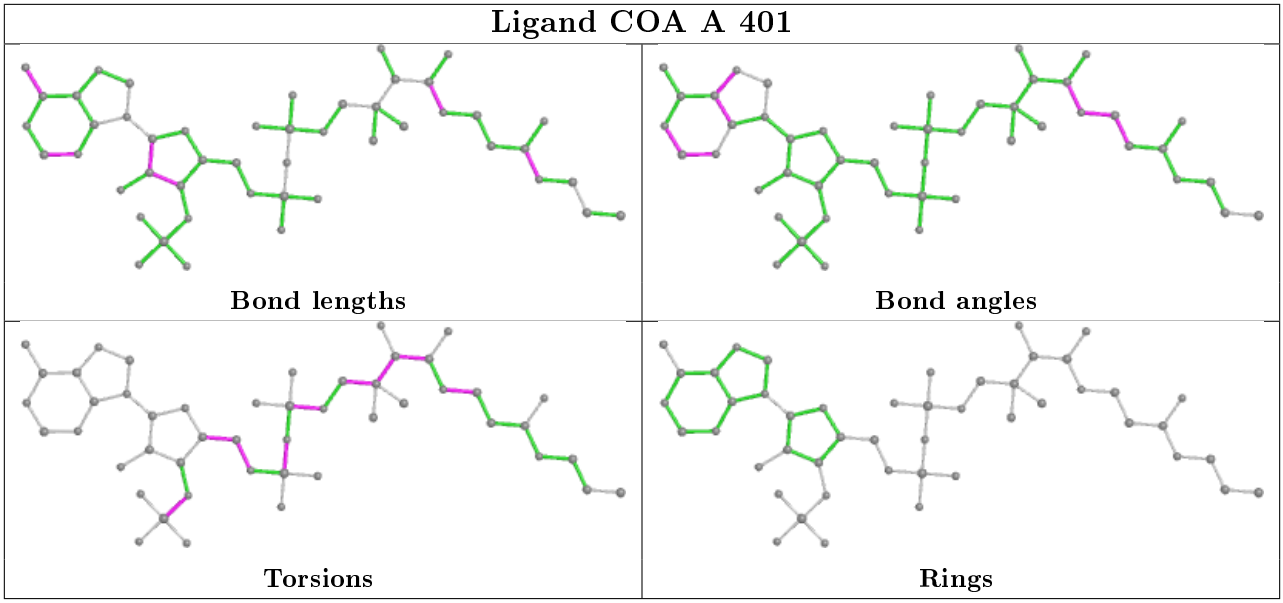
Mol	Chain	Res	Type	Atoms
4	A	401	COA	CCP-O6A-P2A-O4A
4	A	401	COA	CAP-CBP-CCP-O6A
4	A	401	COA	C9P-CAP-CBP-CCP
4	A	401	COA	C9P-CAP-CBP-CEP
4	A	401	COA	C6P-C7P-N8P-C9P
4	A	401	COA	O4B-C4B-C5B-O5B
4	A	401	COA	CEP-CBP-CCP-O6A
4	A	401	COA	OAP-CAP-CBP-CEP
4	A	401	COA	N8P-C9P-CAP-CBP
4	A	401	COA	OAP-CAP-CBP-CCP
4	A	401	COA	CDP-CBP-CCP-O6A
4	A	401	COA	O9P-C9P-CAP-CBP
4	A	401	COA	C4B-C5B-O5B-P1A
4	A	401	COA	C3B-O3B-P3B-O7A
4	A	401	COA	C9P-CAP-CBP-CDP
4	A	401	COA	C3B-O3B-P3B-O9A
4	A	401	COA	CCP-O6A-P2A-O3A
4	A	401	COA	OAP-CAP-CBP-CDP
4	A	401	COA	P2A-O3A-P1A-O2A

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	401	COA	4	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.



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	316/317 (99%)	0.18	18 (5%)	23	29	20, 39, 69, 106	0
2	B	365/401 (91%)	-0.24	6 (1%)	72	75	14, 22, 49, 83	0
3	C	38/38 (100%)	1.30	10 (26%)	0	0	24, 40, 115, 132	0
All	All	719/756 (95%)	0.03	34 (4%)	31	37	14, 30, 67, 132	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	30	GLY	7.4
3	C	29	GLN	5.9
3	C	28	ILE	5.7
3	C	31	ILE	5.7
1	A	6	PHE	5.3
3	C	21	ARG	5.1
2	B	8	LEU	4.8
1	A	78	ASP	4.8
2	B	194	GLY	4.5
1	A	320	SER	4.2
2	B	7	PRO	4.0
2	B	390	GLY	3.8
3	C	32	THR	3.8
1	A	115	HIS	3.5
1	A	209	ILE	3.5
2	B	193	GLY	3.4
1	A	79	ASN	3.3
1	A	5	ASP	3.3
1	A	7	LYS	3.3
3	C	20	HIS	2.9
3	C	34	PRO	2.9
1	A	155	ILE	2.8
1	A	130	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
3	C	33	LYS	2.6
1	A	153	VAL	2.6
1	A	76	GLY	2.5
1	A	228	ASN	2.4
1	A	9	GLU	2.4
3	C	27	ASN	2.4
2	B	192	SER	2.4
1	A	26	GLU	2.3
1	A	110	GLU	2.2
1	A	42	ASP	2.1
1	A	190	PHE	2.1

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
2	TPO	B	34	11/12	0.85	0.22	27,38,114,152	0

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

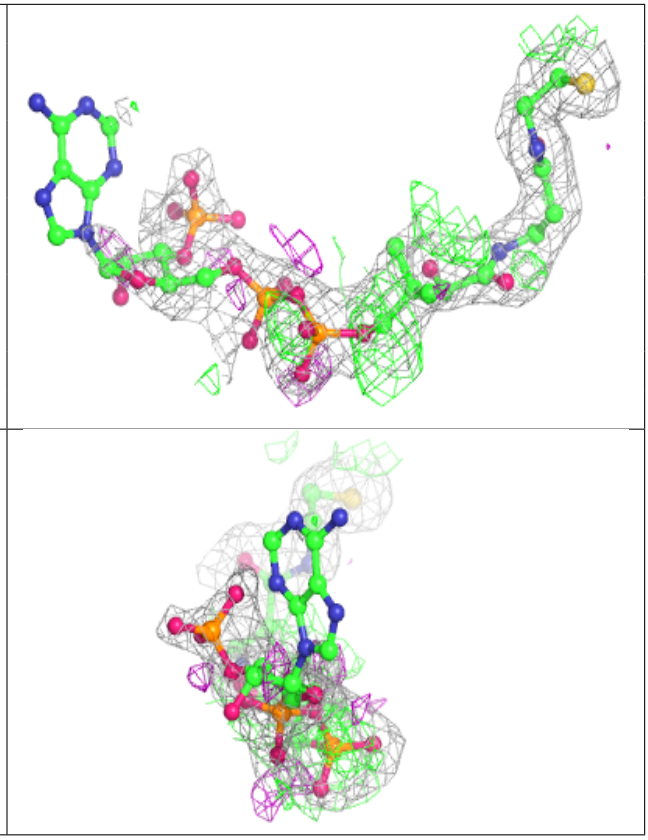
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	COA	A	401	48/48	0.75	0.30	33,105,129,154	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 COA A 401:

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



6.5 Other polymers (i)

There are no such residues in this entry.