



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 24, 2024 – 11:53 AM EDT

PDB ID : 6Z81
Title : TsaBD bound to the inhibitor
Authors : Missouri, S.; Van Tilbeurgh, H.
Deposited on : 2020-06-02
Resolution : 2.31 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 ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
EDS : 2.37.1
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) : 2.37.1

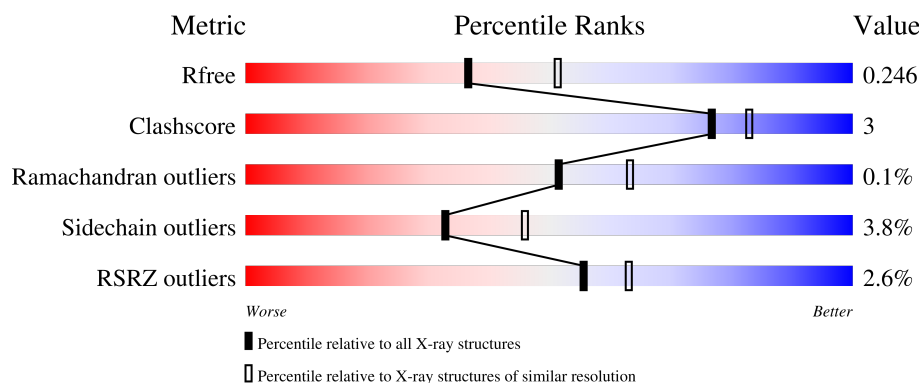
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

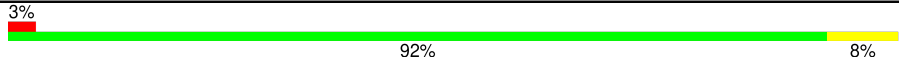
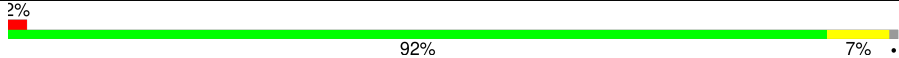


The reported resolution of this entry is 2.31 Å.

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	5974 (2.34-2.30)
Clashscore	141614	6604 (2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)
RSRZ outliers	127900	5855 (2.34-2.30)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	343	
1	B	343	
2	C	237	
2	D	237	

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
8	ACT	C	304	-	-	-	X

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 8886 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 tRNA N6-adenosine threonylcarbamoyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	342	Total	C	N	O	S	0	2	0
			2564	1629	444	477	14			
1	B	341	Total	C	N	O	S	0	0	0
			2553	1618	447	474	14			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	338	HIS	-	expression tag	UNP P05852
A	339	HIS	-	expression tag	UNP P05852
A	340	HIS	-	expression tag	UNP P05852
A	341	HIS	-	expression tag	UNP P05852
A	342	HIS	-	expression tag	UNP P05852
A	343	HIS	-	expression tag	UNP P05852
B	338	HIS	-	expression tag	UNP P05852
B	339	HIS	-	expression tag	UNP P05852
B	340	HIS	-	expression tag	UNP P05852
B	341	HIS	-	expression tag	UNP P05852
B	342	HIS	-	expression tag	UNP P05852
B	343	HIS	-	expression tag	UNP P05852

- Molecule 2 is a protein called tRNA threonylcarbamoyladenine biosynthesis protein Tsab.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	229	Total	C	N	O	S	0	0	0
			1733	1098	299	324	12			
2	D	228	Total	C	N	O	S	0	1	0
			1738	1100	298	328	12			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	232	HIS	-	expression tag	UNP P76256
C	233	HIS	-	expression tag	UNP P76256
C	234	HIS	-	expression tag	UNP P76256
C	235	HIS	-	expression tag	UNP P76256
C	236	HIS	-	expression tag	UNP P76256
C	237	HIS	-	expression tag	UNP P76256
D	232	HIS	-	expression tag	UNP P76256
D	233	HIS	-	expression tag	UNP P76256
D	234	HIS	-	expression tag	UNP P76256
D	235	HIS	-	expression tag	UNP P76256
D	236	HIS	-	expression tag	UNP P76256
D	237	HIS	-	expression tag	UNP P76256

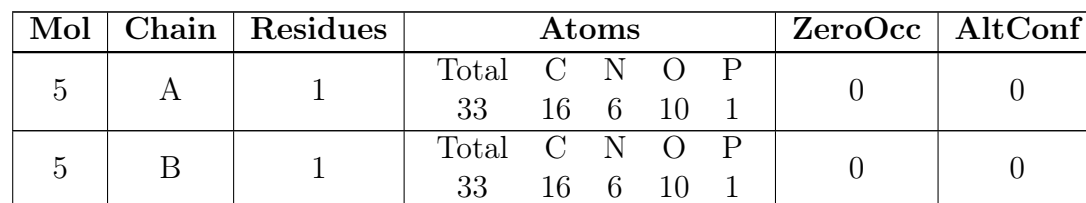
- Molecule 3 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Ni 2 2	0	0
3	B	2	Total Ni 2 2	0	0

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Zn 1 1	0	0
4	B	1	Total Zn 1 1	0	0

- Molecule 5 is (2 {S},3 {R})-2-[2-[(2 {R},3 {S},4 {R},5 {R})-5-(6-aminopurin-9-yl)-3,4-bis(oxidanyl)oxolan-2-yl]methoxy-oxidanyl-phosphoryl]ethanoylamino]-3-oxidanyl-butanoic acid (three-letter code: QCB) (formula: C₁₆H₂₃N₆O₁₀P) (labeled as "Ligand of Interest" by depositor).



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



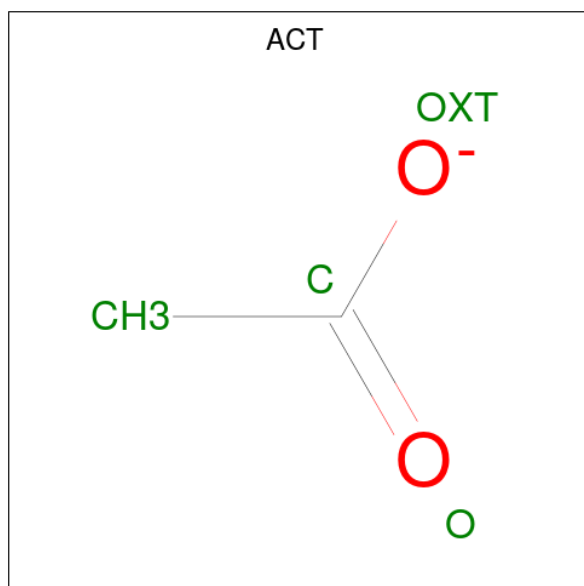
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Na	0	0
			1	1		
7	C	1	Total	Na	0	0
			1	1		
7	D	1	Total	Na	0	0
			1	1		

- Molecule 8 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



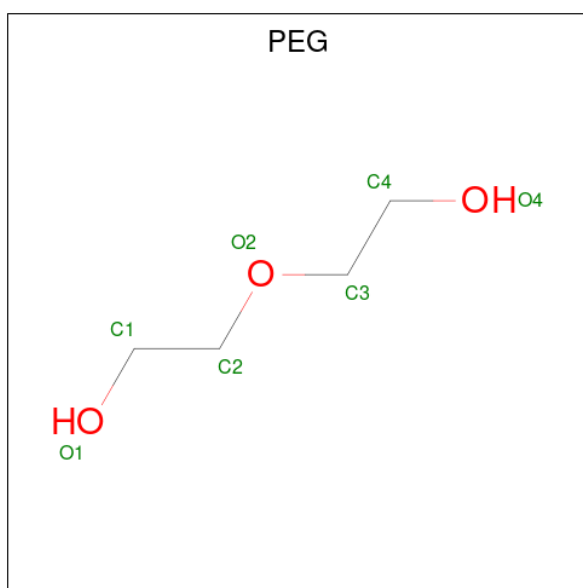
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			4	2	2		
8	A	1	Total	C	O	0	0
			4	2	2		
8	A	1	Total	C	O	0	0
			4	2	2		
8	B	1	Total	C	O	0	0
			4	2	2		

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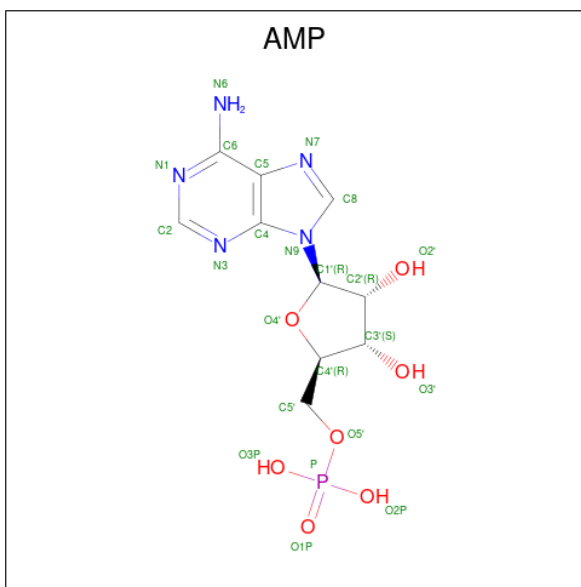
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	C	O	0	0
			4	2	2		
8	C	1	Total	C	O	0	0
			4	2	2		
8	C	1	Total	C	O	0	0
			4	2	2		
8	D	1	Total	C	O	0	0
			4	2	2		
8	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 9 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			7	4	3		
9	A	1	Total	C	O	0	0
			7	4	3		
9	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 10 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	C	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
10	D	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

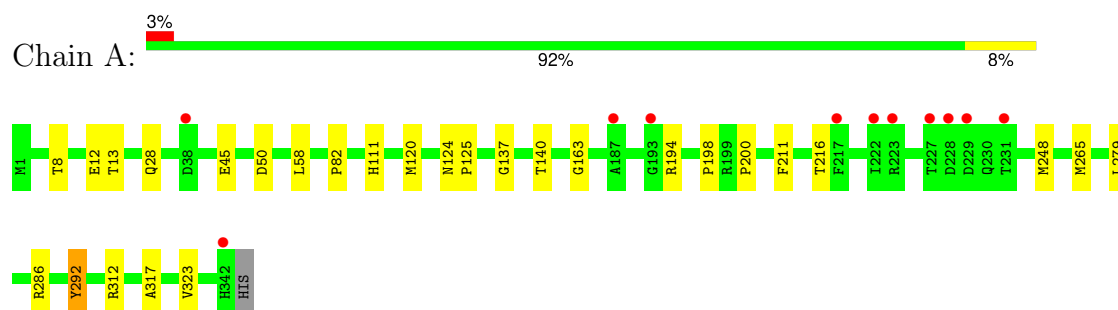
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	30	Total	O	0	0
			30	30		
11	B	32	Total	O	0	0
			32	32		
11	C	18	Total	O	0	0
			18	18		
11	D	19	Total	O	0	1
			20	20		

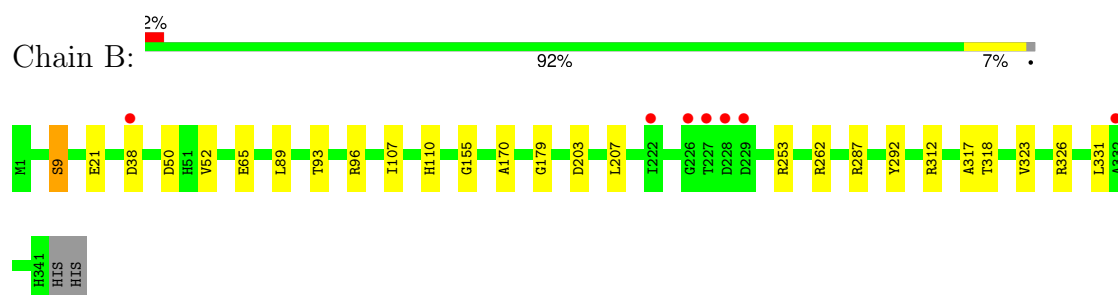
3 Residue-property plots [i](#)

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.

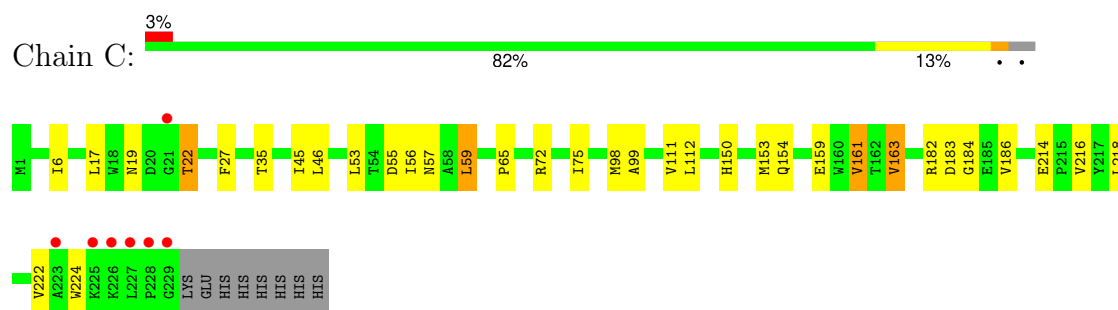
- Molecule 1: tRNA N6-adenosine threonylcarbamoyltransferase



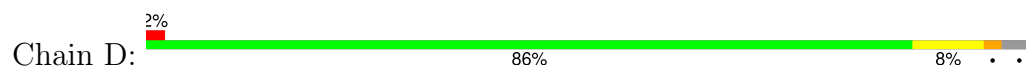
- Molecule 1: tRNA N6-adenosine threonylcarbamoyltransferase

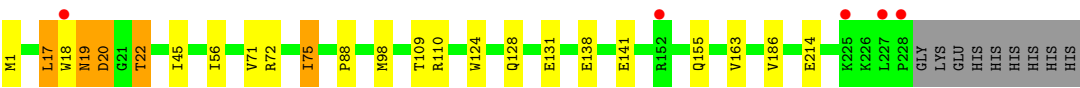


- Molecule 2: tRNA threonylcarbamoyladenosine biosynthesis protein TsaB



- Molecule 2: tRNA threonylcarbamoyladenosine biosynthesis protein TsaB





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	63.23Å 69.25Å 86.54Å 109.38° 92.00° 116.94°	Depositor
Resolution (Å)	42.47 – 2.31 42.47 – 2.31	Depositor EDS
% Data completeness (in resolution range)	96.2 (42.47-2.31) 96.3 (42.47-2.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.32 (at 2.32Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.182 , 0.233 0.190 , 0.246	Depositor DCC
R_{free} test set	2557 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	34.2	Xtriage
Anisotropy	0.037	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 53.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.084 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8886	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.98% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ACT, NI, AMP, NA, QCB, SO4, ZN, PEG

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	0.50	0/2624	0.67	0/3561
1	B	0.50	0/2606	0.68	0/3535
2	C	0.52	0/1770	0.71	0/2409
2	D	0.50	0/1778	0.72	1/2421 (0.0%)
All	All	0.50	0/8778	0.69	1/11926 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	19	ASN	C-N-CA	5.09	134.44	121.70

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	2564	0	2530	14	0
1	B	2553	0	2541	12	0
2	C	1733	0	1709	19	0
2	D	1738	0	1714	13	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	33	0	0	0	0
5	B	33	0	0	1	0
6	A	10	0	0	0	0
6	B	10	0	0	0	0
7	A	1	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
8	A	12	0	9	0	0
8	B	4	0	3	1	0
8	C	12	0	9	2	0
8	D	8	0	6	0	0
9	A	14	0	20	0	0
9	B	7	0	10	1	0
10	C	23	0	12	0	0
10	D	23	0	12	0	0
11	A	30	0	0	0	0
11	B	32	0	0	0	0
11	C	18	0	0	0	0
11	D	20	0	0	0	0
All	All	8886	0	8575	52	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 (52) 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)
2:C:163:VAL:HG22	2:C:186:VAL:HB	1.63	0.79
2:D:163:VAL:HG22	2:D:186:VAL:HB	1.71	0.72
1:B:253:ARG:HH21	8:B:407:ACT:H1	1.58	0.68
1:B:96:ARG:HG2	1:B:323:VAL:HG22	1.80	0.63
2:D:1:MET:HB3	2:D:18:TRP:HZ3	1.64	0.62
2:D:19:ASN:HB3	2:D:22:THR:HG23	1.82	0.62
1:B:65:GLU:HA	2:C:224:TRP:HB2	1.85	0.58
2:C:6:ILE:HD12	2:C:59:LEU:HD21	1.86	0.57
2:C:98:MET:HB3	2:C:163:VAL:HG13	1.87	0.57
2:D:98:MET:HB3	2:D:163:VAL:CG1	2.37	0.54
1:B:262:ARG:HH22	9:B:408:PEG:H12	1.73	0.54
2:C:19:ASN:HB2	2:C:22:THR:HB	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:GLY:HA2	1:A:163:GLY:HA3	1.90	0.54
2:D:110:ARG:HG2	2:D:128:GLN:HG2	1.89	0.54
2:D:98:MET:HB3	2:D:163:VAL:HG13	1.90	0.53
2:C:72:ARG:HA	2:C:75:ILE:HG22	1.93	0.51
2:C:216:VAL:HA	8:C:303:ACT:H3	1.92	0.51
1:A:216:THR:HG21	2:D:88:PRO:HG3	1.93	0.50
2:D:71:VAL:O	2:D:75:ILE:HG23	2.12	0.48
2:C:112:LEU:HD13	2:C:153:MET:HE3	1.96	0.48
2:D:18:TRP:CE2	2:D:20:ASP:O	2.67	0.48
1:A:45:GLU:HG2	2:C:222:VAL:HB	1.96	0.47
1:B:312:ARG:HB3	1:B:317:ALA:HB3	1.96	0.46
1:A:8:THR:HG22	1:A:13:THR:HG23	1.98	0.46
2:C:27:PHE:HB2	8:C:304:ACT:H3	1.97	0.46
2:C:98:MET:HB3	2:C:163:VAL:CG1	2.45	0.46
1:A:120:MET:HA	1:A:125:PRO:HB3	1.98	0.46
1:A:198:PRO:O	1:A:200:PRO:HD3	2.16	0.46
1:B:52:VAL:HG21	2:D:72:ARG:HG2	1.97	0.46
2:C:182:ARG:HE	2:C:183:ASP:H	1.62	0.46
2:D:17:LEU:HD12	2:D:45:ILE:HG23	1.97	0.46
2:C:161:VAL:HG13	2:C:184:GLY:CA	2.46	0.45
1:A:323:VAL:HB	2:C:35:THR:HB	1.97	0.45
1:B:170:ALA:CB	1:B:179:GLY:HA3	2.47	0.45
2:C:65:PRO:HG3	2:C:218:LEU:HD12	1.98	0.45
1:A:82:PRO:HD2	1:A:111:HIS:HB3	1.98	0.44
1:A:248:MET:HG3	1:A:279:LEU:HD23	2.00	0.44
2:D:131:GLU:H	2:D:131:GLU:CD	2.20	0.44
1:A:28:GLN:HB3	1:A:58:LEU:HD22	1.99	0.44
2:C:99:ALA:HA	2:C:111:VAL:HG11	1.98	0.44
1:A:45:GLU:OE2	2:C:72:ARG:NH2	2.51	0.43
1:B:107:ILE:CD1	1:B:318:THR:HG22	2.49	0.43
1:B:110:HIS:CE1	1:B:331:LEU:HD13	2.54	0.43
1:B:155:GLY:HA3	1:B:207:LEU:O	2.20	0.42
1:A:140:THR:HG21	1:A:211:PHE:HE2	1.84	0.42
2:C:46:LEU:HD11	2:C:53:LEU:HD13	2.02	0.41
2:C:150:HIS:O	2:C:154:GLN:HG2	2.20	0.41
2:D:124:TRP:O	2:D:141:GLU:HA	2.21	0.41
1:A:265:MET:HE3	1:A:292:TYR:HD2	1.85	0.41
1:A:312:ARG:HB3	1:A:317:ALA:HB3	2.02	0.41
1:B:9:SER:HB3	5:B:404:QCB:CGX	2.51	0.40
1:B:89:LEU:O	1:B:93:THR:HG23	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	342/343 (100%)	331 (97%)	11 (3%)	0	100	100
1	B	339/343 (99%)	330 (97%)	9 (3%)	0	100	100
2	C	227/237 (96%)	216 (95%)	11 (5%)	0	100	100
2	D	227/237 (96%)	219 (96%)	7 (3%)	1 (0%)	34	41
All	All	1135/1160 (98%)	1096 (97%)	38 (3%)	1 (0%)	51	63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	20	ASP

5.3.2 Protein sidechains

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	255/264 (97%)	248 (97%)	7 (3%)	44	60
1	B	257/264 (97%)	249 (97%)	8 (3%)	40	55
2	C	174/187 (93%)	163 (94%)	11 (6%)	18	24
2	D	178/187 (95%)	170 (96%)	8 (4%)	27	38
All	All	864/902 (96%)	830 (96%)	34 (4%)	33	45

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	GLU
1	A	50	ASP
1	A	124	ASN
1	A	194	ARG
1	A	286[B]	ARG
1	A	286[C]	ARG
1	A	292	TYR
1	B	9	SER
1	B	21	GLU
1	B	38	ASP
1	B	50	ASP
1	B	203	ASP
1	B	287	ARG
1	B	292	TYR
1	B	326	ARG
2	C	17	LEU
2	C	22	THR
2	C	45	ILE
2	C	55	ASP
2	C	56	ILE
2	C	57	ASN
2	C	59	LEU
2	C	159	GLU
2	C	161	VAL
2	C	163	VAL
2	C	214	GLU
2	D	17	LEU
2	D	22	THR
2	D	56	ILE
2	D	75	ILE
2	D	109	THR
2	D	138	GLU
2	D	155	GLN
2	D	214	GLU

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

Mol	Chain	Res	Type
1	B	28	GLN
2	C	24	ASN
2	D	212	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 29 ligands modelled in this entry, 9 are monoatomic - leaving 20 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	$\# Z > 2$
5	QCB	A	404	4	30,35,35	1.97	7 (23%)	33,52,52	2.06	8 (24%)
8	ACT	D	303	-	3,3,3	1.34	0	3,3,3	0.81	0
10	AMP	C	302	-	21,25,25	0.86	0	23,38,38	0.82	1 (4%)
8	ACT	C	305	-	3,3,3	1.23	0	3,3,3	1.04	0
8	ACT	C	303	-	3,3,3	1.22	0	3,3,3	0.66	0
8	ACT	A	409	-	3,3,3	1.17	0	3,3,3	0.90	0
8	ACT	A	412	-	3,3,3	1.45	0	3,3,3	0.77	0
9	PEG	B	408	-	6,6,6	0.21	0	5,5,5	0.10	0
5	QCB	B	404	4	30,35,35	2.01	5 (16%)	33,52,52	1.74	6 (18%)
8	ACT	B	407	-	3,3,3	1.12	0	3,3,3	1.11	0
6	SO4	A	405	-	4,4,4	0.26	0	6,6,6	0.13	0
6	SO4	B	405	-	4,4,4	0.28	0	6,6,6	0.14	0
8	ACT	A	408	-	3,3,3	1.23	0	3,3,3	1.05	0
6	SO4	A	406	-	4,4,4	0.27	0	6,6,6	0.09	0
9	PEG	A	410	7	6,6,6	0.15	0	5,5,5	0.15	0
8	ACT	C	304	-	3,3,3	1.65	1 (33%)	3,3,3	0.60	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	AMP	D	302	-	21,25,25	0.63	0	23,38,38	0.82	1 (4%)
9	PEG	A	411	-	6,6,6	0.24	0	5,5,5	0.17	0
6	SO4	B	406	-	4,4,4	0.29	0	6,6,6	0.05	0
8	ACT	D	304	-	3,3,3	1.01	0	3,3,3	0.71	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
5	QCB	B	404	4	-	5/23/43/43	0/3/3/3
5	QCB	A	404	4	-	5/23/43/43	0/3/3/3
10	AMP	D	302	-	-	3/6/26/26	0/3/3/3
10	AMP	C	302	-	-	1/6/26/26	0/3/3/3
9	PEG	A	411	-	-	0/4/4/4	-
9	PEG	A	410	7	-	3/4/4/4	-
9	PEG	B	408	-	-	4/4/4/4	-

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	404	QCB	CCA-NX	5.88	1.46	1.34
5	B	404	QCB	O4'-C1'	5.86	1.48	1.40
5	A	404	QCB	CCA-NX	5.51	1.45	1.34
5	A	404	QCB	O4'-C1'	5.42	1.48	1.40
5	B	404	QCB	C6-N6	3.30	1.45	1.34
5	A	404	QCB	C6-N6	3.12	1.45	1.34
5	A	404	QCB	P1-CP2	2.53	1.87	1.80
5	A	404	QCB	P1-OP1	-2.50	1.50	1.56
5	A	404	QCB	C1'-N9	-2.42	1.43	1.49
5	A	404	QCB	OCA-CCA	-2.41	1.18	1.23
5	B	404	QCB	P1-OP1	-2.39	1.50	1.56
5	B	404	QCB	P1-CP2	2.06	1.86	1.80
8	C	304	ACT	OXT-C	-2.06	1.21	1.30

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	404	QCB	CP2-CCA-NX	6.59	121.46	115.19
5	B	404	QCB	CP2-CCA-NX	4.84	119.80	115.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	404	QCB	C4'-O4'-C1'	-3.96	106.30	109.92
5	B	404	QCB	CAX-NX-CCA	-3.95	113.99	121.80
5	A	404	QCB	OGX-CBX-CAX	3.57	116.28	109.07
5	B	404	QCB	O4'-C1'-N9	3.48	113.36	108.75
5	A	404	QCB	OP1-P1-CP2	3.47	113.56	105.87
5	A	404	QCB	CAX-NX-CCA	-3.46	114.97	121.80
5	B	404	QCB	OGX-CBX-CAX	2.95	115.03	109.07
5	B	404	QCB	OP3-P1-CP2	2.66	114.88	109.02
5	A	404	QCB	OP3-P1-CP2	-2.41	103.71	109.02
10	D	302	AMP	C5-C6-N6	2.37	123.92	120.31
5	A	404	QCB	OXT-CX-OX	-2.36	118.72	124.08
5	B	404	QCB	C4'-O4'-C1'	-2.29	107.83	109.92
5	A	404	QCB	C1'-N9-C4	-2.25	122.69	126.64
10	C	302	AMP	C5-C6-N6	2.16	123.61	120.31

There are no chirality outliers.

All (21) torsion outliers are listed below:

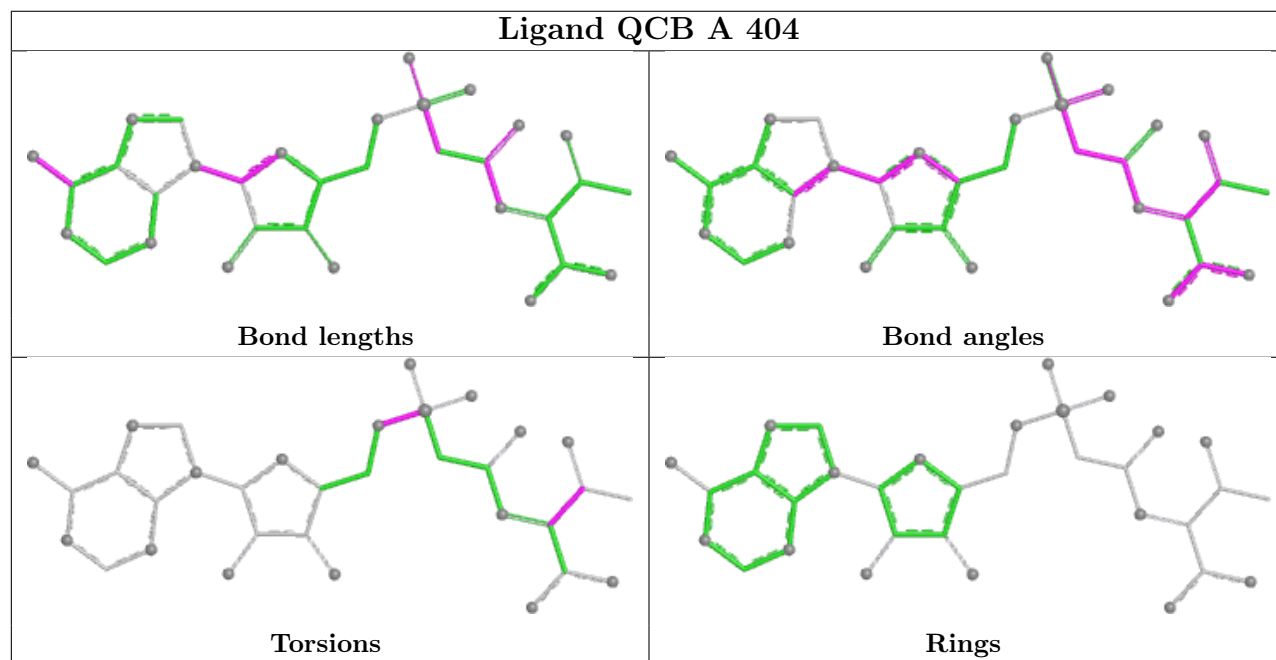
Mol	Chain	Res	Type	Atoms
5	A	404	QCB	CX-CAX-CBX-CGX
5	A	404	QCB	CX-CAX-CBX-OGX
5	A	404	QCB	NX-CAX-CBX-CGX
5	A	404	QCB	NX-CAX-CBX-OGX
5	B	404	QCB	CX-CAX-CBX-CGX
5	B	404	QCB	CX-CAX-CBX-OGX
5	B	404	QCB	NX-CAX-CBX-CGX
5	B	404	QCB	NX-CAX-CBX-OGX
10	D	302	AMP	C5'-O5'-P-O1P
10	D	302	AMP	C5'-O5'-P-O2P
10	D	302	AMP	C5'-O5'-P-O3P
9	A	410	PEG	O1-C1-C2-O2
9	A	410	PEG	C1-C2-O2-C3
9	A	410	PEG	C4-C3-O2-C2
9	B	408	PEG	C1-C2-O2-C3
5	A	404	QCB	C5'-O5'-P1-CP2
9	B	408	PEG	O1-C1-C2-O2
9	B	408	PEG	O2-C3-C4-O4
9	B	408	PEG	C4-C3-O2-C2
5	B	404	QCB	C5'-O5'-P1-CP2
10	C	302	AMP	C5'-O5'-P-O3P

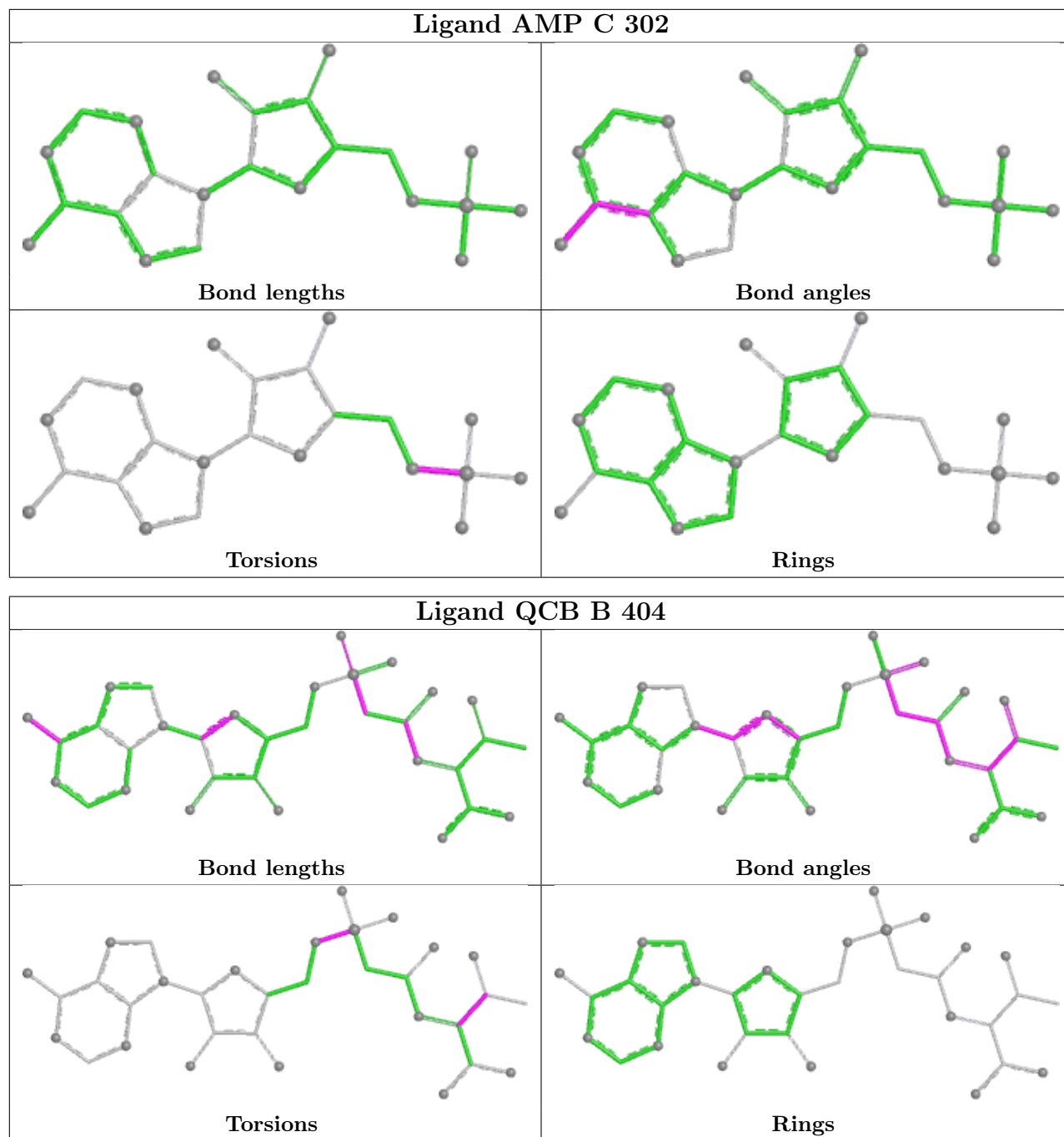
There are no ring outliers.

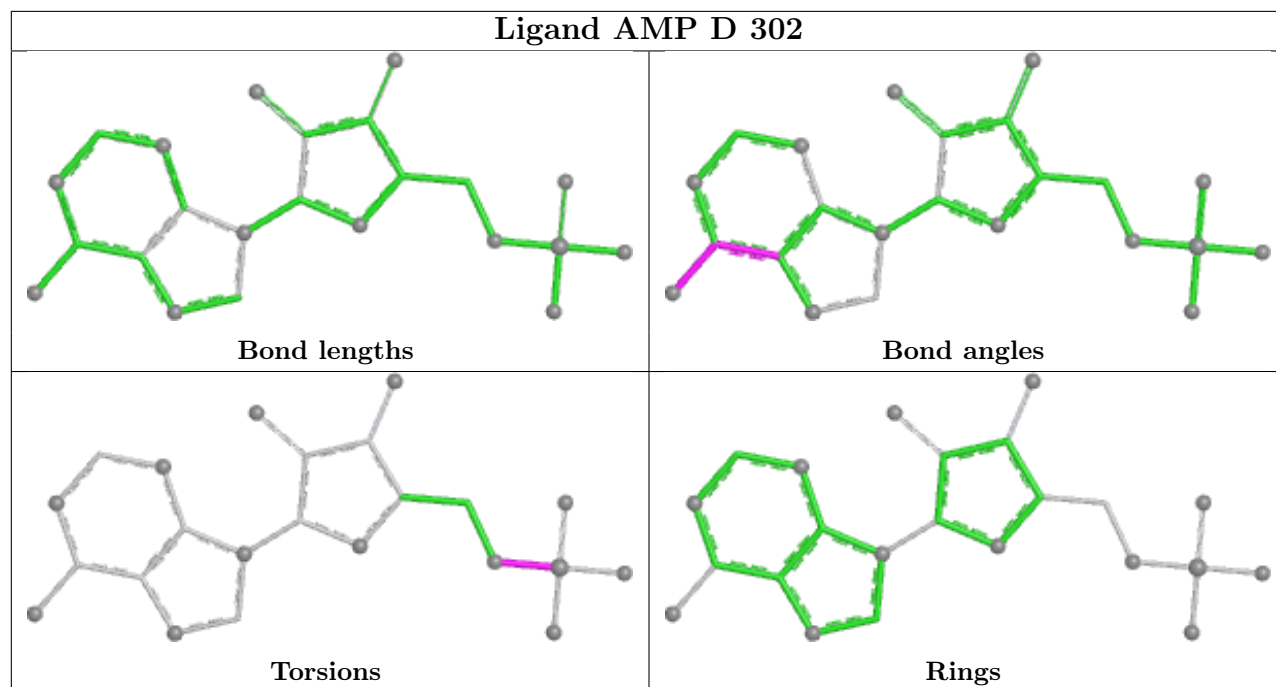
5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	C	303	ACT	1	0
9	B	408	PEG	1	0
5	B	404	QCB	1	0
8	B	407	ACT	1	0
8	C	304	ACT	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 than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	342/343 (99%)	-0.12	11 (3%) 47 55	24, 35, 58, 77	1 (0%)
1	B	341/343 (99%)	-0.14	7 (2%) 63 70	22, 33, 53, 73	1 (0%)
2	C	229/237 (96%)	-0.27	7 (3%) 49 56	24, 35, 60, 92	2 (0%)
2	D	228/237 (96%)	-0.30	5 (2%) 62 69	24, 36, 62, 77	1 (0%)
All	All	1140/1160 (98%)	-0.19	30 (2%) 56 63	22, 35, 59, 92	5 (0%)

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	227	THR	4.9
2	D	227	LEU	4.6
1	A	229	ASP	4.2
2	D	228	PRO	3.5
2	D	18	TRP	3.4
1	A	217	PHE	3.2
1	A	227	THR	3.2
2	C	229	GLY	3.1
1	B	229	ASP	3.0
1	A	193	GLY	3.0
1	A	342	HIS	2.9
2	C	223	ALA	2.7
1	B	332	ALA	2.7
1	B	226	GLY	2.6
1	A	222	ILE	2.5
1	A	231	THR	2.5
2	C	228	PRO	2.5
1	B	228	ASP	2.3
1	A	223	ARG	2.3
2	C	227	LEU	2.3
1	B	222	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	228	ASP	2.2
2	C	21	GLY	2.2
2	D	152	ARG	2.1
2	D	225	LYS	2.1
1	B	38	ASP	2.1
1	A	38	ASP	2.0
2	C	225	LYS	2.0
1	A	187	ALA	2.0
2	C	226	LYS	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

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.

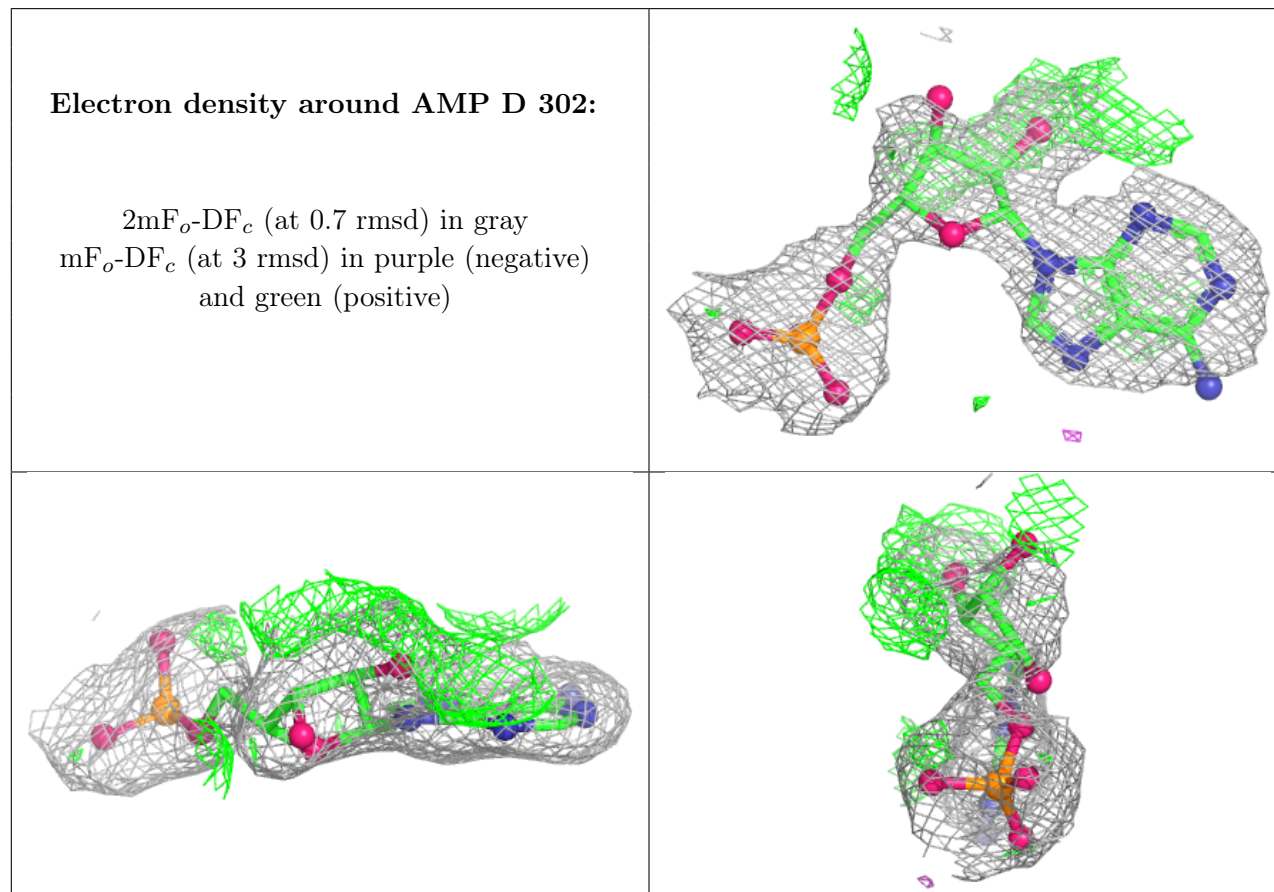
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
9	PEG	A	411	7/7	0.67	0.26	40,45,51,53	0
8	ACT	C	304	4/4	0.69	0.42	48,52,52,56	0
9	PEG	B	408	7/7	0.73	0.21	47,50,51,52	0
10	AMP	D	302	23/23	0.74	0.26	47,54,69,71	23
6	SO4	B	406	5/5	0.78	0.20	128,129,129,130	0
8	ACT	A	408	4/4	0.81	0.22	47,48,49,49	0
8	ACT	A	412	4/4	0.81	0.15	47,49,49,50	0
6	SO4	A	406	5/5	0.83	0.20	124,125,125,125	0
10	AMP	C	302	23/23	0.84	0.20	37,44,59,60	23
6	SO4	B	405	5/5	0.84	0.16	90,91,91,93	0
6	SO4	A	405	5/5	0.89	0.12	117,117,118,118	0
8	ACT	D	304	4/4	0.90	0.19	38,40,41,47	0
8	ACT	C	303	4/4	0.91	0.13	47,48,48,51	0
9	PEG	A	410	7/7	0.92	0.17	46,51,53,54	0

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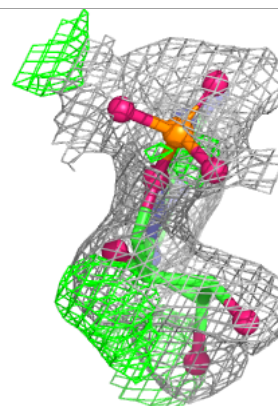
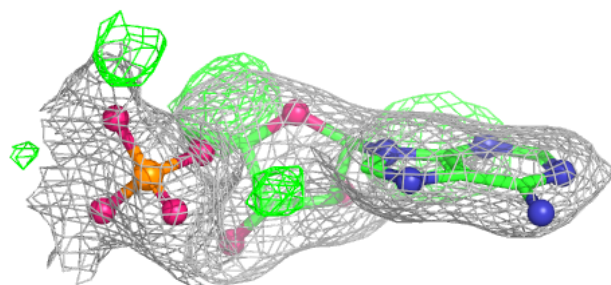
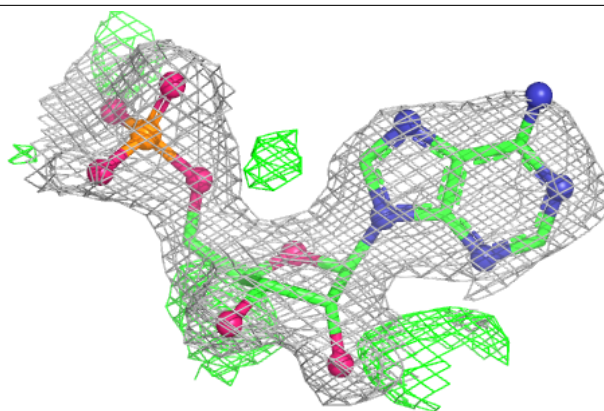
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
8	ACT	C	305	4/4	0.93	0.10	43,44,46,50	0
8	ACT	A	409	4/4	0.94	0.09	62,63,63,63	0
7	NA	A	407	1/1	0.95	0.15	42,42,42,42	0
7	NA	C	301	1/1	0.95	0.34	53,53,53,53	0
5	QCB	A	404	33/33	0.96	0.13	27,32,43,46	0
8	ACT	B	407	4/4	0.96	0.12	42,43,44,46	0
7	NA	D	301	1/1	0.96	0.14	41,41,41,41	0
3	NI	A	401	1/1	0.96	0.08	75,75,75,75	0
3	NI	B	402	1/1	0.96	0.21	105,105,105,105	0
8	ACT	D	303	4/4	0.96	0.07	40,41,42,43	0
5	QCB	B	404	33/33	0.97	0.10	17,27,32,33	0
3	NI	A	402	1/1	0.97	0.11	75,75,75,75	0
3	NI	B	401	1/1	0.98	0.06	63,63,63,63	0
4	ZN	B	403	1/1	1.00	0.04	43,43,43,43	0
4	ZN	A	403	1/1	1.00	0.05	43,43,43,43	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.

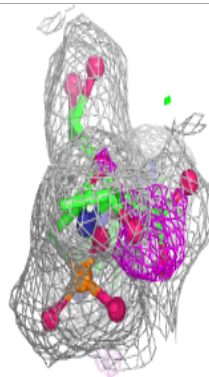
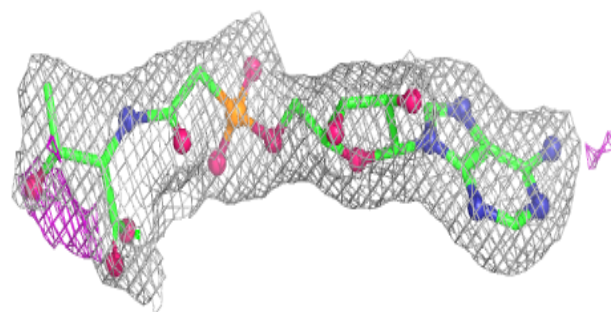
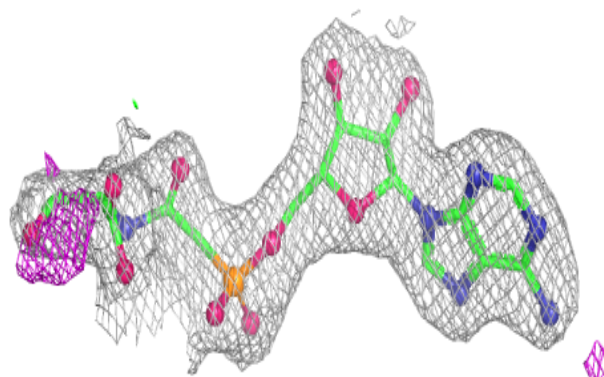


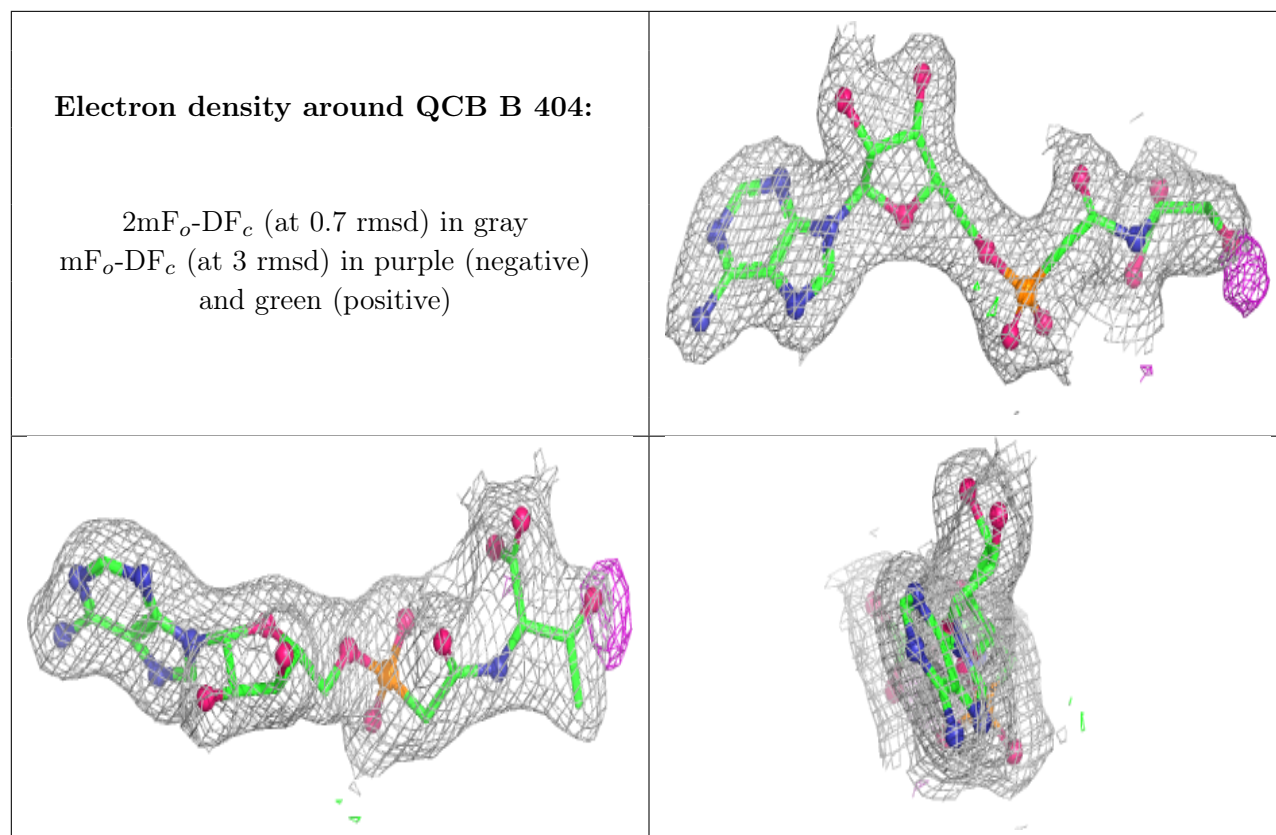
Electron density around AMP C 302:

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

**Electron density around QCB A 404:**

$2mF_o-DF_c$ (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.