Full wwPDB X-ray Structure Validation Report (i)

Sep 1, 2022 – 01:16 pm BST

PDB ID	:	6SH0
Title	:	Crystal structure of AcAChBP in complex with anatoxin
Authors	:	Hunter, W.N.; Dawson, A.; Parker, H.
Deposited on	:	2019-08-05
Resolution	:	2.50 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 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:

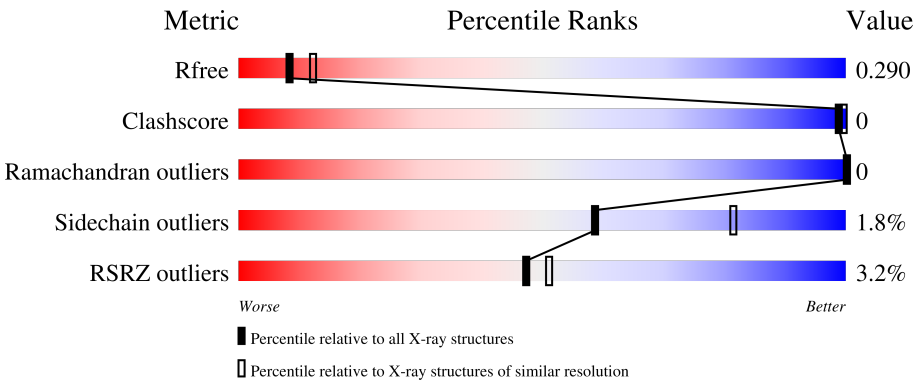
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.30
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.30

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 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	249	6%, 80%, 18%
1	B	249	2%, 81%, 17%
1	C	249	3%, 81%, 18%
1	D	249	2%, 80%, 18%
1	E	249	2%, 81%, 18%

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Mol	Chain	Length	Quality of chain
1	F	249	2% 82% 18%
1	G	249	2% 80% 18%
1	H	249	2% 81% 17%
1	I	249	4% 82% 15%
1	J	249	% 80% 17%

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
2	NAG	C	302	-	-	-	X
2	NAG	D	301	-	-	-	X
2	NAG	H	302	-	-	-	X
2	NAG	I	301	-	-	-	X

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 17754 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 Acetylcholine binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	205	1641	1039	266	325	11	0	2	0
1	B	206	1649	1043	270	326	10	0	1	0
1	C	205	1641	1038	267	326	10	0	1	0
1	D	205	1641	1038	267	326	10	0	1	0
1	E	205	1638	1037	266	325	10	0	1	0
1	F	205	1638	1037	266	325	10	0	1	0
1	G	205	1644	1040	269	325	10	0	2	0
1	H	206	1647	1042	270	326	9	0	0	0
1	I	211	1687	1069	276	332	10	0	1	0
1	J	206	1655	1047	271	327	10	0	2	0

There are 150 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	60	VAL	ALA	conflict	UNP Q8WSF8
A	155	VAL	ALA	conflict	UNP Q8WSF8
A	237	GLU	-	expression tag	UNP Q8WSF8
A	238	ASN	-	expression tag	UNP Q8WSF8
A	239	LEU	-	expression tag	UNP Q8WSF8
A	240	TYR	-	expression tag	UNP Q8WSF8
A	241	PHE	-	expression tag	UNP Q8WSF8
A	242	GLN	-	expression tag	UNP Q8WSF8
A	243	GLY	-	expression tag	UNP Q8WSF8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	244	HIS	-	expression tag	UNP Q8WSF8
A	245	HIS	-	expression tag	UNP Q8WSF8
A	246	HIS	-	expression tag	UNP Q8WSF8
A	247	HIS	-	expression tag	UNP Q8WSF8
A	248	HIS	-	expression tag	UNP Q8WSF8
A	249	HIS	-	expression tag	UNP Q8WSF8
B	60	VAL	ALA	conflict	UNP Q8WSF8
B	155	VAL	ALA	conflict	UNP Q8WSF8
B	237	GLU	-	expression tag	UNP Q8WSF8
B	238	ASN	-	expression tag	UNP Q8WSF8
B	239	LEU	-	expression tag	UNP Q8WSF8
B	240	TYR	-	expression tag	UNP Q8WSF8
B	241	PHE	-	expression tag	UNP Q8WSF8
B	242	GLN	-	expression tag	UNP Q8WSF8
B	243	GLY	-	expression tag	UNP Q8WSF8
B	244	HIS	-	expression tag	UNP Q8WSF8
B	245	HIS	-	expression tag	UNP Q8WSF8
B	246	HIS	-	expression tag	UNP Q8WSF8
B	247	HIS	-	expression tag	UNP Q8WSF8
B	248	HIS	-	expression tag	UNP Q8WSF8
B	249	HIS	-	expression tag	UNP Q8WSF8
C	60	VAL	ALA	conflict	UNP Q8WSF8
C	155	VAL	ALA	conflict	UNP Q8WSF8
C	237	GLU	-	expression tag	UNP Q8WSF8
C	238	ASN	-	expression tag	UNP Q8WSF8
C	239	LEU	-	expression tag	UNP Q8WSF8
C	240	TYR	-	expression tag	UNP Q8WSF8
C	241	PHE	-	expression tag	UNP Q8WSF8
C	242	GLN	-	expression tag	UNP Q8WSF8
C	243	GLY	-	expression tag	UNP Q8WSF8
C	244	HIS	-	expression tag	UNP Q8WSF8
C	245	HIS	-	expression tag	UNP Q8WSF8
C	246	HIS	-	expression tag	UNP Q8WSF8
C	247	HIS	-	expression tag	UNP Q8WSF8
C	248	HIS	-	expression tag	UNP Q8WSF8
C	249	HIS	-	expression tag	UNP Q8WSF8
D	60	VAL	ALA	conflict	UNP Q8WSF8
D	155	VAL	ALA	conflict	UNP Q8WSF8
D	237	GLU	-	expression tag	UNP Q8WSF8
D	238	ASN	-	expression tag	UNP Q8WSF8
D	239	LEU	-	expression tag	UNP Q8WSF8
D	240	TYR	-	expression tag	UNP Q8WSF8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	241	PHE	-	expression tag	UNP Q8WSF8
D	242	GLN	-	expression tag	UNP Q8WSF8
D	243	GLY	-	expression tag	UNP Q8WSF8
D	244	HIS	-	expression tag	UNP Q8WSF8
D	245	HIS	-	expression tag	UNP Q8WSF8
D	246	HIS	-	expression tag	UNP Q8WSF8
D	247	HIS	-	expression tag	UNP Q8WSF8
D	248	HIS	-	expression tag	UNP Q8WSF8
D	249	HIS	-	expression tag	UNP Q8WSF8
E	60	VAL	ALA	conflict	UNP Q8WSF8
E	155	VAL	ALA	conflict	UNP Q8WSF8
E	237	GLU	-	expression tag	UNP Q8WSF8
E	238	ASN	-	expression tag	UNP Q8WSF8
E	239	LEU	-	expression tag	UNP Q8WSF8
E	240	TYR	-	expression tag	UNP Q8WSF8
E	241	PHE	-	expression tag	UNP Q8WSF8
E	242	GLN	-	expression tag	UNP Q8WSF8
E	243	GLY	-	expression tag	UNP Q8WSF8
E	244	HIS	-	expression tag	UNP Q8WSF8
E	245	HIS	-	expression tag	UNP Q8WSF8
E	246	HIS	-	expression tag	UNP Q8WSF8
E	247	HIS	-	expression tag	UNP Q8WSF8
E	248	HIS	-	expression tag	UNP Q8WSF8
E	249	HIS	-	expression tag	UNP Q8WSF8
F	60	VAL	ALA	conflict	UNP Q8WSF8
F	155	VAL	ALA	conflict	UNP Q8WSF8
F	237	GLU	-	expression tag	UNP Q8WSF8
F	238	ASN	-	expression tag	UNP Q8WSF8
F	239	LEU	-	expression tag	UNP Q8WSF8
F	240	TYR	-	expression tag	UNP Q8WSF8
F	241	PHE	-	expression tag	UNP Q8WSF8
F	242	GLN	-	expression tag	UNP Q8WSF8
F	243	GLY	-	expression tag	UNP Q8WSF8
F	244	HIS	-	expression tag	UNP Q8WSF8
F	245	HIS	-	expression tag	UNP Q8WSF8
F	246	HIS	-	expression tag	UNP Q8WSF8
F	247	HIS	-	expression tag	UNP Q8WSF8
F	248	HIS	-	expression tag	UNP Q8WSF8
F	249	HIS	-	expression tag	UNP Q8WSF8
G	60	VAL	ALA	conflict	UNP Q8WSF8
G	155	VAL	ALA	conflict	UNP Q8WSF8
G	237	GLU	-	expression tag	UNP Q8WSF8

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Chain	Residue	Modelled	Actual	Comment	Reference
G	238	ASN	-	expression tag	UNP Q8WSF8
G	239	LEU	-	expression tag	UNP Q8WSF8
G	240	TYR	-	expression tag	UNP Q8WSF8
G	241	PHE	-	expression tag	UNP Q8WSF8
G	242	GLN	-	expression tag	UNP Q8WSF8
G	243	GLY	-	expression tag	UNP Q8WSF8
G	244	HIS	-	expression tag	UNP Q8WSF8
G	245	HIS	-	expression tag	UNP Q8WSF8
G	246	HIS	-	expression tag	UNP Q8WSF8
G	247	HIS	-	expression tag	UNP Q8WSF8
G	248	HIS	-	expression tag	UNP Q8WSF8
G	249	HIS	-	expression tag	UNP Q8WSF8
H	60	VAL	ALA	conflict	UNP Q8WSF8
H	155	VAL	ALA	conflict	UNP Q8WSF8
H	237	GLU	-	expression tag	UNP Q8WSF8
H	238	ASN	-	expression tag	UNP Q8WSF8
H	239	LEU	-	expression tag	UNP Q8WSF8
H	240	TYR	-	expression tag	UNP Q8WSF8
H	241	PHE	-	expression tag	UNP Q8WSF8
H	242	GLN	-	expression tag	UNP Q8WSF8
H	243	GLY	-	expression tag	UNP Q8WSF8
H	244	HIS	-	expression tag	UNP Q8WSF8
H	245	HIS	-	expression tag	UNP Q8WSF8
H	246	HIS	-	expression tag	UNP Q8WSF8
H	247	HIS	-	expression tag	UNP Q8WSF8
H	248	HIS	-	expression tag	UNP Q8WSF8
H	249	HIS	-	expression tag	UNP Q8WSF8
I	60	VAL	ALA	conflict	UNP Q8WSF8
I	155	VAL	ALA	conflict	UNP Q8WSF8
I	237	GLU	-	expression tag	UNP Q8WSF8
I	238	ASN	-	expression tag	UNP Q8WSF8
I	239	LEU	-	expression tag	UNP Q8WSF8
I	240	TYR	-	expression tag	UNP Q8WSF8
I	241	PHE	-	expression tag	UNP Q8WSF8
I	242	GLN	-	expression tag	UNP Q8WSF8
I	243	GLY	-	expression tag	UNP Q8WSF8
I	244	HIS	-	expression tag	UNP Q8WSF8
I	245	HIS	-	expression tag	UNP Q8WSF8
I	246	HIS	-	expression tag	UNP Q8WSF8
I	247	HIS	-	expression tag	UNP Q8WSF8
I	248	HIS	-	expression tag	UNP Q8WSF8
I	249	HIS	-	expression tag	UNP Q8WSF8

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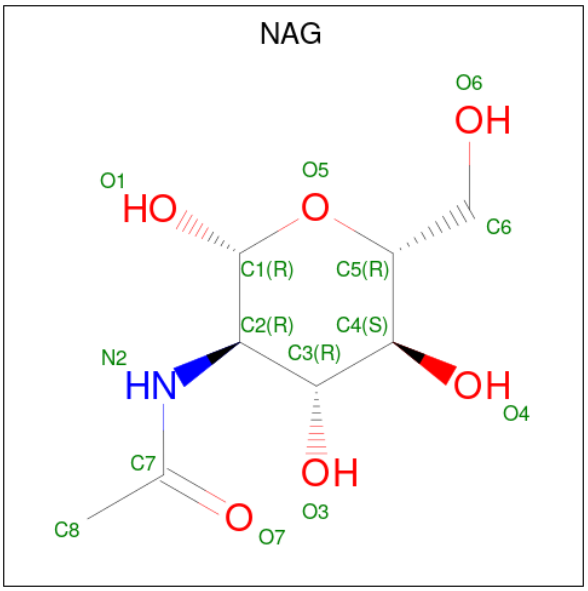
Chain	Residue	Modelled	Actual	Comment	Reference
J	60	VAL	ALA	conflict	UNP Q8WSF8
J	155	VAL	ALA	conflict	UNP Q8WSF8
J	237	GLU	-	expression tag	UNP Q8WSF8
J	238	ASN	-	expression tag	UNP Q8WSF8
J	239	LEU	-	expression tag	UNP Q8WSF8
J	240	TYR	-	expression tag	UNP Q8WSF8
J	241	PHE	-	expression tag	UNP Q8WSF8
J	242	GLN	-	expression tag	UNP Q8WSF8
J	243	GLY	-	expression tag	UNP Q8WSF8
J	244	HIS	-	expression tag	UNP Q8WSF8
J	245	HIS	-	expression tag	UNP Q8WSF8
J	246	HIS	-	expression tag	UNP Q8WSF8
J	247	HIS	-	expression tag	UNP Q8WSF8
J	248	HIS	-	expression tag	UNP Q8WSF8
J	249	HIS	-	expression tag	UNP Q8WSF8

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	14	8	1	5	0	0
			Total	C	N	O		
2	B	1	14	8	1	5	0	0
			Total	C	N	O		
2	C	1	14	8	1	5	0	0

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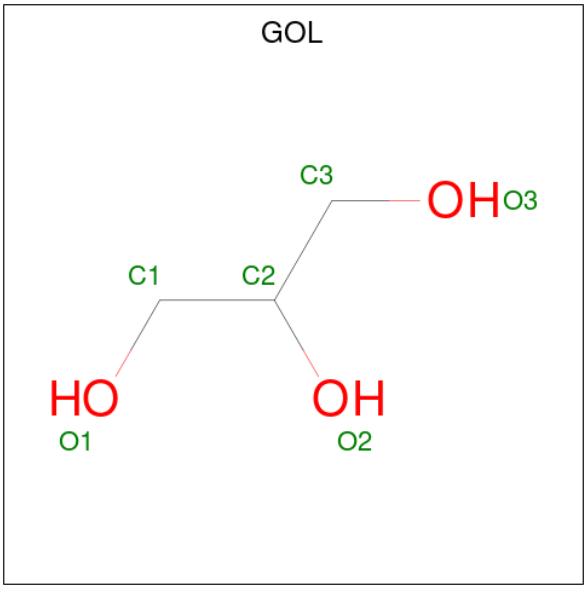
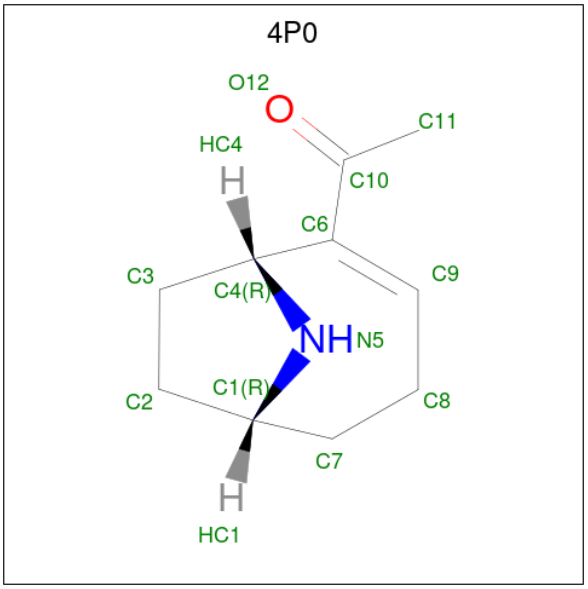
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	D	1	14	8	1	5	0	0
2	E	1	14	8	1	5	0	0
2	F	1	14	8	1	5	0	0
2	H	1	14	8	1	5	0	0
2	I	1	14	8	1	5	0	0
2	J	1	14	8	1	5	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



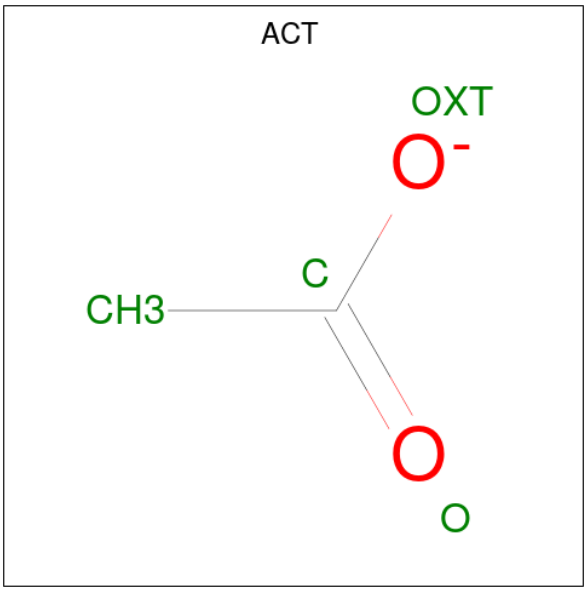
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	6	3	3	0	0
3	B	1	6	3	3	0	0
3	D	1	6	3	3	0	0
3	E	1	6	3	3	0	0
3	I	1	6	3	3	0	0

- Molecule 4 is 1-[(1R,6R)-9-azabicyclo[4.2.1]non-2-en-2-yl]ethanone (three-letter code: 4P0) (formula: $C_{10}H_{15}NO$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	12	10	1	1	0	0
			Total	C	N	O		
4	B	1	12	10	1	1	0	0
			Total	C	N	O		
4	C	1	12	10	1	1	0	0
			Total	C	N	O		
4	D	1	12	10	1	1	0	0
			Total	C	N	O		
4	E	1	12	10	1	1	0	0
			Total	C	N	O		
4	F	1	12	10	1	1	0	0
			Total	C	N	O		
4	G	1	12	10	1	1	0	0
			Total	C	N	O		
4	H	1	12	10	1	1	0	0
			Total	C	N	O		
4	I	1	12	10	1	1	0	0
			Total	C	N	O		
4	J	1	12	10	1	1	0	0

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	B	1	4	2	2	0	0
5	C	1	4	2	2	0	0
5	C	1	4	2	2	0	0
5	F	1	4	2	2	0	0
5	F	1	4	2	2	0	0
5	F	1	4	2	2	0	0
5	F	1	4	2	2	0	0
5	G	1	4	2	2	0	0
5	H	1	4	2	2	0	0
5	H	1	4	2	2	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	82	82	82	0	0
6	B	89	89	89	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	C	85	Total O 85 85	0	0
6	D	97	Total O 97 97	0	0
6	E	91	Total O 91 91	0	0
6	F	103	Total O 103 103	0	0
6	G	92	Total O 92 92	0	0
6	H	107	Total O 107 107	0	0
6	I	105	Total O 105 105	0	0
6	J	106	Total O 106 106	0	0

3 Residue-property plots (i)

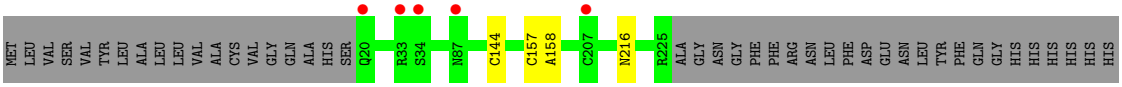
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Acetylcholine binding protein

Chain A:

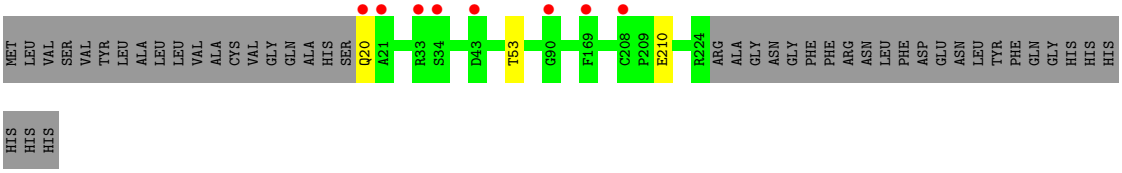
• Molecule 1: Acetylcholine binding protein

Chain B:



• Molecule 1: Acetylcholine binding protein

Chain C:

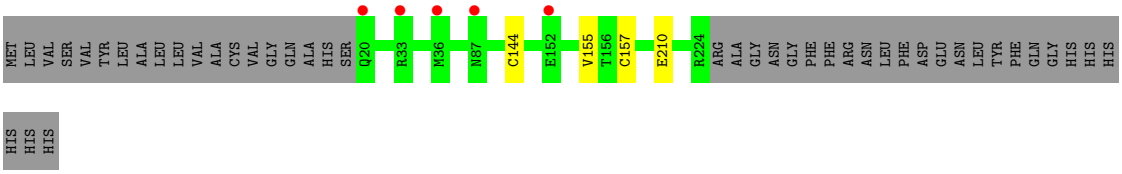


• Molecule 1: Acetylcholine binding protein

Chain D:

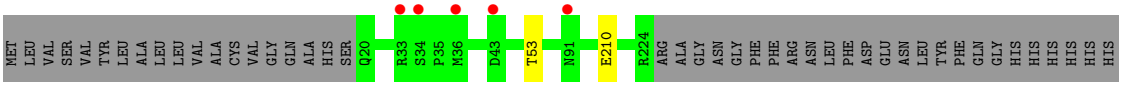
• Molecule 1: Acetylcholine binding protein

Chain E:



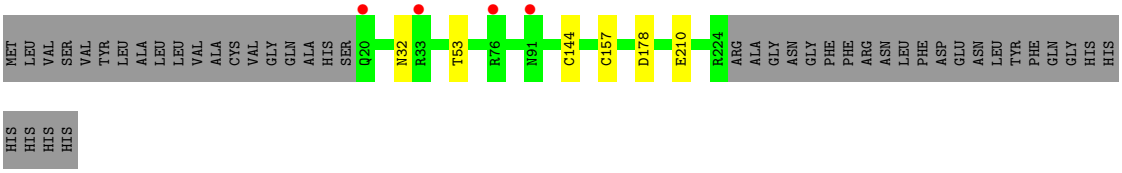
- Molecule 1: Acetylcholine binding protein

Chain F:



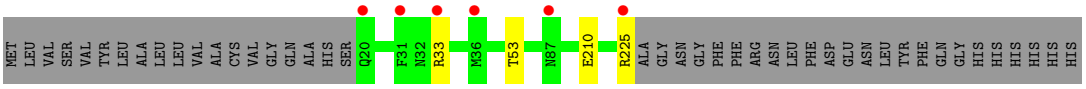
- Molecule 1: Acetylcholine binding protein

Chain G:



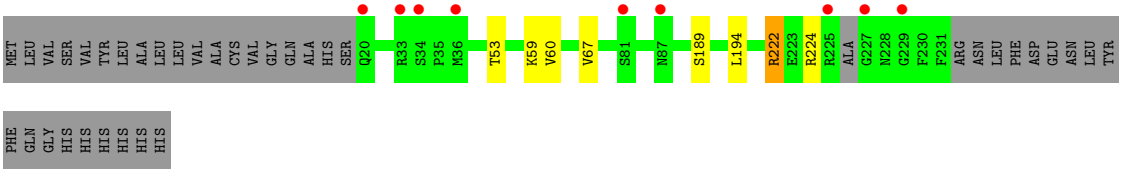
- Molecule 1: Acetylcholine binding protein

Chain H:



- Molecule 1: Acetylcholine binding protein

Chain I:



- Molecule 1: Acetylcholine binding protein

Chain J:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	211.97Å 129.87Å 131.32Å 90.00° 103.17° 90.00°	Depositor
Resolution (Å)	59.77 – 2.50 59.77 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.5 (59.77-2.50) 99.5 (59.77-2.50)	Depositor EDS
R_{merge}	0.23	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.01 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.253 , 0.289 0.254 , 0.290	Depositor DCC
R_{free} test set	6041 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	27.1	Xtriage
Anisotropy	0.394	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.55$, $< L^2 > = 0.40$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	17754	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.54% 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: 4P0, GOL, ACT, NAG

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	0.37	0/1688	0.57	0/2303
1	B	0.36	0/1693	0.58	0/2309
1	C	0.37	0/1682	0.58	0/2295
1	D	0.38	0/1682	0.58	0/2295
1	E	0.36	0/1682	0.59	0/2295
1	F	0.35	0/1682	0.58	0/2295
1	G	0.36	0/1693	0.57	0/2309
1	H	0.36	0/1687	0.58	0/2301
1	I	0.35	0/1732	0.58	0/2359
1	J	0.35	0/1702	0.58	0/2322
All	All	0.36	0/16923	0.58	0/23083

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	J	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	J	207	CYS	Peptide

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	1641	0	1573	1	0
1	B	1649	0	1582	2	0
1	C	1641	0	1572	0	0
1	D	1641	0	1572	1	0
1	E	1638	0	1569	1	0
1	F	1638	0	1569	0	0
1	G	1644	0	1579	1	0
1	H	1647	0	1581	0	0
1	I	1687	0	1611	3	0
1	J	1655	0	1588	0	0
2	A	14	0	13	0	0
2	B	14	0	13	0	0
2	C	14	0	13	0	0
2	D	14	0	13	0	0
2	E	14	0	13	0	0
2	F	14	0	13	0	0
2	H	14	0	13	0	0
2	I	14	0	13	0	0
2	J	14	0	13	0	0
3	A	6	0	8	0	0
3	B	6	0	8	0	0
3	D	6	0	8	0	0
3	E	6	0	8	0	0
3	I	6	0	8	0	0
4	A	12	0	15	0	0
4	B	12	0	15	0	0
4	C	12	0	15	0	0
4	D	12	0	15	0	0
4	E	12	0	15	0	0
4	F	12	0	15	0	0
4	G	12	0	15	1	0
4	H	12	0	15	1	0
4	I	12	0	15	1	0
4	J	12	0	15	0	0
5	B	4	0	3	0	0
5	C	8	0	6	0	0
5	F	16	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	G	4	0	3	0	0
5	H	8	0	6	0	0
6	A	82	0	0	1	0
6	B	89	0	0	0	0
6	C	85	0	0	0	0
6	D	97	0	0	0	0
6	E	91	0	0	0	0
6	F	103	0	0	0	0
6	G	92	0	0	0	0
6	H	107	0	0	0	0
6	I	105	0	0	0	0
6	J	106	0	0	0	0
All	All	17754	0	16133	12	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 0.

All (12) 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:D:189:SER:O	1:D:224:ARG:HD3	1.90	0.72
1:I:60:VAL:HG22	1:I:67:VAL:HG22	1.84	0.58
1:B:158:ALA:HB1	1:B:216:ASN:HD21	1.70	0.56
1:B:144:CYS:SG	1:B:157[B]:CYS:HB3	2.52	0.50
1:E:144:CYS:SG	1:E:157[B]:CYS:HB3	2.55	0.46
1:G:144:CYS:SG	1:G:157[B]:CYS:HB3	2.57	0.44
4:G:302:4P0:HC9	4:G:302:4P0:H111	1.84	0.44
1:A:20:GLN:N	6:A:402:HOH:O	2.51	0.43
1:I:194:LEU:HD21	1:I:222:ARG:HD3	1.99	0.43
4:I:303:4P0:HC9	4:I:303:4P0:H111	1.86	0.43
1:I:189:SER:O	1:I:224:ARG:NH2	2.54	0.41
4:H:304:4P0:H111	4:H:304:4P0:HC9	1.84	0.40

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	205/249 (82%)	202 (98%)	3 (2%)	0	100	100
1	B	205/249 (82%)	203 (99%)	2 (1%)	0	100	100
1	C	204/249 (82%)	202 (99%)	2 (1%)	0	100	100
1	D	204/249 (82%)	196 (96%)	8 (4%)	0	100	100
1	E	204/249 (82%)	202 (99%)	2 (1%)	0	100	100
1	F	204/249 (82%)	202 (99%)	2 (1%)	0	100	100
1	G	205/249 (82%)	204 (100%)	1 (0%)	0	100	100
1	H	204/249 (82%)	201 (98%)	3 (2%)	0	100	100
1	I	208/249 (84%)	207 (100%)	1 (0%)	0	100	100
1	J	205/249 (82%)	201 (98%)	4 (2%)	0	100	100
All	All	2048/2490 (82%)	2020 (99%)	28 (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	190/224 (85%)	185 (97%)	5 (3%)	46	72
1	B	190/224 (85%)	190 (100%)	0	100	100
1	C	189/224 (84%)	186 (98%)	3 (2%)	62	84
1	D	189/224 (84%)	183 (97%)	6 (3%)	39	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	189/224 (84%)	187 (99%)	2 (1%)	73	89
1	F	189/224 (84%)	187 (99%)	2 (1%)	73	89
1	G	190/224 (85%)	186 (98%)	4 (2%)	53	78
1	H	189/224 (84%)	185 (98%)	4 (2%)	53	78
1	I	193/224 (86%)	190 (98%)	3 (2%)	62	84
1	J	191/224 (85%)	186 (97%)	5 (3%)	46	72
All	All	1899/2240 (85%)	1865 (98%)	34 (2%)	59	81

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

Mol	Chain	Res	Type
1	A	20	GLN
1	A	36	MET
1	A	53	THR
1	A	76	ARG
1	A	210	GLU
1	C	20	GLN
1	C	53	THR
1	C	210	GLU
1	D	33	ARG
1	D	36	MET
1	D	53	THR
1	D	76	ARG
1	D	210	GLU
1	D	224	ARG
1	E	155	VAL
1	E	210	GLU
1	F	53	THR
1	F	210	GLU
1	G	32	ASN
1	G	53	THR
1	G	178	ASP
1	G	210	GLU
1	H	33	ARG
1	H	53	THR
1	H	210	GLU
1	H	225	ARG
1	I	53	THR
1	I	59	LYS
1	I	222	ARG

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Mol	Chain	Res	Type
1	J	53	THR
1	J	76	ARG
1	J	174	LYS
1	J	210	GLU
1	J	225	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	20	GLN
1	B	32	ASN
1	B	216	ASN
1	C	20	GLN
1	C	32	ASN
1	C	55	GLN
1	C	74	GLN
1	C	216	ASN
1	D	74	GLN
1	D	216	ASN
1	E	32	ASN
1	E	216	ASN
1	F	20	GLN
1	F	80	ASN
1	F	216	ASN
1	G	32	ASN
1	G	216	ASN
1	H	32	ASN
1	H	216	ASN
1	I	20	GLN
1	I	87	ASN
1	I	216	ASN
1	J	203	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

34 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAG	F	301	1	14,14,15	0.38	0	17,19,21	1.07	1 (5%)
4	4P0	E	303	-	13,13,13	0.67	1 (7%)	8,18,18	0.47	0
2	NAG	A	301	1	14,14,15	0.41	0	17,19,21	1.11	1 (5%)
3	GOL	B	302	-	5,5,5	0.31	0	5,5,5	0.12	0
2	NAG	J	301	1	14,14,15	0.46	0	17,19,21	1.25	2 (11%)
4	4P0	G	302	-	13,13,13	0.67	1 (7%)	8,18,18	0.59	0
4	4P0	B	304	-	13,13,13	0.68	1 (7%)	8,18,18	0.53	0
3	GOL	D	302	-	5,5,5	0.38	0	5,5,5	0.19	0
2	NAG	D	301	1	14,14,15	0.43	0	17,19,21	0.79	1 (5%)
4	4P0	D	303	-	13,13,13	0.74	1 (7%)	8,18,18	0.64	0
5	ACT	H	303	-	3,3,3	0.78	0	3,3,3	0.66	0
4	4P0	C	304	-	13,13,13	0.70	1 (7%)	8,18,18	0.57	0
3	GOL	I	302	-	5,5,5	0.35	0	5,5,5	0.28	0
4	4P0	J	302	-	13,13,13	0.58	0	8,18,18	0.58	0
4	4P0	F	306	-	13,13,13	0.53	0	8,18,18	0.57	0
4	4P0	I	303	-	13,13,13	0.78	1 (7%)	8,18,18	0.51	0
5	ACT	F	304	-	3,3,3	0.80	0	3,3,3	0.63	0
5	ACT	G	301	-	3,3,3	0.78	0	3,3,3	0.71	0
2	NAG	B	301	1	14,14,15	0.42	0	17,19,21	1.34	3 (17%)
3	GOL	A	302	-	5,5,5	0.31	0	5,5,5	0.35	0
5	ACT	C	303	-	3,3,3	0.77	0	3,3,3	0.73	0
2	NAG	I	301	1	14,14,15	0.50	0	17,19,21	0.99	1 (5%)
2	NAG	C	302	1	14,14,15	0.57	0	17,19,21	1.07	1 (5%)
5	ACT	H	301	-	3,3,3	0.76	0	3,3,3	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	ACT	F	302	-	3,3,3	0.74	0	3,3,3	0.85	0
2	NAG	E	301	1	14,14,15	0.51	0	17,19,21	0.90	0
5	ACT	F	303	-	3,3,3	0.77	0	3,3,3	0.70	0
3	GOL	E	302	-	5,5,5	0.30	0	5,5,5	0.22	0
2	NAG	H	302	1	14,14,15	0.49	0	17,19,21	1.10	1 (5%)
4	4P0	A	303	-	13,13,13	0.82	1 (7%)	8,18,18	0.51	0
4	4P0	H	304	-	13,13,13	0.68	1 (7%)	8,18,18	0.58	0
5	ACT	B	303	-	3,3,3	0.72	0	3,3,3	0.87	0
5	ACT	C	301	-	3,3,3	0.77	0	3,3,3	0.77	0
5	ACT	F	305	-	3,3,3	0.77	0	3,3,3	0.69	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
2	NAG	F	301	1	-	2/6/23/26	0/1/1/1
4	4P0	E	303	-	-	0/4/23/23	0/2/2/2
2	NAG	A	301	1	-	2/6/23/26	0/1/1/1
3	GOL	B	302	-	-	2/4/4/4	-
2	NAG	J	301	1	-	2/6/23/26	0/1/1/1
4	4P0	G	302	-	-	0/4/23/23	0/2/2/2
4	4P0	B	304	-	-	0/4/23/23	0/2/2/2
3	GOL	D	302	-	-	2/4/4/4	-
2	NAG	D	301	1	-	2/6/23/26	0/1/1/1
4	4P0	D	303	-	-	1/4/23/23	0/2/2/2
4	4P0	C	304	-	-	2/4/23/23	0/2/2/2
3	GOL	I	302	-	-	2/4/4/4	-
4	4P0	J	302	-	-	0/4/23/23	0/2/2/2
4	4P0	F	306	-	-	0/4/23/23	0/2/2/2
4	4P0	I	303	-	-	0/4/23/23	0/2/2/2
2	NAG	B	301	1	-	2/6/23/26	0/1/1/1
3	GOL	A	302	-	-	0/4/4/4	-
2	NAG	I	301	1	-	0/6/23/26	0/1/1/1
2	NAG	C	302	1	-	0/6/23/26	0/1/1/1
2	NAG	E	301	1	-	0/6/23/26	0/1/1/1
3	GOL	E	302	-	-	0/4/4/4	-
2	NAG	H	302	1	-	2/6/23/26	0/1/1/1
4	4P0	A	303	-	-	0/4/23/23	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	4P0	H	304	-	-	0/4/23/23	0/2/2/2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	303	4P0	C7-C1	2.82	1.56	1.52
4	I	303	4P0	C7-C1	2.61	1.55	1.52
4	D	303	4P0	C7-C1	2.47	1.55	1.52
4	C	304	4P0	C7-C1	2.33	1.55	1.52
4	B	304	4P0	C7-C1	2.18	1.55	1.52
4	G	302	4P0	C7-C1	2.16	1.55	1.52
4	H	304	4P0	C7-C1	2.14	1.55	1.52
4	E	303	4P0	C7-C1	2.14	1.55	1.52

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	302	NAG	C1-O5-C5	3.58	117.04	112.19
2	F	301	NAG	C1-O5-C5	3.18	116.50	112.19
2	H	302	NAG	C1-O5-C5	2.97	116.21	112.19
2	A	301	NAG	O5-C5-C6	2.95	111.83	107.20
2	B	301	NAG	O5-C1-C2	-2.87	106.75	111.29
2	J	301	NAG	C1-O5-C5	2.75	115.91	112.19
2	B	301	NAG	C1-O5-C5	2.54	115.63	112.19
2	I	301	NAG	C1-O5-C5	2.50	115.58	112.19
2	D	301	NAG	C1-O5-C5	2.29	115.30	112.19
2	B	301	NAG	C1-C2-N2	2.15	114.16	110.49
2	J	301	NAG	C2-N2-C7	2.13	125.93	122.90

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	304	4P0	C11-C10-C6-C9
2	D	301	NAG	O5-C5-C6-O6
2	D	301	NAG	C4-C5-C6-O6
3	D	302	GOL	O1-C1-C2-O2
2	A	301	NAG	O5-C5-C6-O6
3	B	302	GOL	C1-C2-C3-O3
3	D	302	GOL	O1-C1-C2-C3
3	I	302	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
2	H	302	NAG	C4-C5-C6-O6
3	I	302	GOL	O2-C2-C3-O3
2	J	301	NAG	O5-C5-C6-O6
2	F	301	NAG	C4-C5-C6-O6
2	H	302	NAG	O5-C5-C6-O6
2	F	301	NAG	O5-C5-C6-O6
3	B	302	GOL	O2-C2-C3-O3
2	J	301	NAG	C3-C2-N2-C7
4	C	304	4P0	O12-C10-C6-C9
2	B	301	NAG	C4-C5-C6-O6
2	B	301	NAG	C3-C2-N2-C7
4	D	303	4P0	C11-C10-C6-C9
2	A	301	NAG	C4-C5-C6-O6

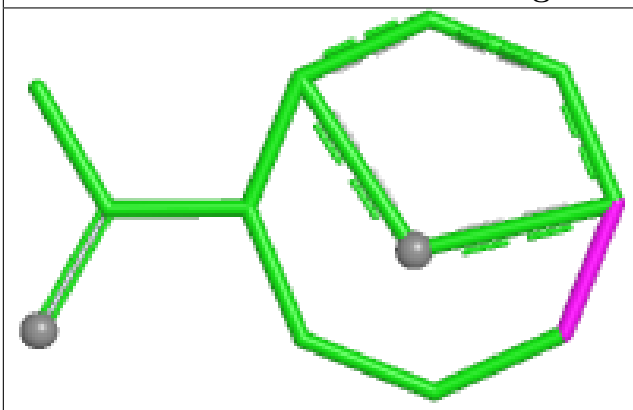
There are no ring outliers.

3 monomers are involved in 3 short contacts:

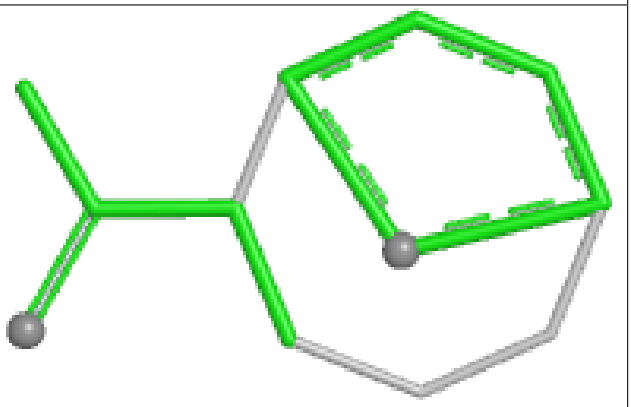
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	302	4P0	1	0
4	I	303	4P0	1	0
4	H	304	4P0	1	0

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.

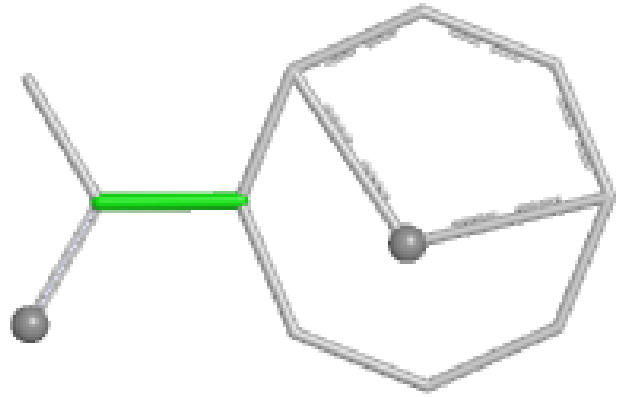
Ligand 4P0 E 303



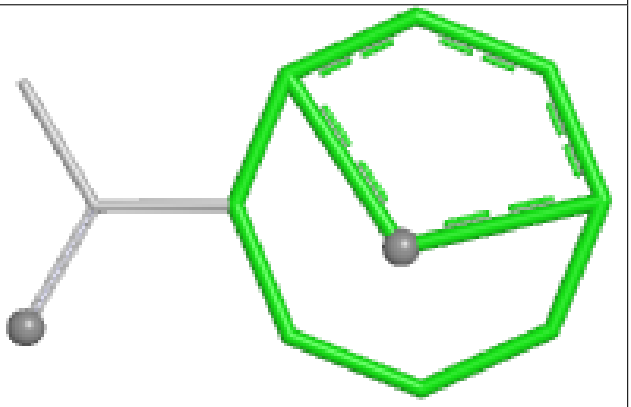
Bond lengths



Bond angles

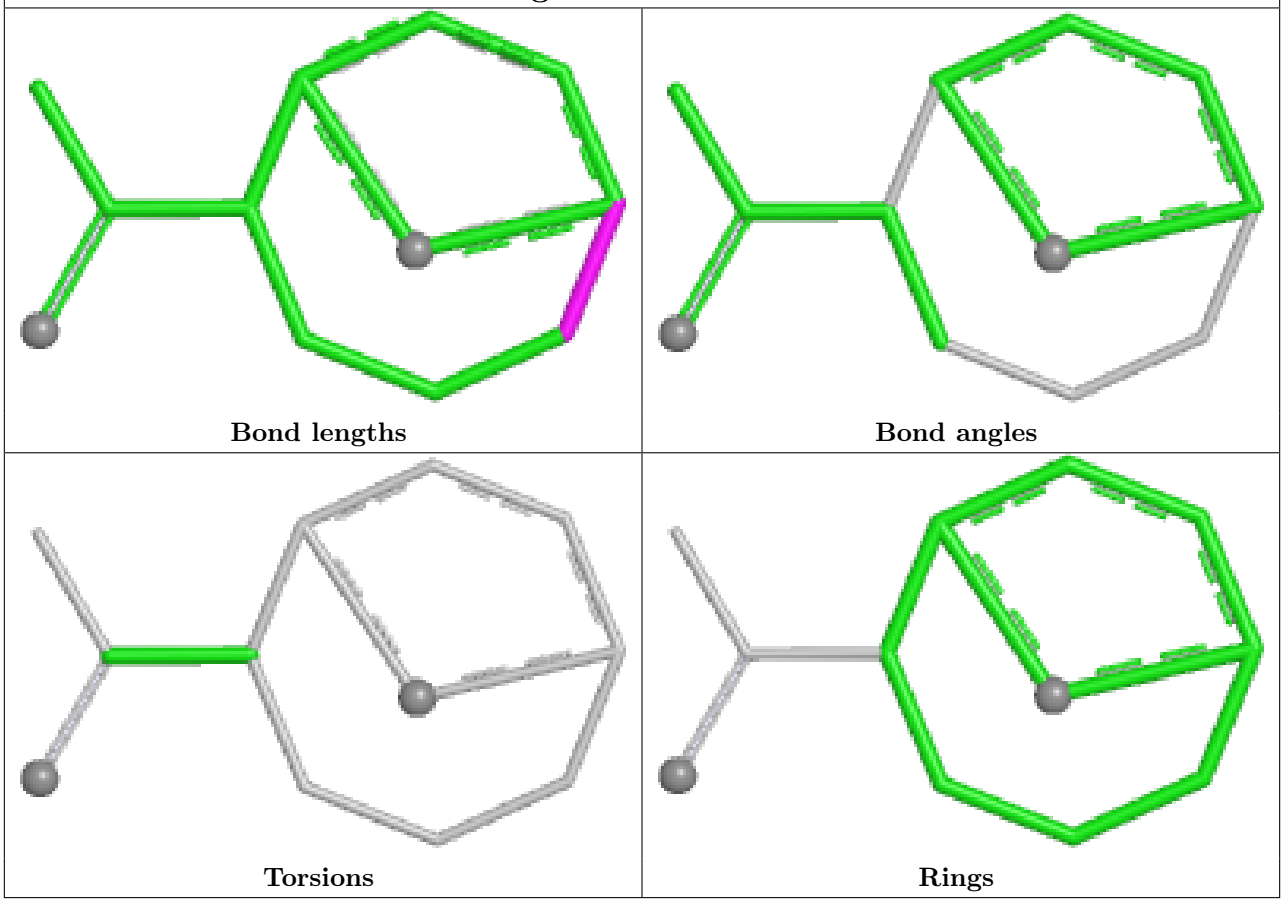


Torsions

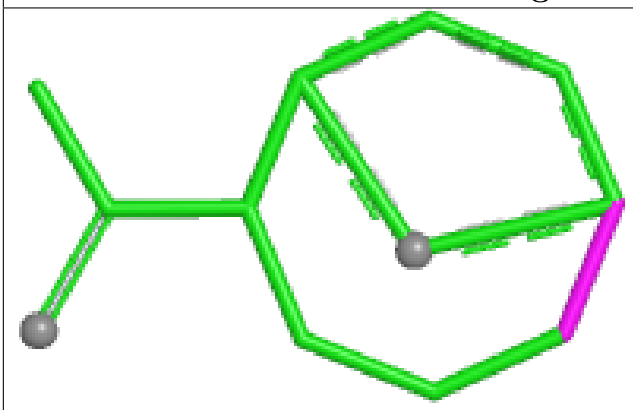


Rings

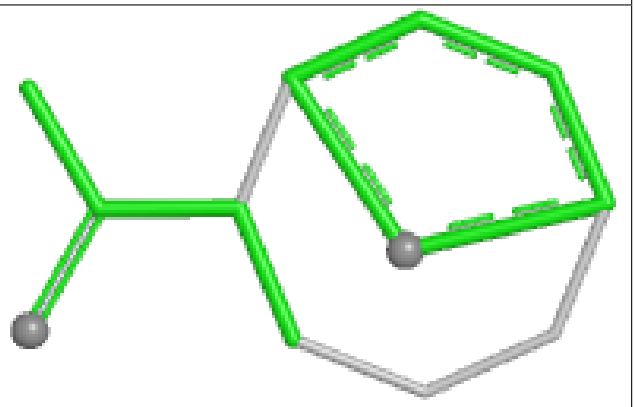
Ligand 4P0 G 302



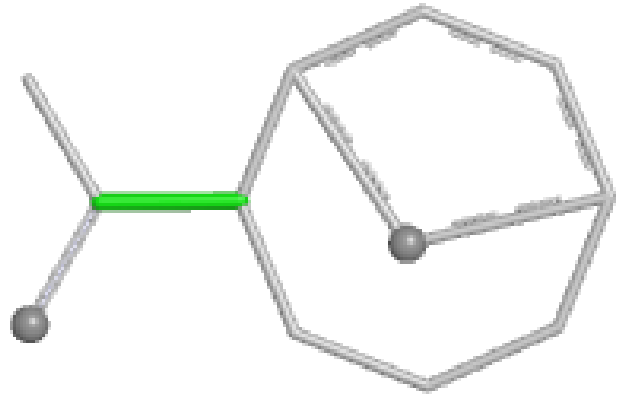
Ligand 4P0 B 304



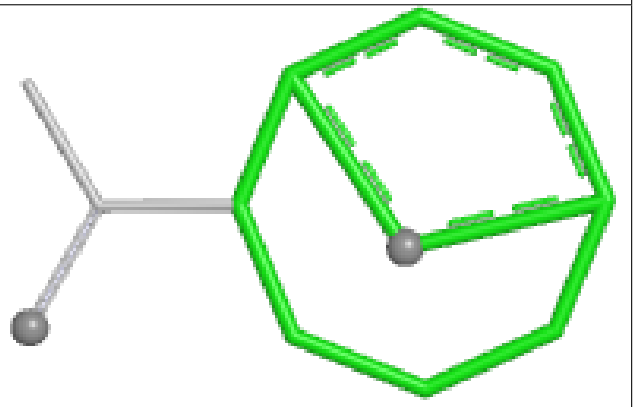
Bond lengths



Bond angles

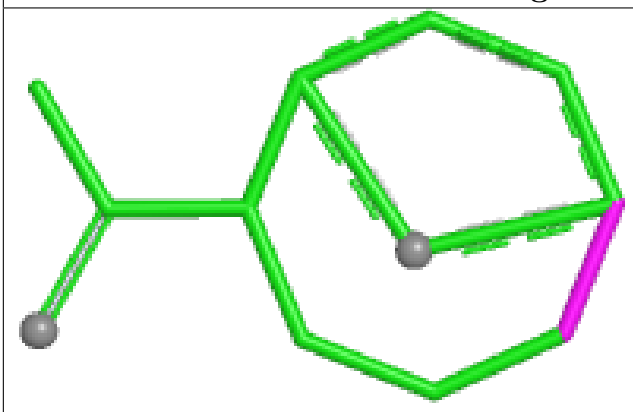


Torsions

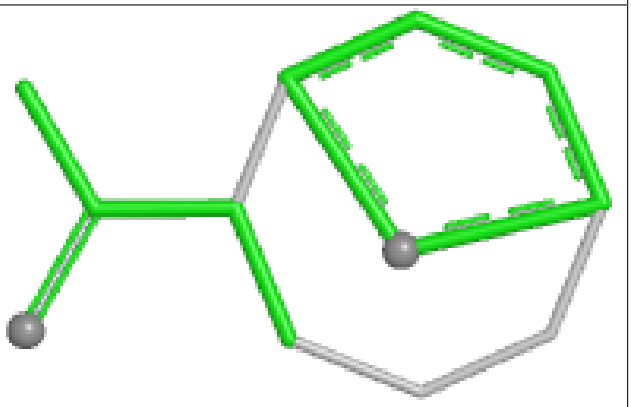


Rings

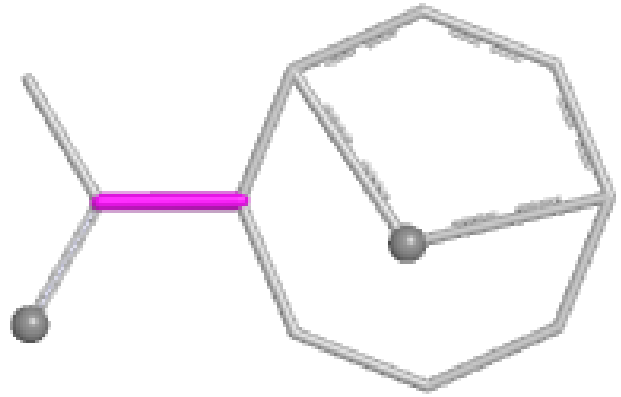
Ligand 4P0 D 303



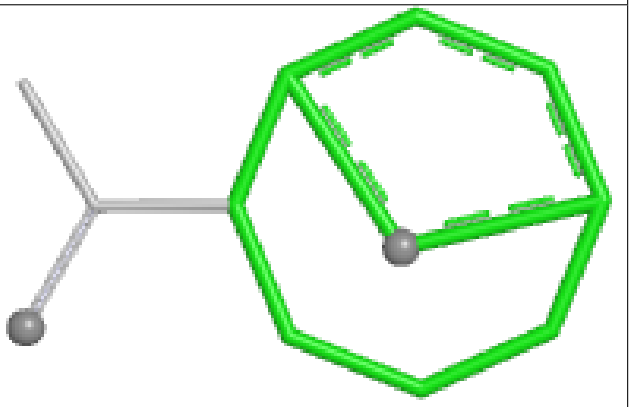
Bond lengths



Bond angles

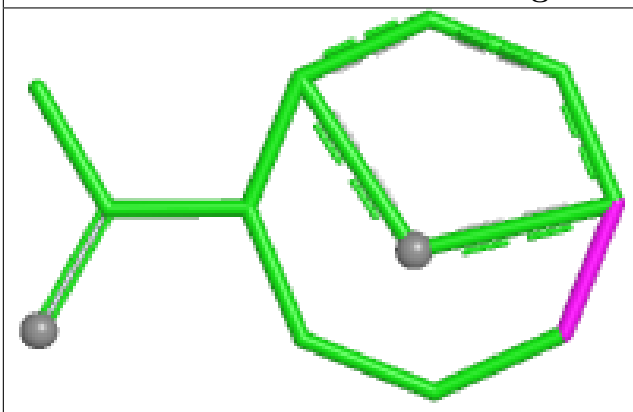


Torsions

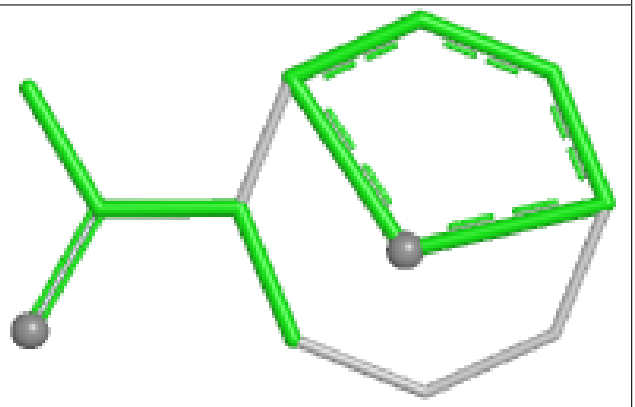


Rings

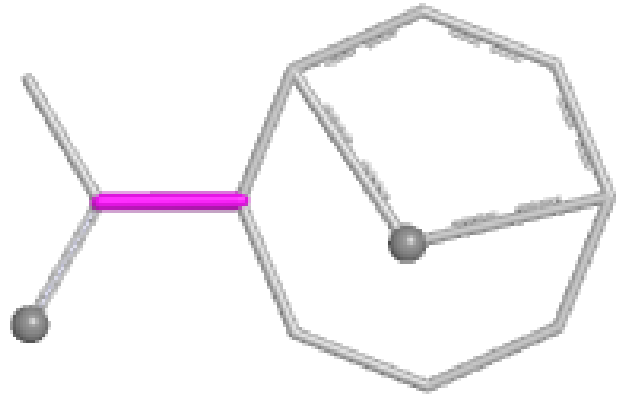
Ligand 4P0 C 304



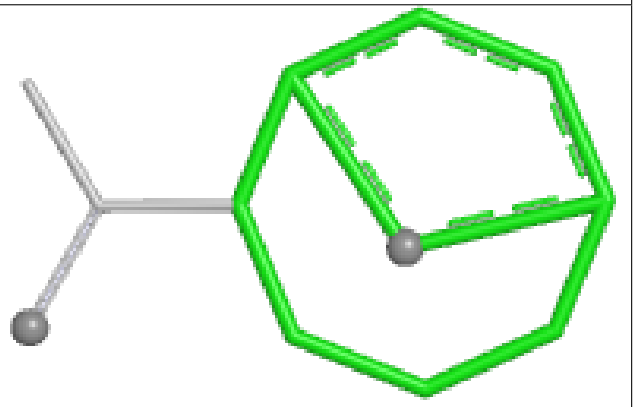
Bond lengths



Bond angles

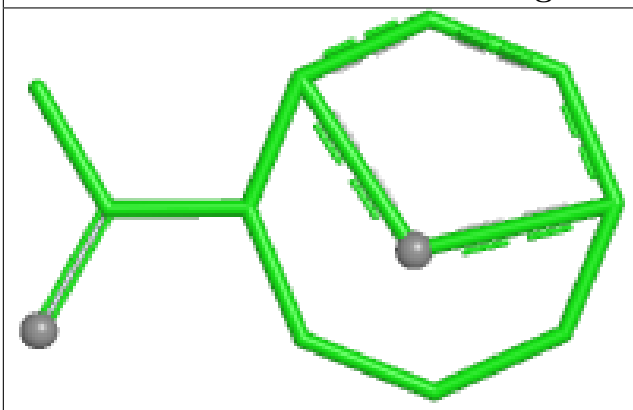


Torsions

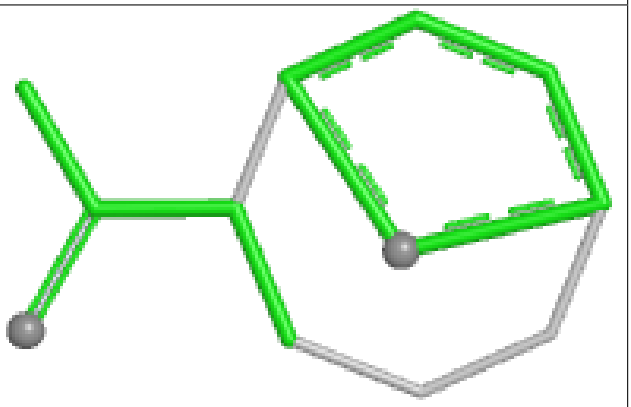


Rings

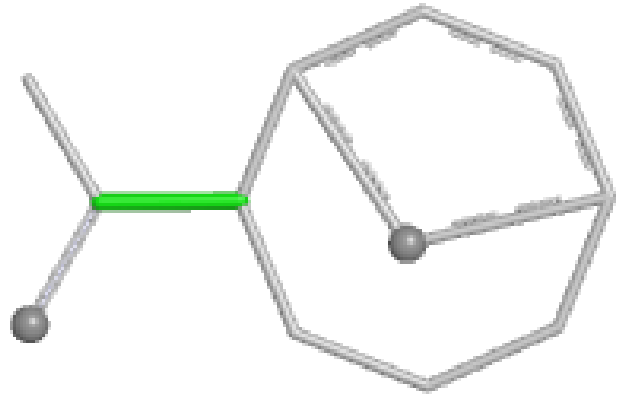
Ligand 4P0 J 302



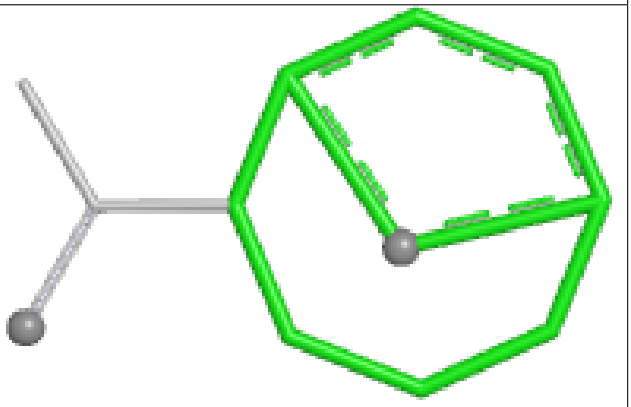
Bond lengths



Bond angles

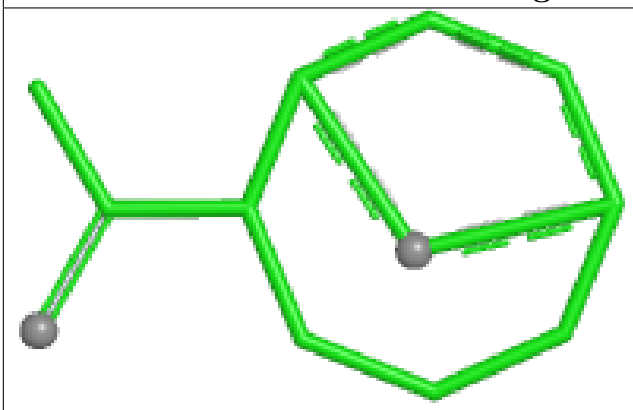


Torsions

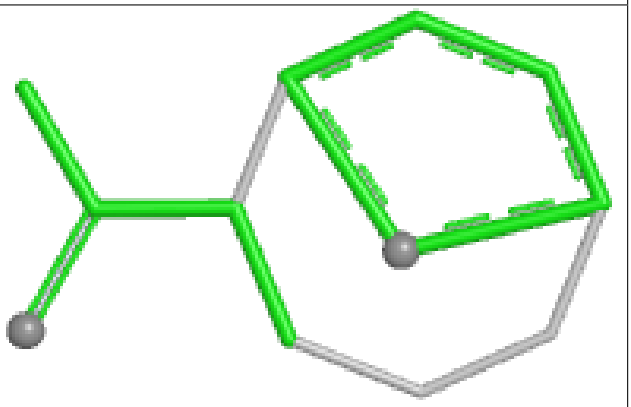


Rings

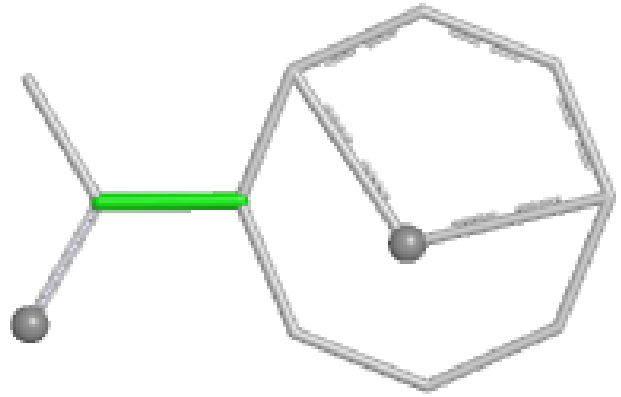
Ligand 4P0 F 306



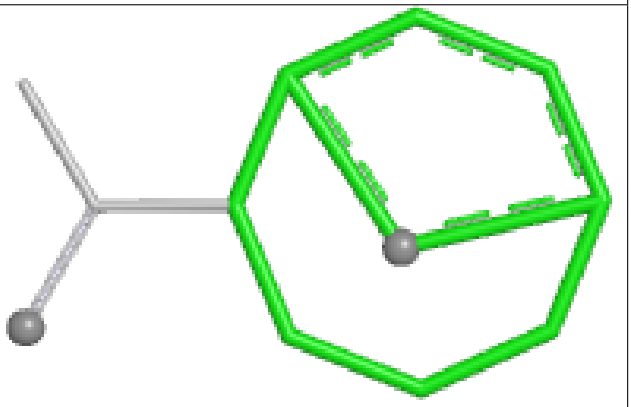
Bond lengths



Bond angles

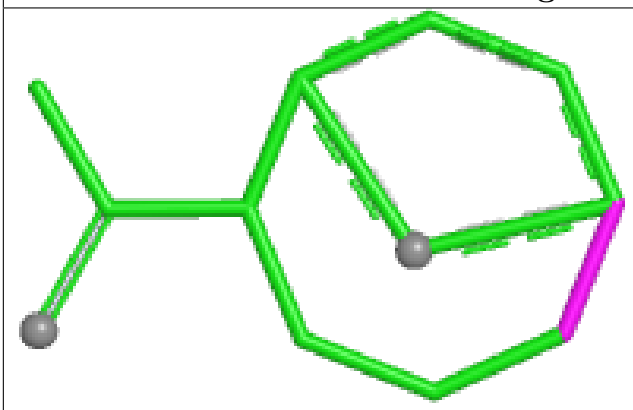


Torsions

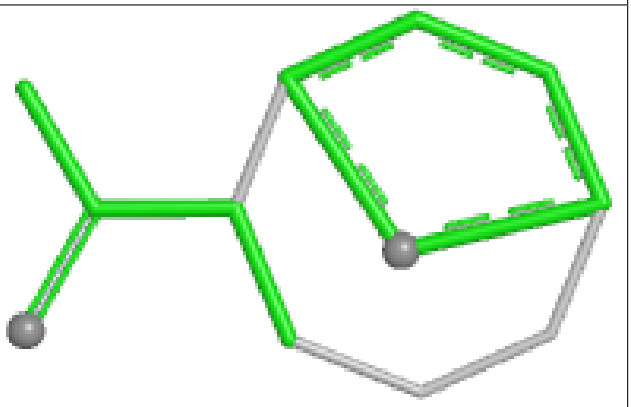


Rings

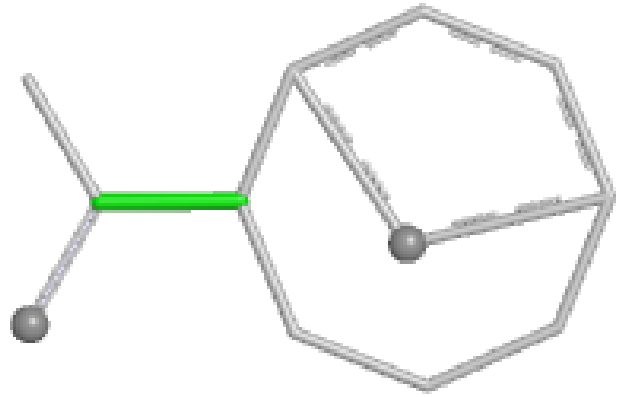
Ligand 4P0 I 303



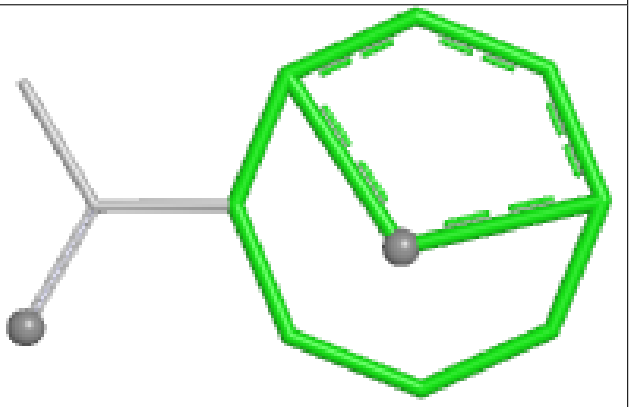
Bond lengths



Bond angles

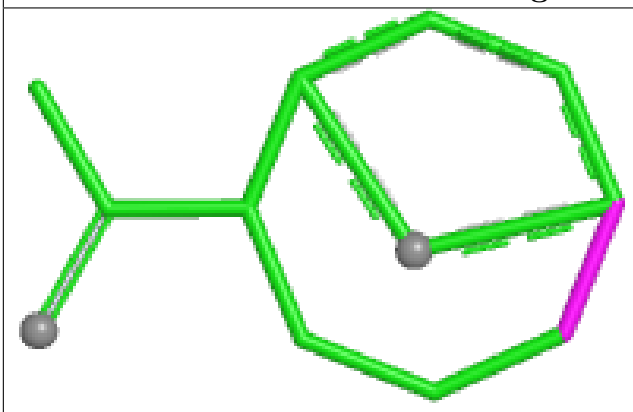


Torsions

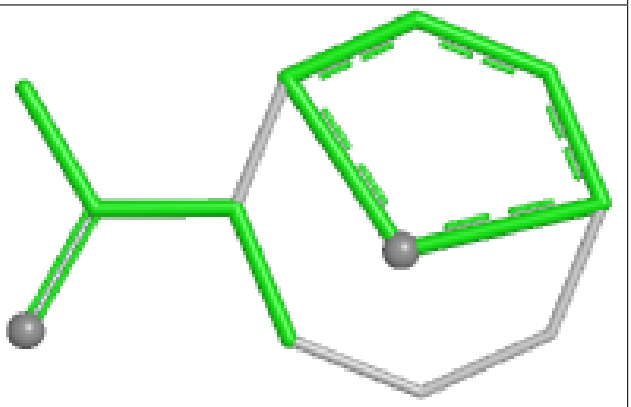


Rings

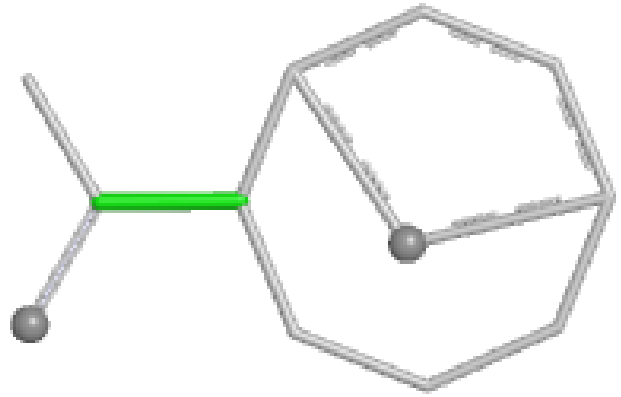
Ligand 4P0 A 303



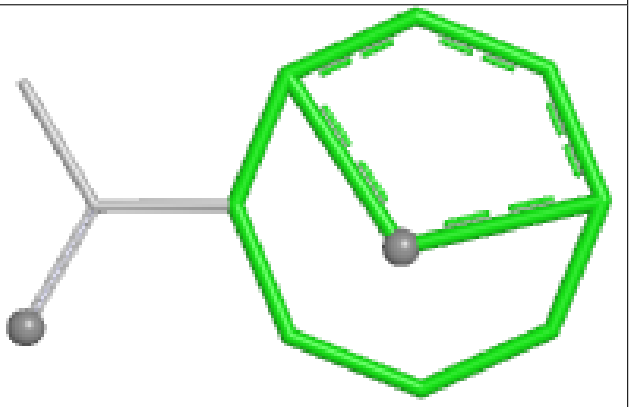
Bond lengths



Bond angles

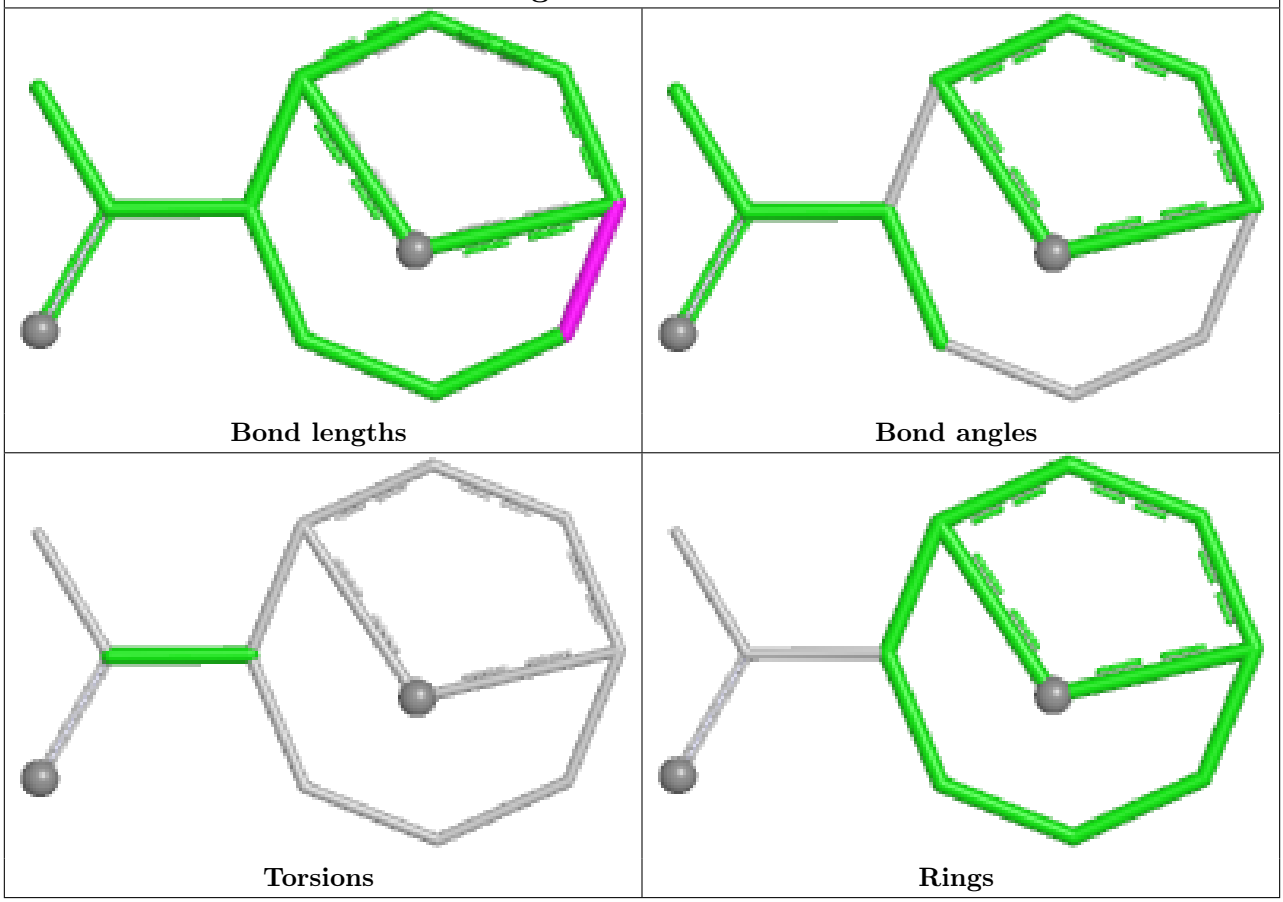


Torsions



Rings

Ligand 4P0 H 304



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	205/249 (82%)	0.71	16 (7%)	13	13	21, 28, 40, 58	1 (0%)
1	B	206/249 (82%)	0.59	5 (2%)	59	62	19, 26, 40, 63	0
1	C	205/249 (82%)	0.57	8 (3%)	39	42	18, 25, 40, 59	0
1	D	205/249 (82%)	0.49	5 (2%)	59	62	19, 25, 39, 59	0
1	E	205/249 (82%)	0.53	5 (2%)	59	62	19, 26, 39, 56	0
1	F	205/249 (82%)	0.51	5 (2%)	59	62	17, 24, 37, 61	0
1	G	205/249 (82%)	0.50	4 (1%)	65	68	17, 24, 38, 60	0
1	H	206/249 (82%)	0.61	6 (2%)	51	55	19, 26, 42, 59	0
1	I	211/249 (84%)	0.50	9 (4%)	35	38	18, 23, 42, 59	0
1	J	206/249 (82%)	0.43	3 (1%)	73	75	15, 22, 35, 55	0
All	All	2059/2490 (82%)	0.54	66 (3%)	47	51	15, 25, 40, 63	1 (0%)

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	225	ARG	3.8
1	I	34	SER	3.7
1	C	34	SER	3.5
1	C	169	PHE	3.5
1	G	20	GLN	3.5
1	H	20	GLN	3.3
1	H	33	ARG	3.2
1	A	54	LEU	3.2
1	C	21	ALA	3.1
1	I	225	ARG	3.1
1	E	20	GLN	3.0
1	I	227	GLY	2.9
1	I	33	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
1	F	33	ARG	2.9
1	F	34	SER	2.8
1	I	36	MET	2.8
1	B	87	ASN	2.8
1	A	46	LEU	2.7
1	D	35	PRO	2.7
1	A	202	VAL	2.7
1	C	20	GLN	2.7
1	H	36	MET	2.7
1	A	20	GLN	2.5
1	A	33	ARG	2.5
1	E	36	MET	2.5
1	J	20[A]	GLN	2.5
1	F	36	MET	2.5
1	A	36	MET	2.5
1	E	87	ASN	2.5
1	J	225	ARG	2.5
1	G	76[A]	ARG	2.4
1	C	33	ARG	2.4
1	C	208	CYS	2.3
1	A	35	PRO	2.3
1	C	43	ASP	2.3
1	I	20	GLN	2.3
1	D	20	GLN	2.3
1	B	34	SER	2.3
1	H	31	PHE	2.3
1	I	229	GLY	2.3
1	A	176	ASP	2.3
1	A	157[A]	CYS	2.3
1	G	33	ARG	2.2
1	H	87	ASN	2.2
1	A	169	PHE	2.2
1	E	152	GLU	2.2
1	I	87	ASN	2.2
1	A	34	SER	2.2
1	A	155	VAL	2.2
1	E	33	ARG	2.2
1	D	34	SER	2.2
1	B	20	GLN	2.2
1	B	207	CYS	2.2
1	I	81	SER	2.2
1	F	43	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	158	ALA	2.1
1	D	79	LEU	2.1
1	G	91	ASN	2.1
1	A	207[B]	CYS	2.1
1	J	34	SER	2.1
1	B	33	ARG	2.1
1	F	91	ASN	2.0
1	A	153	GLU	2.0
1	C	90	GLY	2.0
1	D	207	CYS	2.0
1	A	212	TYR	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
2	NAG	C	302	14/15	0.14	0.45	58,62,64,65	0
2	NAG	I	301	14/15	0.45	0.43	58,62,63,64	0
2	NAG	J	301	14/15	0.48	0.35	54,57,59,61	0
2	NAG	B	301	14/15	0.52	0.39	56,60,60,61	0
2	NAG	E	301	14/15	0.52	0.37	63,66,68,68	0
2	NAG	D	301	14/15	0.58	0.44	64,68,71,72	0
2	NAG	F	301	14/15	0.60	0.32	55,57,59,59	0
2	NAG	H	302	14/15	0.66	0.46	61,64,65,65	0
5	ACT	G	301	4/4	0.67	0.31	47,47,48,48	0
3	GOL	E	302	6/6	0.70	0.37	44,45,46,47	0
2	NAG	A	301	14/15	0.70	0.32	57,59,61,61	0
5	ACT	C	301	4/4	0.72	0.29	42,43,43,44	0

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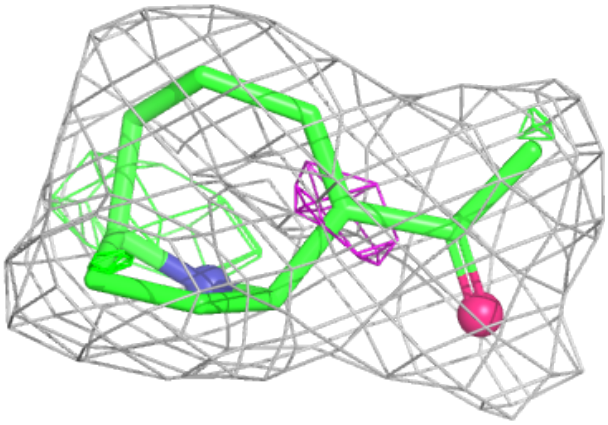
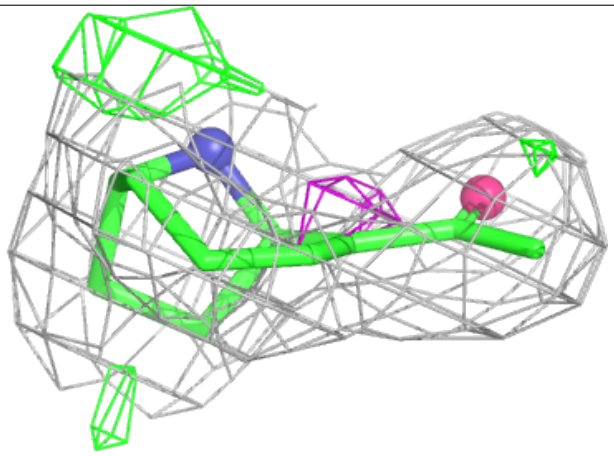
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	GOL	A	302	6/6	0.79	0.36	44,46,47,47	0
5	ACT	B	303	4/4	0.79	0.22	42,42,42,43	0
5	ACT	H	303	4/4	0.79	0.25	46,47,47,47	0
3	GOL	B	302	6/6	0.80	0.31	41,42,42,43	0
3	GOL	I	302	6/6	0.81	0.34	52,52,52,52	0
4	4P0	G	302	12/12	0.81	0.22	20,20,20,20	0
3	GOL	D	302	6/6	0.81	0.24	34,35,35,35	0
5	ACT	H	301	4/4	0.82	0.31	40,40,40,40	0
5	ACT	F	302	4/4	0.85	0.25	56,56,57,58	0
4	4P0	J	302	12/12	0.87	0.19	16,16,17,17	0
5	ACT	C	303	4/4	0.87	0.23	41,41,41,41	0
4	4P0	C	304	12/12	0.89	0.21	25,25,25,25	0
4	4P0	E	303	12/12	0.90	0.18	24,25,26,26	0
5	ACT	F	305	4/4	0.91	0.28	48,48,48,49	0
4	4P0	I	303	12/12	0.91	0.19	19,20,20,20	0
4	4P0	D	303	12/12	0.91	0.22	22,22,22,22	0
5	ACT	F	303	4/4	0.91	0.20	39,39,39,40	0
5	ACT	F	304	4/4	0.92	0.20	38,39,39,39	0
4	4P0	A	303	12/12	0.93	0.19	21,21,22,22	0
4	4P0	F	306	12/12	0.93	0.18	13,13,14,14	0
4	4P0	B	304	12/12	0.93	0.21	20,20,22,22	0
4	4P0	H	304	12/12	0.93	0.23	18,18,19,19	0

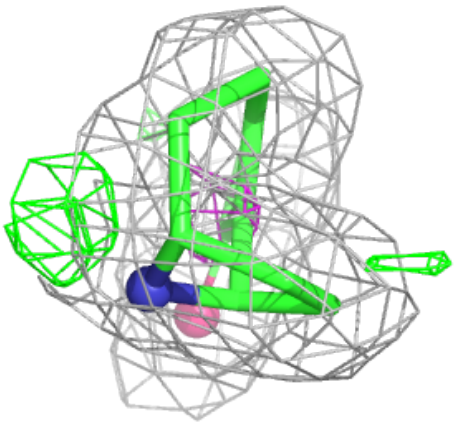
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 4P0 G 302:

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

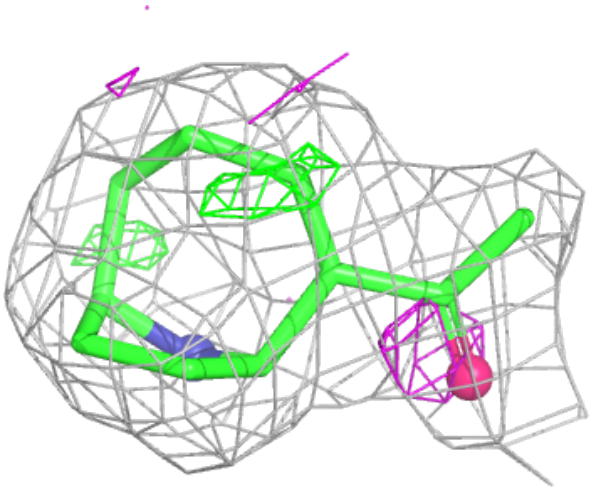


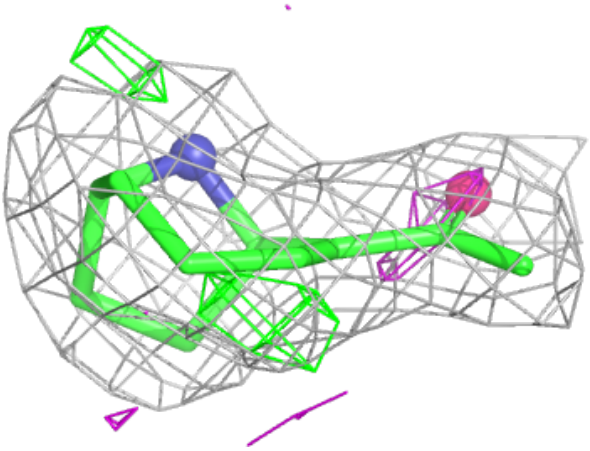


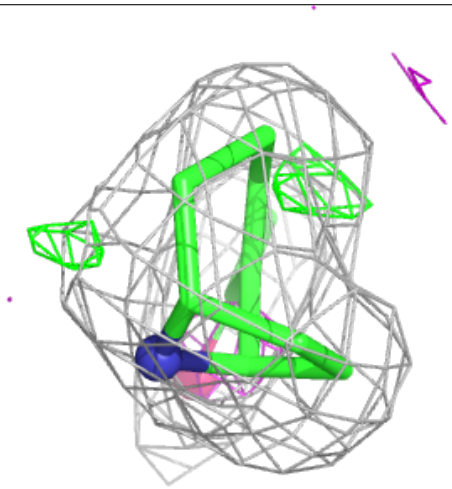


Electron density around 4P0 J 302:

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

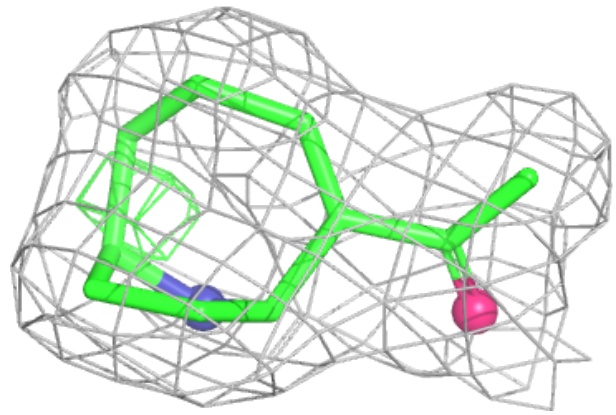


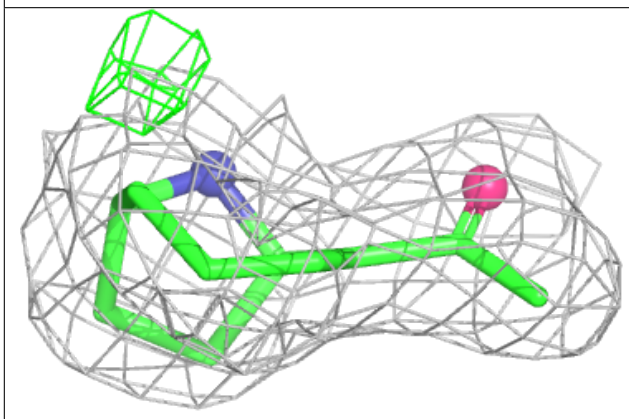


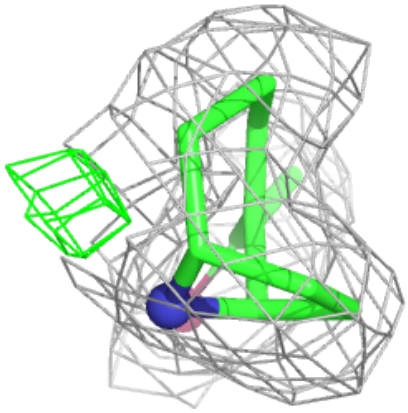


Electron density around 4P0 C 304:

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

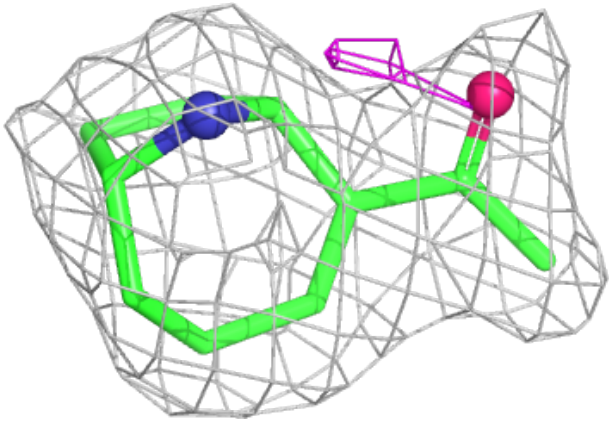


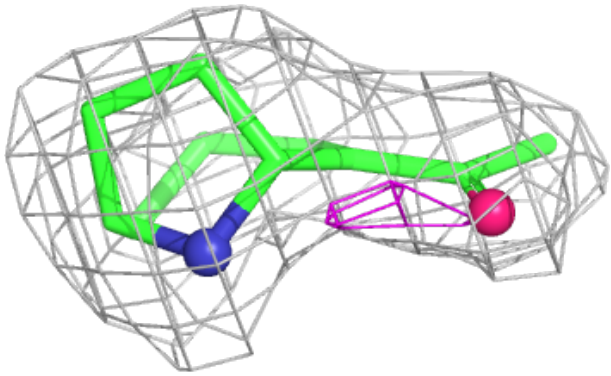


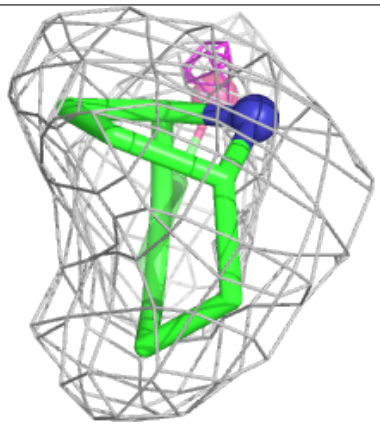


Electron density around 4P0 E 303:

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

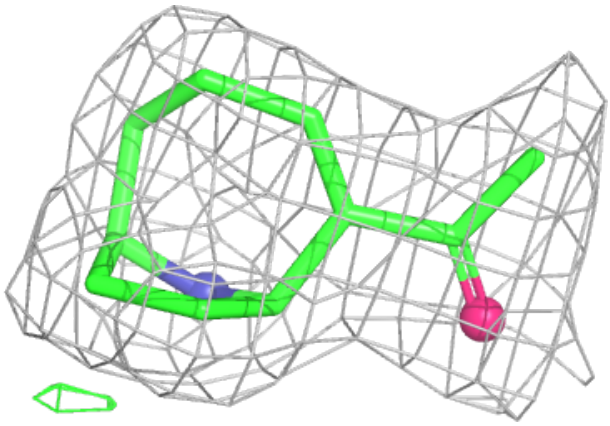


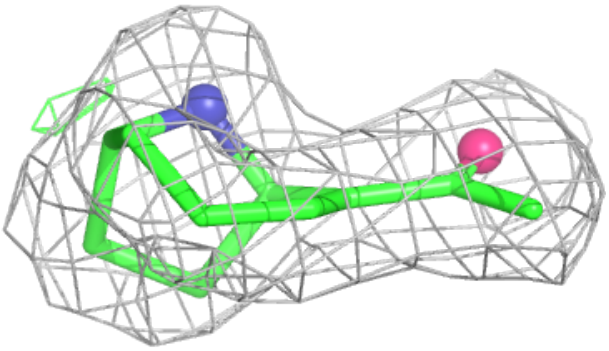


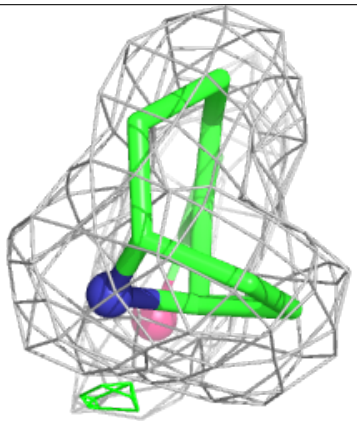


Electron density around 4P0 I 303:

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

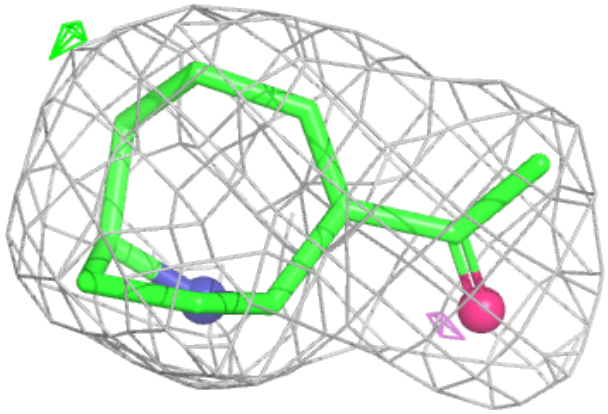


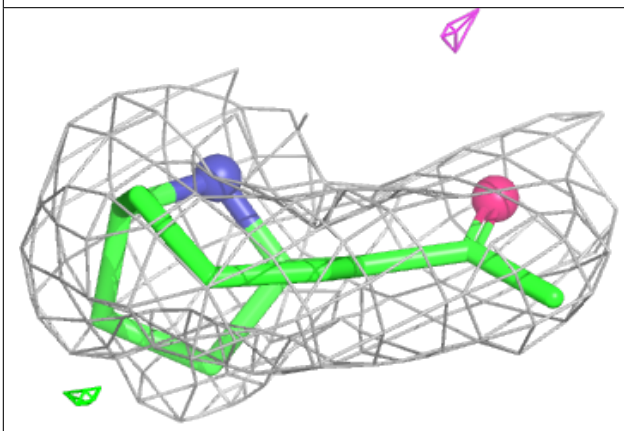


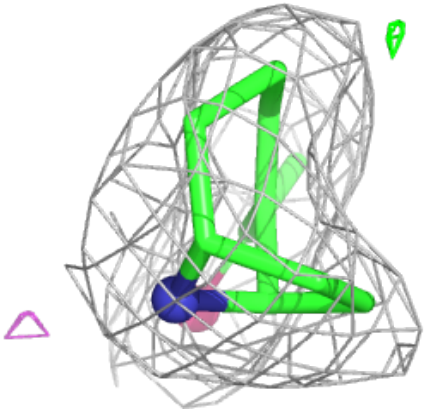


Electron density around 4P0 D 303:

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

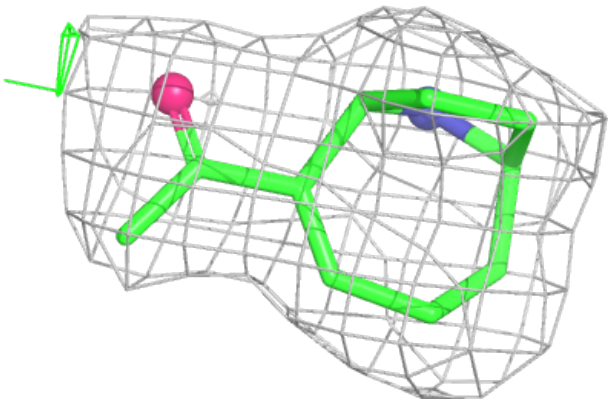


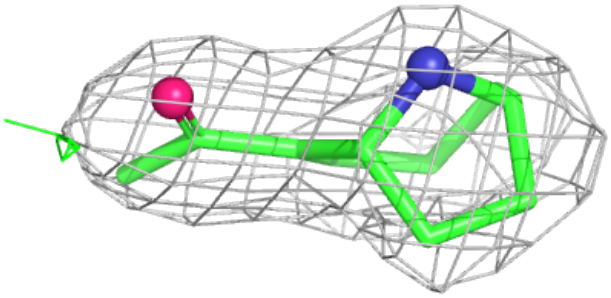


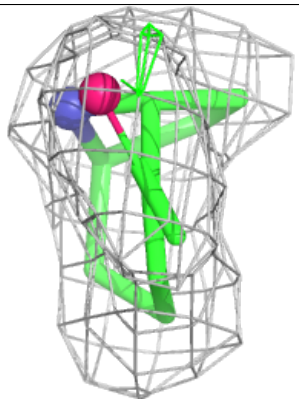


Electron density around 4P0 A 303:

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

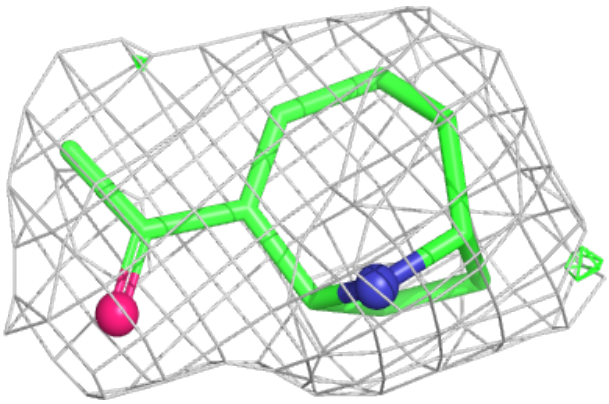


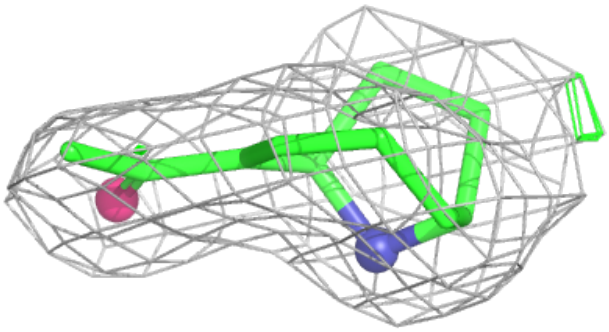


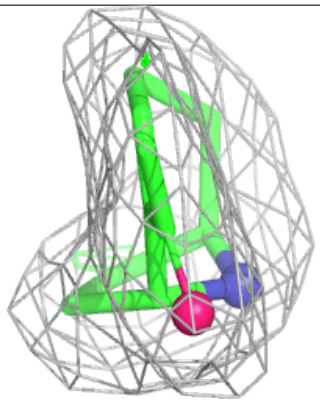


Electron density around 4P0 F 306:

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

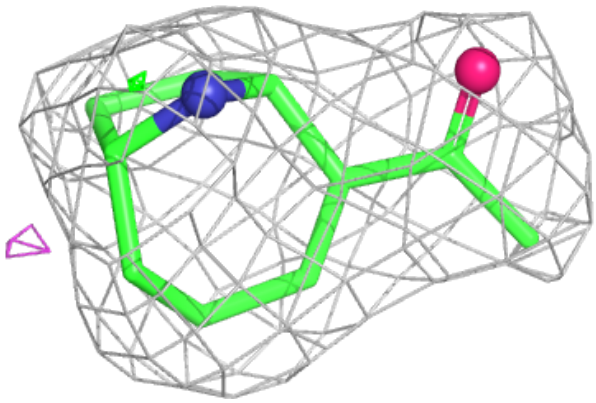


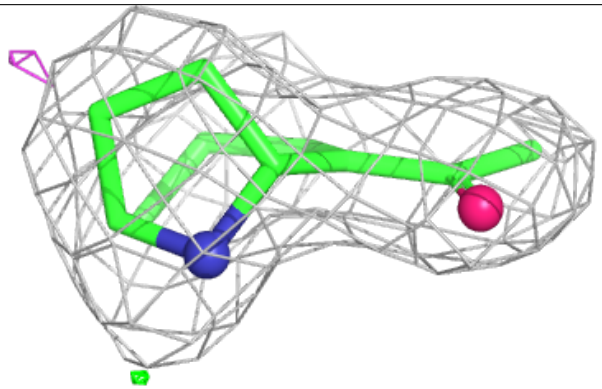


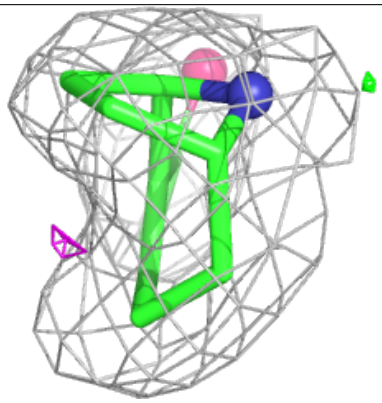


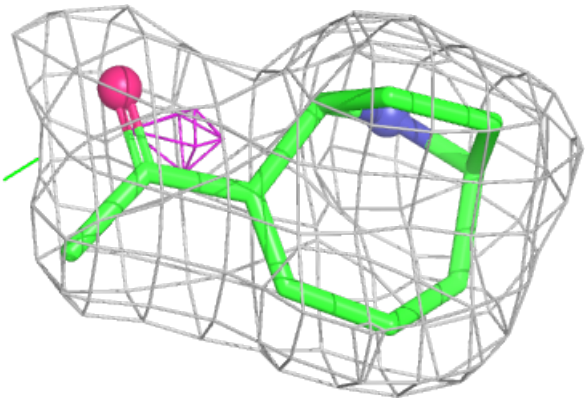
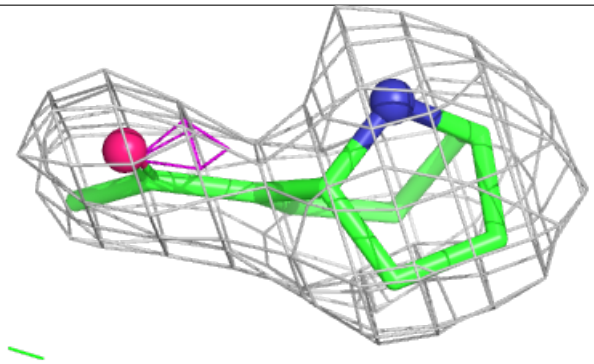
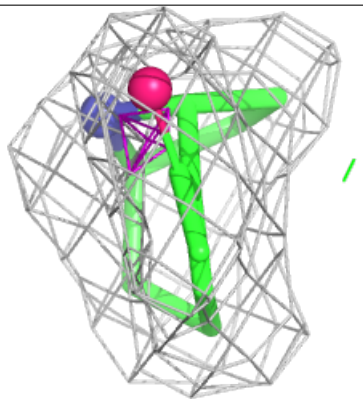
Electron density around 4P0 B 304:

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







Electron density around 4P0 H 304: $2mF_o$-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.