Full wwPDB X-ray Structure Validation Report (i)

Dec 18, 2023 – 06:13 am GMT

PDB ID	:	4C1I
Title	:	Selective Inhibitors of PDE2, PDE9, and PDE10: Modulators of Activity of the Central Nervous System
Authors	:	Jorgensen, M.; Kehler, J.; Langgard, M.; Svenstrup, N.; Tagmose, L.
Deposited on	:	2013-08-12
Resolution	:	2.40 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:

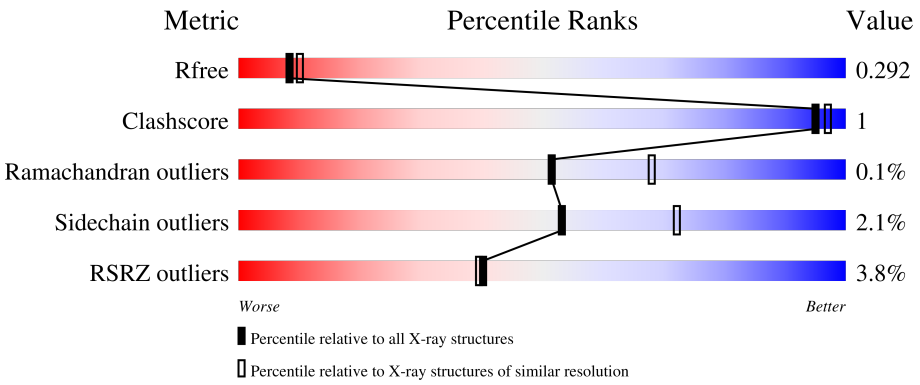
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	353	3%, 87%, 5%, 8%
1	B	353	3%, 85%, 5%, 9%
1	C	353	3%, 87%, ·, 10%
1	D	353	5%, 87%, ·, 10%

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	EH9	A	1906	X	-	-	-
2	EH9	B	1900	X	-	-	-
2	EH9	C	1900	X	-	-	-
2	EH9	D	1900	X	-	-	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 10670 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 CGMP-DEPENDENT 3', 5'-CYCLIC PHOSPHODIESTERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	325	2625	1673	451	476	25	0	0	0
1	B	320	2581	1646	437	473	25	0	0	0
1	C	319	2577	1641	440	472	24	0	0	0
1	D	319	2551	1626	434	466	25	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	576	MET	-	expression tag	UNP O00408
A	577	GLY	-	expression tag	UNP O00408
A	922	ARG	-	expression tag	UNP O00408
A	923	HIS	-	expression tag	UNP O00408
A	924	HIS	-	expression tag	UNP O00408
A	925	HIS	-	expression tag	UNP O00408
A	926	HIS	-	expression tag	UNP O00408
A	927	HIS	-	expression tag	UNP O00408
A	928	HIS	-	expression tag	UNP O00408
B	576	MET	-	expression tag	UNP O00408
B	577	GLY	-	expression tag	UNP O00408
B	922	ARG	-	expression tag	UNP O00408
B	923	HIS	-	expression tag	UNP O00408
B	924	HIS	-	expression tag	UNP O00408
B	925	HIS	-	expression tag	UNP O00408
B	926	HIS	-	expression tag	UNP O00408
B	927	HIS	-	expression tag	UNP O00408
B	928	HIS	-	expression tag	UNP O00408
C	576	MET	-	expression tag	UNP O00408
C	577	GLY	-	expression tag	UNP O00408
C	922	ARG	-	expression tag	UNP O00408

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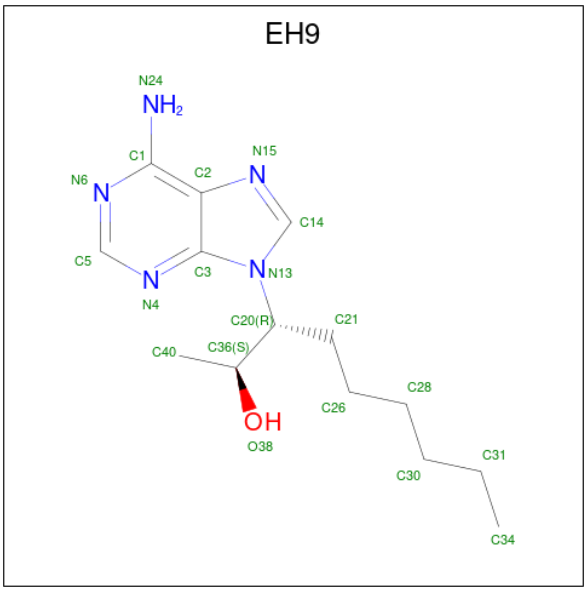
Chain	Residue	Modelled	Actual	Comment	Reference
C	923	HIS	-	expression tag	UNP O00408
C	924	HIS	-	expression tag	UNP O00408
C	925	HIS	-	expression tag	UNP O00408
C	926	HIS	-	expression tag	UNP O00408
C	927	HIS	-	expression tag	UNP O00408
C	928	HIS	-	expression tag	UNP O00408
D	576	MET	-	expression tag	UNP O00408
D	577	GLY	-	expression tag	UNP O00408
D	922	ARG	-	expression tag	UNP O00408
D	923	HIS	-	expression tag	UNP O00408
D	924	HIS	-	expression tag	UNP O00408
D	925	HIS	-	expression tag	UNP O00408
D	926	HIS	-	expression tag	UNP O00408
D	927	HIS	-	expression tag	UNP O00408
D	928	HIS	-	expression tag	UNP O00408

- Molecule 2 is (2S,3R)-3-(6-amino-9H-purin-9-yl)nonan-2-ol (three-letter code: EH9) (formula: $C_{14}H_{23}N_5O$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	20	14	5	1	0	0
			Total	C	N	O		
2	B	1	20	14	5	1	0	0
			Total	C	N	O		
2	C	1	20	14	5	1	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	D	1	20	14	5	1	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
3	A	1	1	1	0	0
3	B	1	1	1	0	0
3	C	1	1	1	0	0
3	D	1	1	1	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 5 is water.

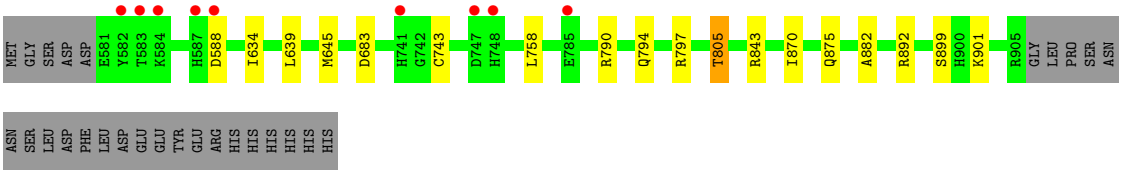
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	68	68	68	0	0
5	B	59	59	59	0	0
5	C	74	74	74	0	0
5	D	47	47	47	0	0

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.

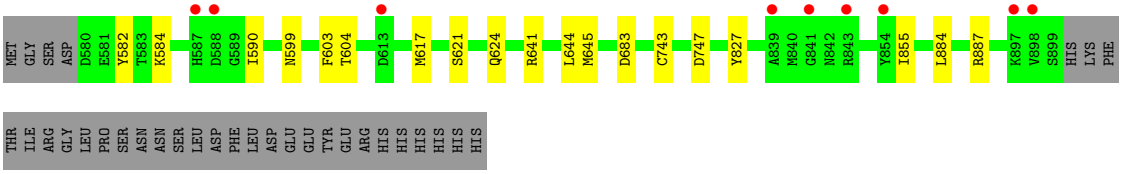
• Molecule 1: CGMP-DEPENDENT 3', 5'-CYCLIC PHOSPHODIESTERASE

Chain A:



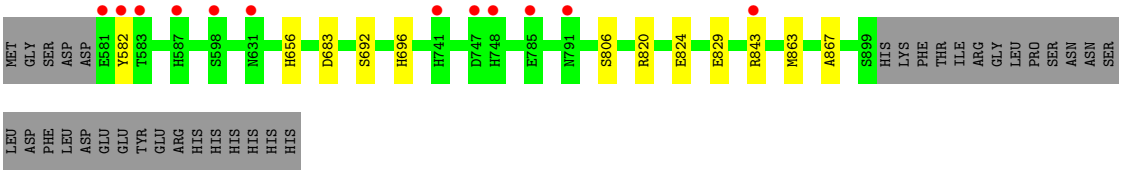
• Molecule 1: CGMP-DEPENDENT 3', 5'-CYCLIC PHOSPHODIESTERASE

Chain B:



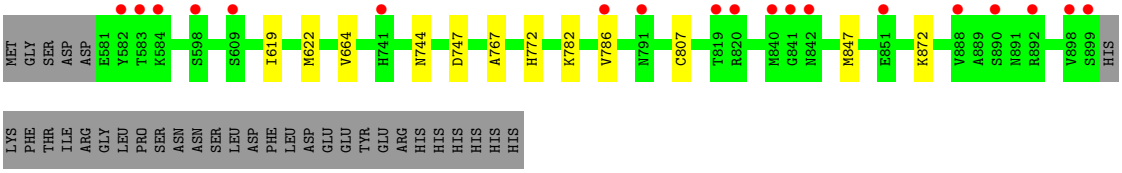
• Molecule 1: CGMP-DEPENDENT 3', 5'-CYCLIC PHOSPHODIESTERASE

Chain C:



• Molecule 1: CGMP-DEPENDENT 3', 5'-CYCLIC PHOSPHODIESTERASE

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	47.05Å 81.81Å 93.34Å 110.16° 95.66° 93.21°	Depositor
Resolution (Å)	18.47 – 2.40 18.41 – 2.40	Depositor EDS
% Data completeness (in resolution range)	94.0 (18.47-2.40) 94.2 (18.41-2.40)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.21 (at 2.40Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.225 , 0.287 0.232 , 0.292	Depositor DCC
R_{free} test set	2434 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å^2)	29.0	Xtriage
Anisotropy	0.123	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 36.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	10670	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.37% 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: EH9, ZN, MG

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	0.31	0/2689	0.48	0/3636
1	B	0.31	0/2644	0.50	0/3577
1	C	0.31	0/2640	0.48	0/3573
1	D	0.30	0/2613	0.47	0/3538
All	All	0.31	0/10586	0.48	0/14324

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2625	0	2531	4	0
1	B	2581	0	2481	8	0
1	C	2577	0	2472	3	0
1	D	2551	0	2437	5	0
2	A	20	0	23	0	0
2	B	20	0	23	2	0
2	C	20	0	23	2	0
2	D	20	0	23	0	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	68	0	0	0	0
5	B	59	0	0	0	0
5	C	74	0	0	0	0
5	D	47	0	0	0	0
All	All	10670	0	10013	24	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 1.

All (24) 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:744:ASN:ND2	1:D:747:ASP:OD1	2.35	0.60
1:A:875:GLN:HE21	1:A:882:ALA:HA	1.74	0.53
2:B:1900:EH9:H402	2:B:1900:EH9:C14	2.40	0.51
1:B:582:TYR:CE1	1:B:641:ARG:HG3	2.46	0.50
2:C:1900:EH9:H402	2:C:1900:EH9:C14	2.42	0.49
1:B:590:ILE:HG21	1:B:624:GLN:CB	2.43	0.49
1:C:863:MET:HA	1:C:867:ALA:HB3	1.96	0.46
1:A:645:MET:HG3	1:A:743:CYS:SG	2.56	0.45
1:B:603:PHE:CD1	1:B:884:LEU:HD21	2.52	0.45
1:B:582:TYR:HA	1:B:644:LEU:HD11	1.99	0.44
1:B:827:TYR:CE2	1:B:855:ILE:HG23	2.53	0.44
1:C:656:HIS:ND1	1:C:829:GLU:OE1	2.49	0.44
1:B:590:ILE:HG23	1:B:621:SER:HA	2.00	0.44
1:D:619:ILE:HA	1:D:622:MET:HE3	2.02	0.42
2:B:1900:EH9:C14	2:B:1900:EH9:C40	2.97	0.42
2:C:1900:EH9:C14	2:C:1900:EH9:C40	2.98	0.42
1:B:645:MET:HG3	1:B:743:CYS:SG	2.60	0.41
1:A:634:ILE:HG21	1:A:639:LEU:HD13	2.02	0.41
1:A:805:THR:HG23	1:A:870:ILE:HD13	2.02	0.41
1:D:664:VAL:HG13	1:D:807:CYS:HB3	2.02	0.41
1:B:599:ASN:ND2	1:B:604:THR:OG1	2.54	0.41
1:D:767:ALA:HA	1:D:772:HIS:CD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:782:LYS:O	1:D:786:VAL:HG22	2.21	0.40
1:C:692:SER:O	1:C:696:HIS:HB3	2.20	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	323/353 (92%)	316 (98%)	7 (2%)	0	100	100
1	B	318/353 (90%)	311 (98%)	6 (2%)	1 (0%)	41	55
1	C	317/353 (90%)	313 (99%)	4 (1%)	0	100	100
1	D	317/353 (90%)	310 (98%)	7 (2%)	0	100	100
All	All	1275/1412 (90%)	1250 (98%)	24 (2%)	1 (0%)	51	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	747	ASP

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	282/319 (88%)	271 (96%)	11 (4%)	32	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	278/319 (87%)	274 (99%)	4 (1%)	67	82
1	C	277/319 (87%)	271 (98%)	6 (2%)	52	71
1	D	272/319 (85%)	270 (99%)	2 (1%)	84	92
All	All	1109/1276 (87%)	1086 (98%)	23 (2%)	53	72

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	588	ASP
1	A	683	ASP
1	A	758	LEU
1	A	790	ARG
1	A	794	GLN
1	A	797	ARG
1	A	805	THR
1	A	843	ARG
1	A	892	ARG
1	A	899	SER
1	A	901	LYS
1	B	584	LYS
1	B	617	MET
1	B	683	ASP
1	B	887	ARG
1	C	582	TYR
1	C	683	ASP
1	C	806	SER
1	C	820	ARG
1	C	824	GLU
1	C	843	ARG
1	D	847	MET
1	D	872	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	599	ASN
1	A	772	HIS
1	A	794	GLN
1	A	875	GLN
1	A	894	HIS

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Mol	Chain	Res	Type
1	B	599	ASN
1	B	772	HIS
1	C	666	HIS
1	C	772	HIS
1	D	708	GLN
1	D	772	HIS

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)

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	EH9	D	1900	-	17,21,21	0.69	0	13,28,28	1.52	1 (7%)
2	EH9	C	1900	-	17,21,21	0.69	0	13,28,28	1.47	1 (7%)
2	EH9	A	1906	-	17,21,21	0.68	0	13,28,28	1.52	1 (7%)
2	EH9	B	1900	-	17,21,21	0.61	0	13,28,28	1.63	2 (15%)

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	EH9	D	1900	-	1/1/2/2	7/10/14/14	0/2/2/2
2	EH9	C	1900	-	1/1/2/2	4/10/14/14	0/2/2/2
2	EH9	A	1906	-	1/1/2/2	6/10/14/14	0/2/2/2
2	EH9	B	1900	-	1/1/2/2	5/10/14/14	0/2/2/2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1906	EH9	N4-C5-N6	-4.61	121.47	128.68
2	C	1900	EH9	N4-C5-N6	-4.52	121.62	128.68
2	D	1900	EH9	N4-C5-N6	-4.49	121.66	128.68
2	B	1900	EH9	N4-C5-N6	-4.44	121.74	128.68
2	B	1900	EH9	C21-C20-N13	-2.43	108.19	112.36

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1906	EH9	C36
2	B	1900	EH9	C36
2	C	1900	EH9	C36
2	D	1900	EH9	C36

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1906	EH9	N13-C20-C36-O38
2	A	1906	EH9	N13-C20-C36-C40
2	A	1906	EH9	C21-C20-C36-O38
2	A	1906	EH9	C21-C20-C36-C40
2	B	1900	EH9	N13-C20-C36-O38
2	B	1900	EH9	N13-C20-C36-C40
2	B	1900	EH9	C21-C20-C36-O38
2	B	1900	EH9	C21-C20-C36-C40
2	C	1900	EH9	N13-C20-C36-O38
2	C	1900	EH9	N13-C20-C36-C40
2	C	1900	EH9	C21-C20-C36-O38
2	C	1900	EH9	C21-C20-C36-C40
2	D	1900	EH9	C36-C20-C21-C26

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Mol	Chain	Res	Type	Atoms
2	D	1900	EH9	N13-C20-C36-O38
2	D	1900	EH9	N13-C20-C36-C40
2	D	1900	EH9	C21-C20-C36-O38
2	D	1900	EH9	C21-C20-C36-C40
2	D	1900	EH9	N13-C20-C21-C26
2	D	1900	EH9	C21-C26-C28-C30
2	A	1906	EH9	C21-C26-C28-C30
2	B	1900	EH9	C21-C26-C28-C30
2	A	1906	EH9	C36-C20-C21-C26

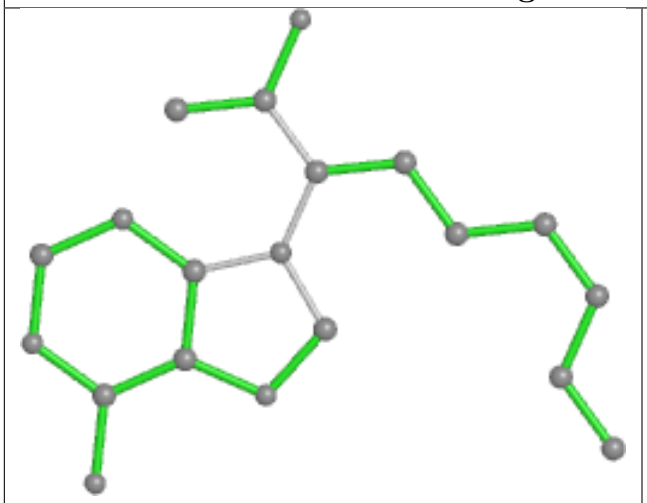
There are no ring outliers.

2 monomers are involved in 4 short contacts:

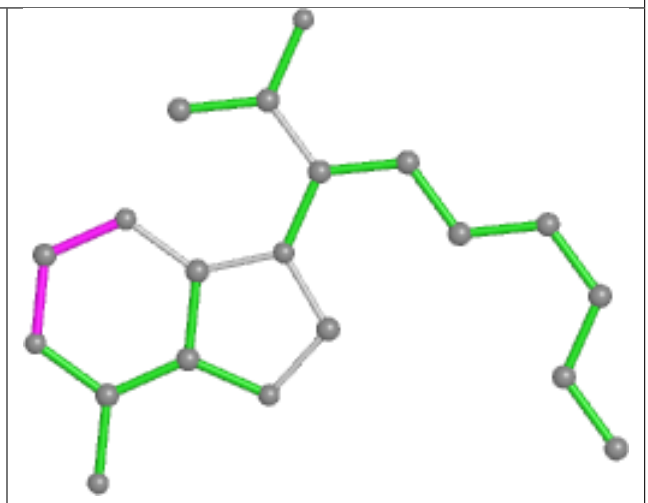
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1900	EH9	2	0
2	B	1900	EH9	2	0

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.

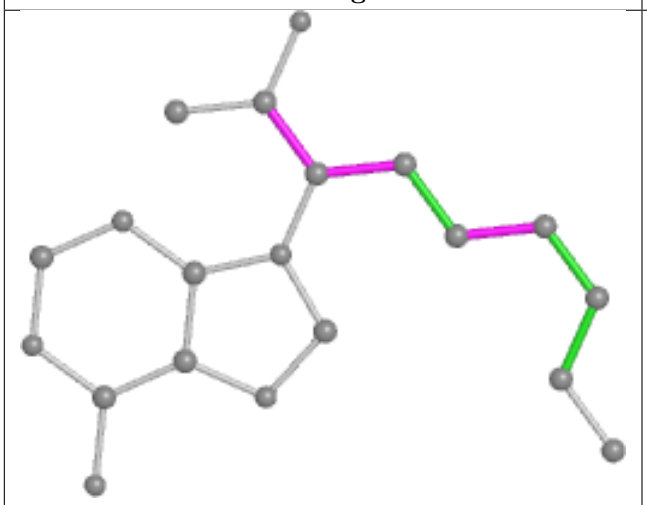
Ligand EH9 D 1900



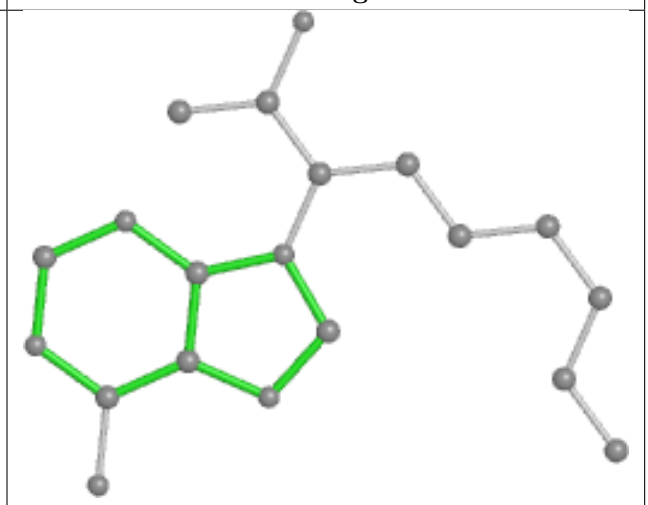
Bond lengths



Bond angles

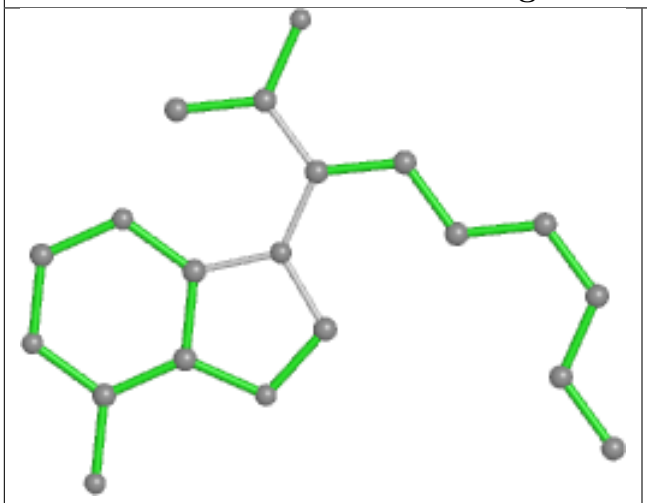


Torsions

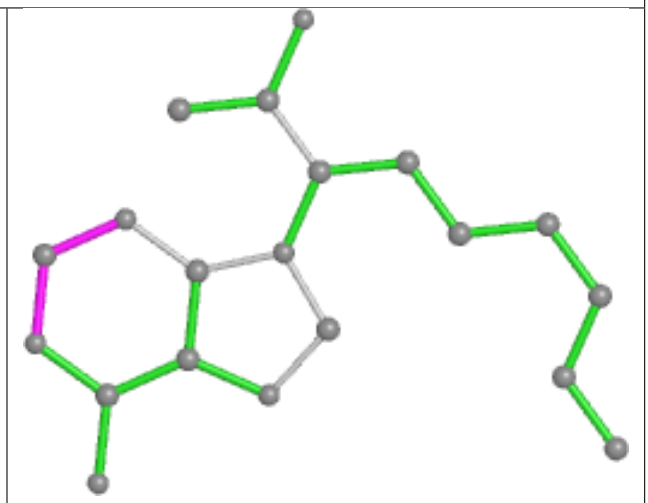


Rings

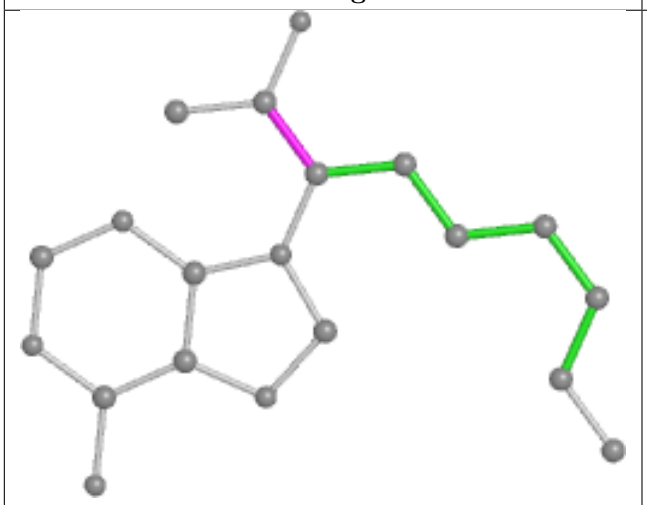
Ligand EH9 C 1900



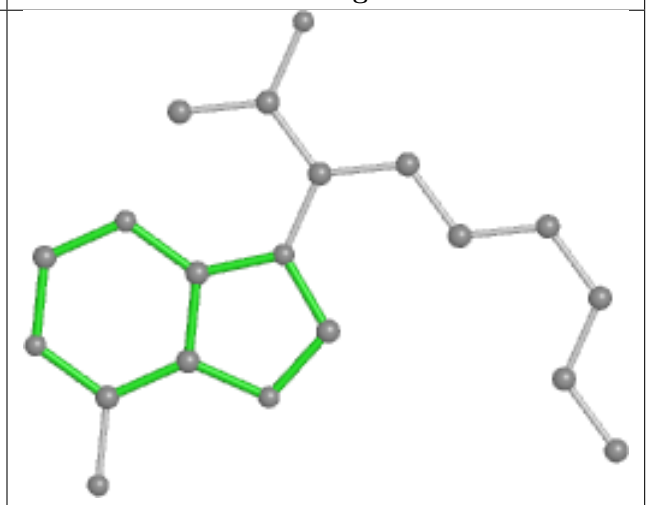
Bond lengths



Bond angles

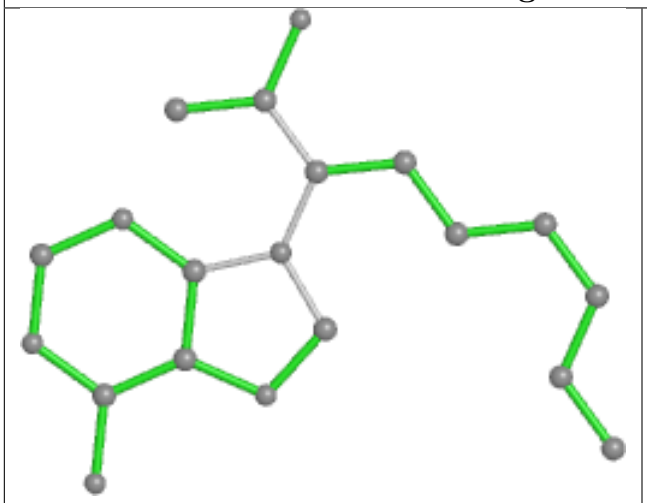


Torsions

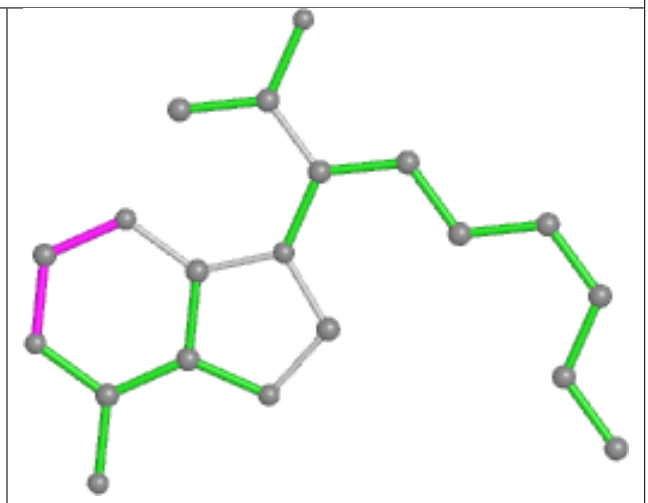


Rings

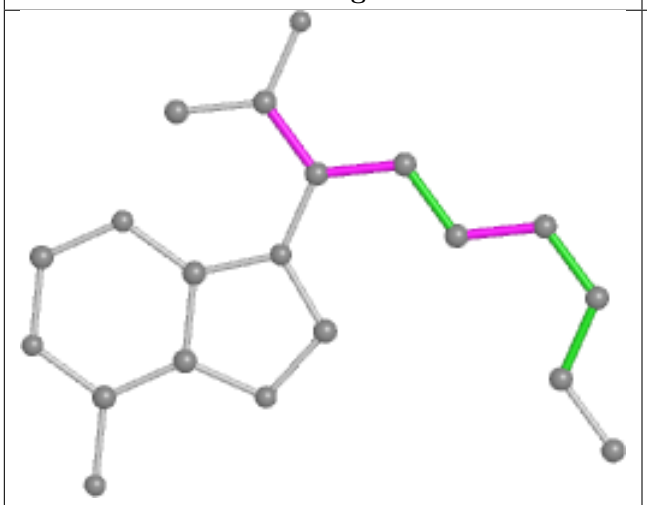
Ligand EH9 A 1906



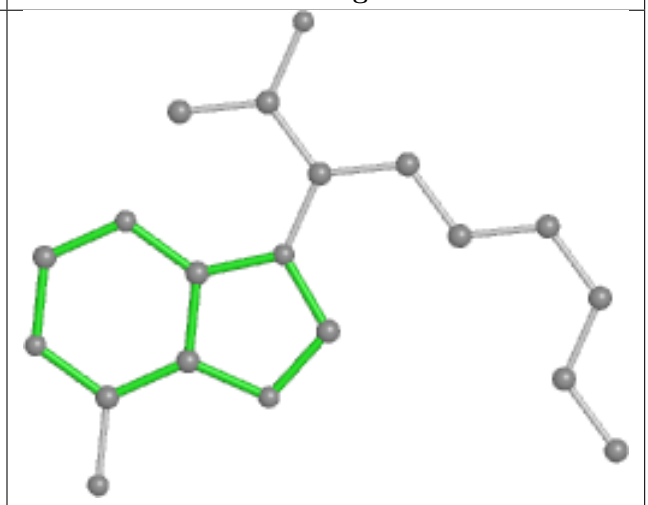
Bond lengths



Bond angles

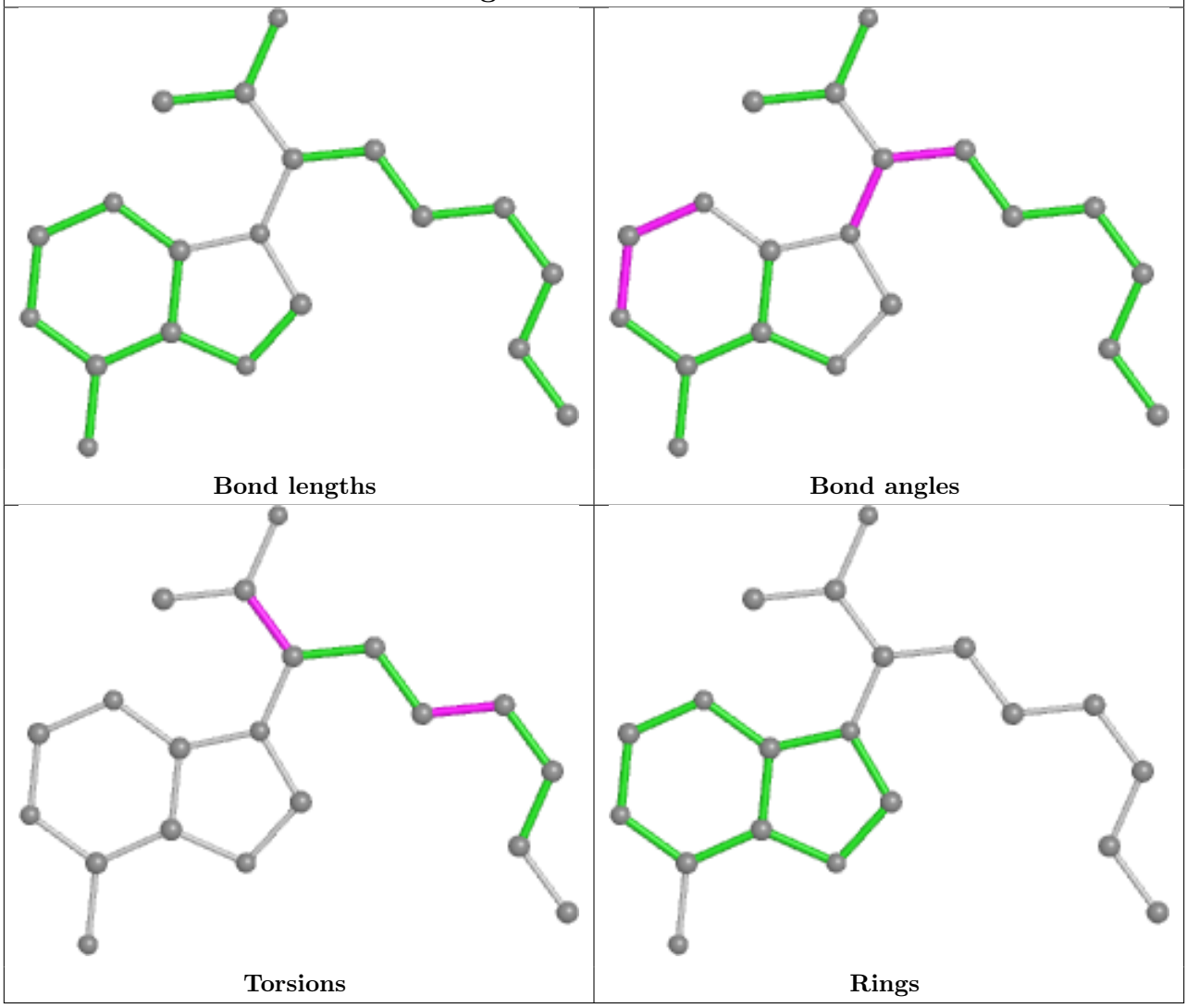


Torsions



Rings

Ligand EH9 B 1900



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	325/353 (92%)	0.11	9 (2%)	53	51	14, 26, 42, 79	0
1	B	320/353 (90%)	0.18	9 (2%)	53	51	16, 28, 45, 60	0
1	C	319/353 (90%)	0.21	12 (3%)	40	39	16, 28, 46, 64	0
1	D	319/353 (90%)	0.46	19 (5%)	21	20	19, 34, 57, 81	0
All	All	1283/1412 (90%)	0.24	49 (3%)	40	39	14, 29, 50, 81	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	587	HIS	6.4
1	D	583	THR	4.9
1	A	582	TYR	4.4
1	D	899	SER	4.1
1	A	741	HIS	4.0
1	D	582	TYR	3.8
1	D	741	HIS	3.8
1	A	583	THR	3.7
1	C	582	TYR	3.5
1	C	587	HIS	3.4
1	D	841	GLY	3.4
1	B	587	HIS	3.1
1	A	588	ASP	3.1
1	D	840	MET	3.0
1	D	791	ASN	3.0
1	D	819	THR	3.0
1	C	598	SER	2.9
1	D	786	VAL	2.8
1	D	598	SER	2.8
1	D	890	SER	2.8
1	C	741	HIS	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	791	ASN	2.7
1	A	747	ASP	2.7
1	B	898	VAL	2.6
1	C	843	ARG	2.6
1	D	820	ARG	2.5
1	B	897	LYS	2.5
1	B	839	ALA	2.5
1	C	631	ASN	2.4
1	A	785	GLU	2.4
1	B	588	ASP	2.4
1	A	584	LYS	2.3
1	D	584	LYS	2.3
1	D	898	VAL	2.3
1	C	581	GLU	2.3
1	B	841	GLY	2.3
1	B	854	TYR	2.3
1	D	892	ARG	2.2
1	D	609	SER	2.2
1	C	583	THR	2.2
1	C	748	HIS	2.2
1	D	888	VAL	2.1
1	C	785	GLU	2.1
1	A	748	HIS	2.1
1	D	851	GLU	2.1
1	D	842	ASN	2.1
1	B	613	ASP	2.0
1	B	843	ARG	2.0
1	C	747	ASP	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,

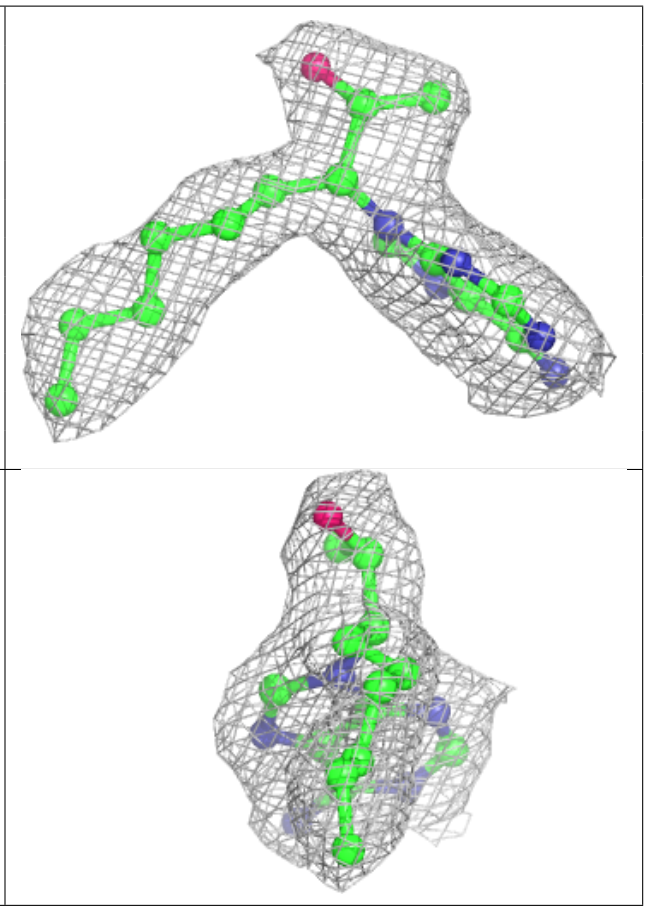
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	MG	A	1908	1/1	0.74	0.11	16,16,16,16	0
2	EH9	D	1900	20/20	0.91	0.14	28,29,30,31	0
2	EH9	B	1900	20/20	0.91	0.15	25,26,26,27	0
2	EH9	A	1906	20/20	0.93	0.15	23,24,26,26	0
2	EH9	C	1900	20/20	0.93	0.15	30,32,34,34	0
4	MG	C	1902	1/1	0.93	0.06	20,20,20,20	0
4	MG	B	1902	1/1	0.95	0.09	16,16,16,16	0
4	MG	D	1902	1/1	0.98	0.07	19,19,19,19	0
3	ZN	C	1901	1/1	0.99	0.03	21,21,21,21	0
3	ZN	D	1901	1/1	0.99	0.04	26,26,26,26	0
3	ZN	B	1901	1/1	0.99	0.04	20,20,20,20	0
3	ZN	A	1907	1/1	1.00	0.02	18,18,18,18	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.

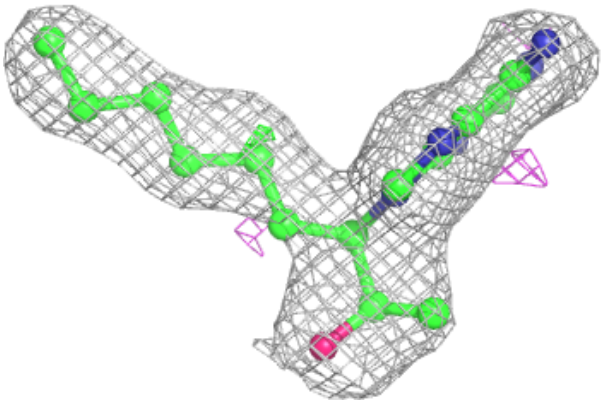
Electron density around EH9 D 1900:

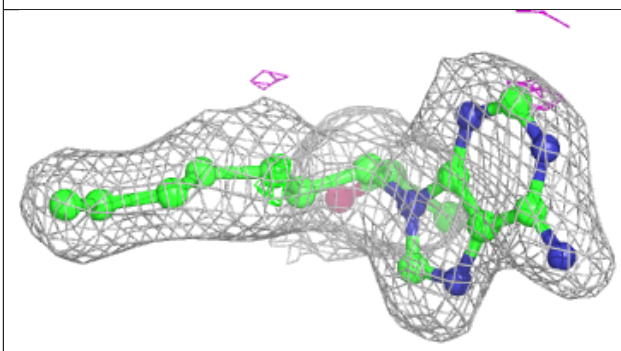
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

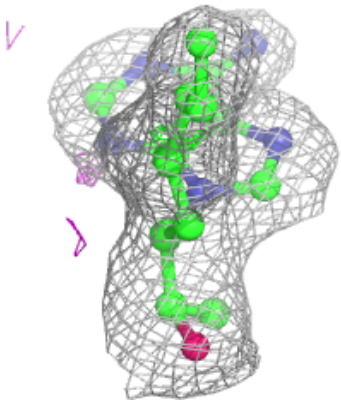


Electron density around EH9 B 1900:

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

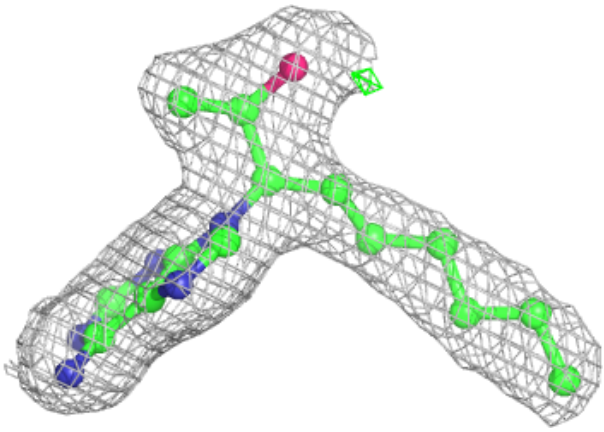


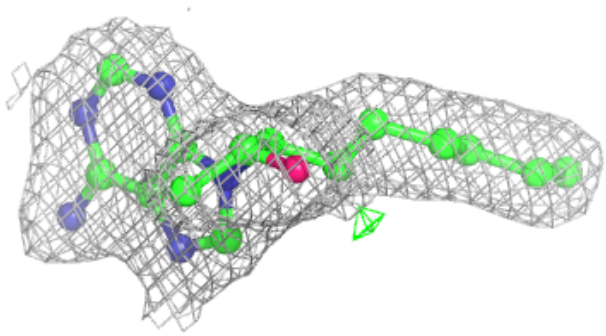


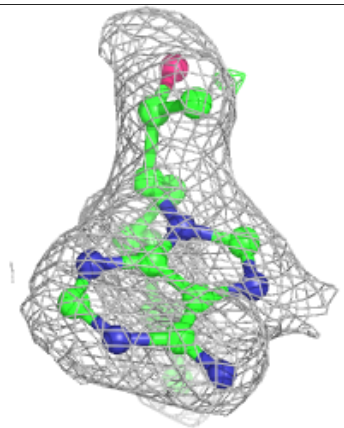


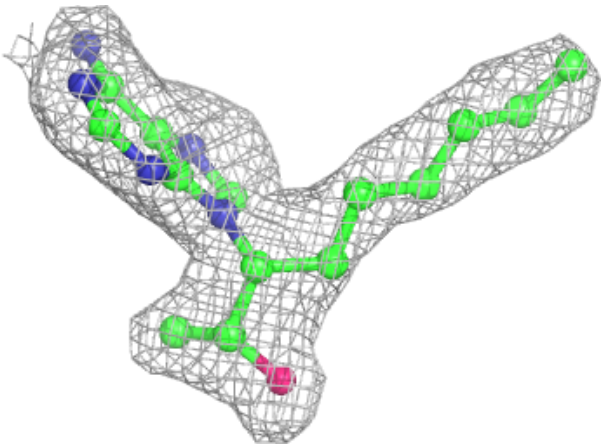
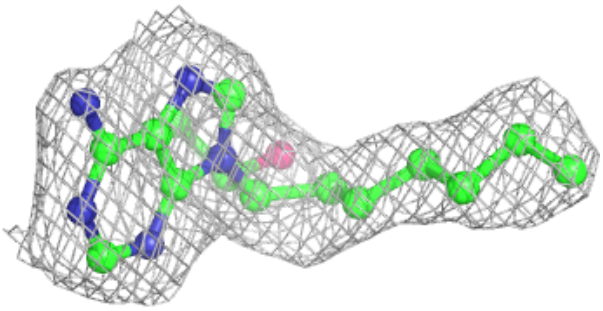
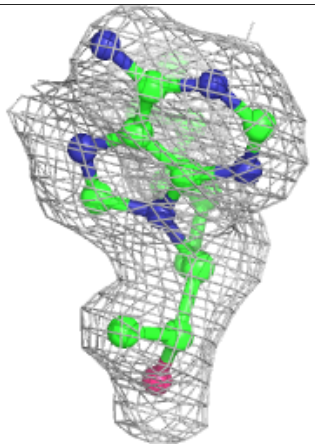
Electron density around EH9 A 1906:

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







Electron density around EH9 C 1900: 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.