



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:40 PM UTC

PDB ID : 9ET6 / pdb_00009et6
Title : CDK2-cyclin A in complex with FragLite 7
Authors : Hope, I.; Martin, M.P.; Waring, M.J.; Noble, M.E.M.; Endicott, J.A.; Tatum, N.J.
Deposited on : 2024-03-26
Resolution : 2.55 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

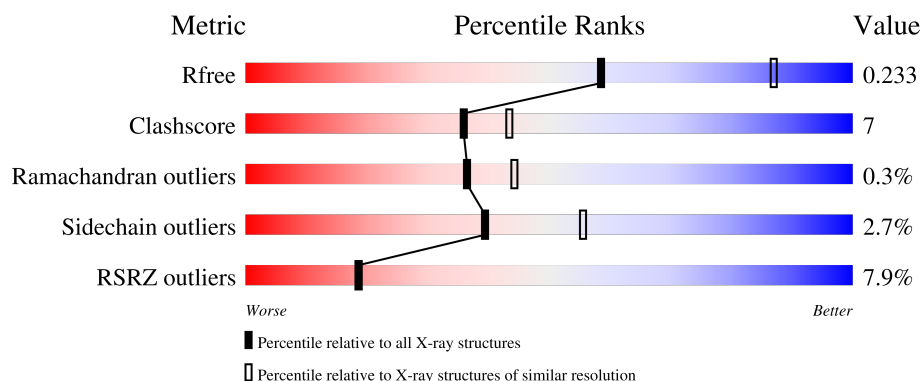
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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}	180053	1853 (2.58-2.54)
Clashscore	190562	1897 (2.58-2.54)
Ramachandran outliers	187476	1875 (2.58-2.54)
Sidechain outliers	187428	1875 (2.58-2.54)
RSRZ outliers	180081	1853 (2.58-2.54)

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	B	268	87% 10% .
1	D	268	12% 84% 14% .
2	A	302	9% 78% 20% .
2	C	302	8% 73% 23% ...

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9320 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 Cyclin-A2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	262	Total	C	N	O	S	0	0	0
			2110	1366	344	390	10			
1	B	262	Total	C	N	O	S	0	1	0
			2116	1369	345	391	11			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	171	GLY	-	expression tag	UNP P30274
D	433	HIS	-	expression tag	UNP P30274
D	434	HIS	-	expression tag	UNP P30274
D	435	HIS	-	expression tag	UNP P30274
D	436	HIS	-	expression tag	UNP P30274
D	437	HIS	-	expression tag	UNP P30274
D	438	HIS	-	expression tag	UNP P30274
B	171	GLY	-	expression tag	UNP P30274
B	433	HIS	-	expression tag	UNP P30274
B	434	HIS	-	expression tag	UNP P30274
B	435	HIS	-	expression tag	UNP P30274
B	436	HIS	-	expression tag	UNP P30274
B	437	HIS	-	expression tag	UNP P30274
B	438	HIS	-	expression tag	UNP P30274

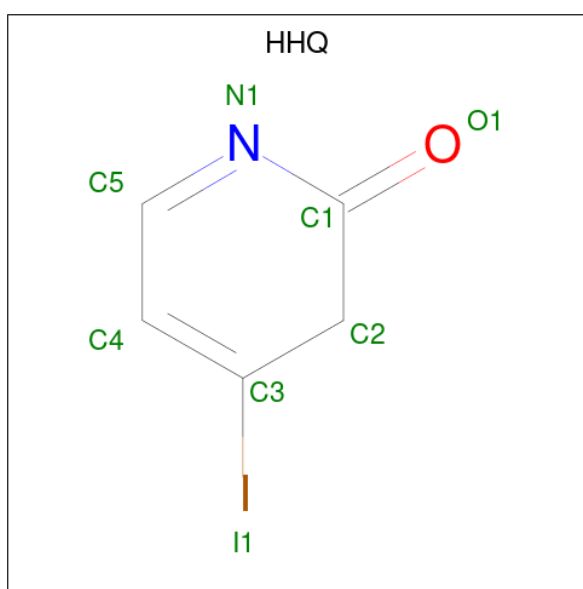
- Molecule 2 is a protein called Cyclin-dependent kinase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	302	Total	C	N	O	P S	0	2	0
			2443	1583	419	432	1 8			
2	C	297	Total	C	N	O	P S	0	0	0
			2388	1550	404	425	1 8			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP P24941
A	-2	PRO	-	expression tag	UNP P24941
A	-1	GLY	-	expression tag	UNP P24941
A	0	SER	-	expression tag	UNP P24941
C	-3	GLY	-	expression tag	UNP P24941
C	-2	PRO	-	expression tag	UNP P24941
C	-1	GLY	-	expression tag	UNP P24941
C	0	SER	-	expression tag	UNP P24941

- Molecule 3 is 4-iodanyl-3 {H}-pyridin-2-one (CCD ID: HHQ) (formula: C₅H₄INO) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	D	1	Total	C	I	N	O	0	0
			8	5	1	1	1		
3	A	1	Total	C	I	N	O	0	0
			8	5	1	1	1		
3	A	1	Total	C	I	N	O	0	0
			8	5	1	1	1		
3	A	1	Total	C	I	N	O	0	0
			8	5	1	1	1		
3	A	1	Total	C	I	N	O	0	0
			8	5	1	1	1		
3	B	1	Total	C	I	N	O	0	0
			8	5	1	1	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	I	N	O	0	0
			8	5	1	1	1		
3	C	1	Total	C	I	N	O	0	1
			16	10	2	2	2		
3	C	1	Total	C	I	N	O	0	0
			8	5	1	1	1		
3	C	1	Total	C	I	N	O	0	0
			8	5	1	1	1		

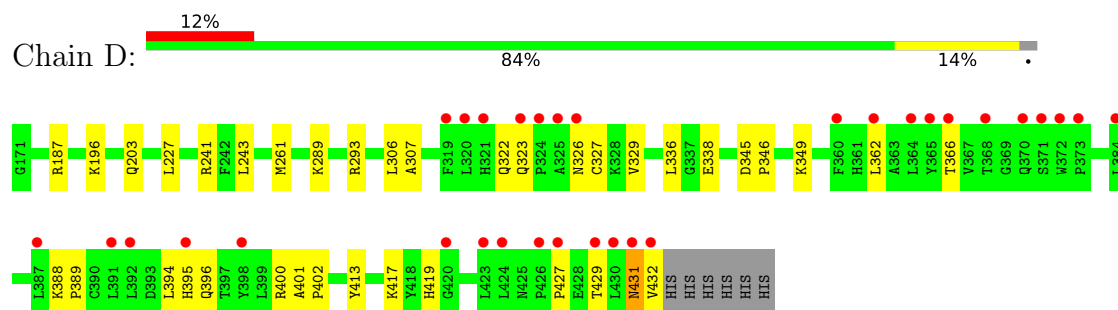
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	19	Total	O	0	0
			19	19		
4	A	68	Total	O	0	0
			68	68		
4	B	54	Total	O	0	0
			54	54		
4	C	26	Total	O	0	0
			26	26		

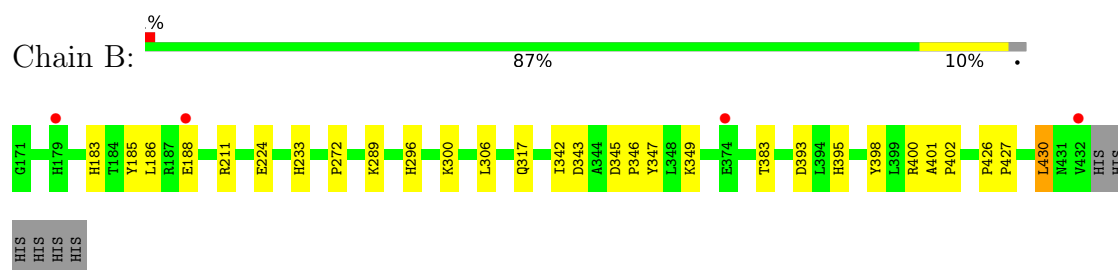
3 Residue-property plots

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.

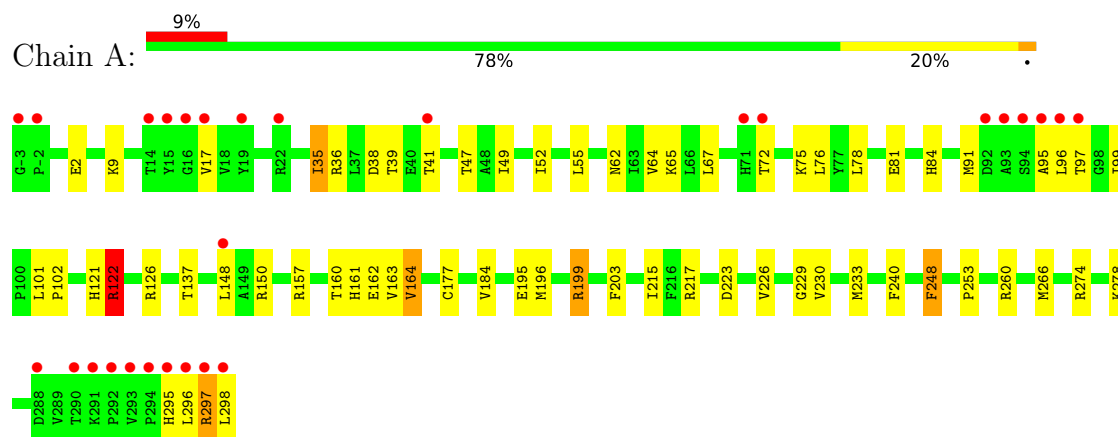
• Molecule 1: Cyclin-A2



• Molecule 1: Cyclin-A2

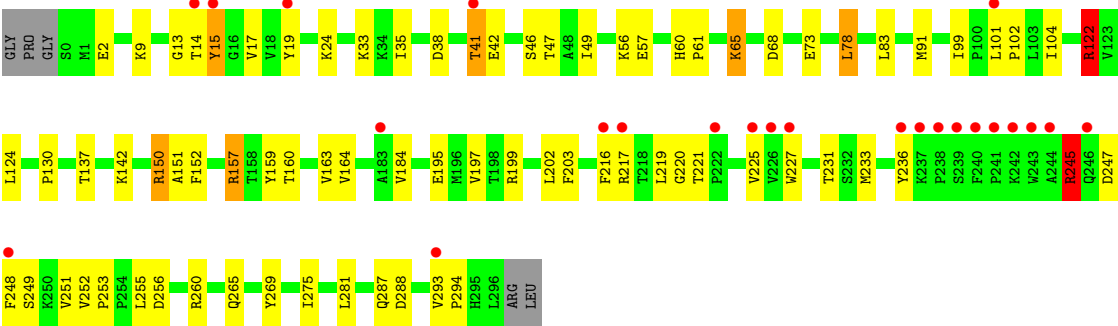


• Molecule 2: Cyclin-dependent kinase 2



• Molecule 2: Cyclin-dependent kinase 2





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	74.25Å 133.57Å 147.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	99.25 – 2.55 99.06 – 2.55	Depositor EDS
% Data completeness (in resolution range)	98.9 (99.25-2.55) 98.8 (99.06-2.55)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.81 (at 2.55Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.223 , 0.239 (Not available) , 0.233	Depositor DCC
R_{free} test set	2580 reflections (5.23%)	wwPDB-VP
Wilson B-factor (Å ²)	64.1	Xtriage
Anisotropy	0.114	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 42.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9320	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TPO, HHQ

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	B	0.76	2/2166 (0.1%)	1.16	5/2945 (0.2%)
1	D	0.59	0/2160	1.14	1/2937 (0.0%)
2	A	0.69	0/2495	1.22	9/3384 (0.3%)
2	C	0.63	0/2438	1.14	3/3308 (0.1%)
All	All	0.67	2/9259 (0.0%)	1.16	18/12574 (0.1%)

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	B	0	2
1	D	0	2
2	A	0	5
2	C	0	4
All	All	0	13

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	343	ASP	C-N	18.24	1.57	1.33
1	B	347	TYR	C-N	7.51	1.45	1.33

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	96	LEU	N-CA-C	-6.55	105.82	113.88
2	A	248	PHE	CA-CB-CG	-6.40	107.40	113.80
2	A	162	GLU	CB-CG-CD	6.39	123.46	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	97	THR	N-CA-C	-6.23	105.68	113.28
1	D	203	GLN	CB-CA-C	-5.91	105.12	110.44
2	C	68	ASP	CA-CB-CG	5.69	118.29	112.60
2	A	240	PHE	CB-CA-C	-5.65	100.86	109.50
1	B	224	GLU	CB-CG-CD	5.44	121.84	112.60
2	C	288	ASP	CA-CB-CG	5.35	117.95	112.60
2	A	62	ASN	CB-CA-C	5.20	119.50	110.72
1	B	393	ASP	CA-CB-CG	5.17	117.77	112.60
1	B	272	PRO	N-CA-C	-5.16	105.06	110.58
1	B	383	THR	CA-CB-OG1	-5.12	101.92	109.60
2	A	253	PRO	N-CA-C	5.12	116.94	110.70
2	A	278	LYS	CB-CA-C	5.08	118.85	110.88
1	B	430	LEU	N-CA-CB	-5.08	104.28	110.98
2	A	41	THR	N-CA-C	-5.01	107.21	113.38
2	C	65	LYS	N-CA-CB	5.01	118.43	110.16

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	122	ARG	Sidechain
2	A	150	ARG	Sidechain
2	A	199	ARG	Sidechain
2	A	217	ARG	Sidechain
2	A	297	ARG	Sidechain
1	B	211	ARG	Sidechain
1	B	400	ARG	Sidechain
2	C	122	ARG	Sidechain
2	C	150	ARG	Sidechain
2	C	217	ARG	Sidechain
2	C	245	ARG	Sidechain
1	D	187	ARG	Sidechain
1	D	241	ARG	Sidechain

5.2 Too-close contacts ⓘ

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	B	2116	0	2132	17	0
1	D	2110	0	2128	21	0
2	A	2443	0	2485	46	0
2	C	2388	0	2430	54	0
3	A	40	0	0	2	0
3	B	16	0	0	0	0
3	C	32	0	0	3	0
3	D	8	0	0	0	0
4	A	68	0	0	1	0
4	B	54	0	0	2	0
4	C	26	0	0	1	0
4	D	19	0	0	0	0
All	All	9320	0	9175	133	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 7.

All (133) 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:197:VAL:HG11	2:C:252:VAL:CG1	1.83	1.08
2:C:197:VAL:HG11	2:C:252:VAL:HG13	1.39	1.03
2:A:91:MET:HE1	2:A:195:GLU:HG2	1.49	0.92
1:B:300:LYS:HE3	4:B:651:HOH:O	1.72	0.90
2:A:126:ARG:O	2:A:148:LEU:HD23	1.72	0.89
2:C:252:VAL:HG12	2:C:255:LEU:HB2	1.55	0.88
2:C:197:VAL:CG1	2:C:252:VAL:HG13	2.04	0.86
1:B:185:TYR:O	1:B:188:GLU:HG2	1.75	0.86
2:A:36:ARG:NH2	2:A:75:LYS:HE2	2.02	0.74
1:B:185:TYR:HD1	1:B:188:GLU:OE2	1.71	0.74
2:A:161:HIS:HD2	4:A:465:HOH:O	1.69	0.73
2:C:252:VAL:CG1	2:C:255:LEU:HB2	2.19	0.72
2:A:81:GLU:O	3:A:303:HHQ:I1	2.78	0.71
2:C:248:PHE:HA	2:C:251:VAL:HB	1.74	0.69
2:A:126:ARG:O	2:A:148:LEU:CD2	2.41	0.69
2:A:177:CYS:SG	2:A:233:MET:SD	2.93	0.66
2:A:36:ARG:CZ	2:A:75:LYS:HE2	2.26	0.66
2:C:38:ASP:HB3	2:C:41:THR:HG23	1.78	0.65
2:C:56:LYS:HD2	3:C:303:HHQ:C4	2.26	0.65
1:D:306:LEU:HD12	2:C:49:ILE:HG23	1.80	0.63
2:C:245:ARG:HD2	2:C:248:PHE:HE1	1.63	0.62
2:C:137:THR:O	2:C:293:VAL:HG13	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:60:HIS:CG	2:C:61:PRO:HD2	2.37	0.59
2:C:293:VAL:HG13	2:C:294:PRO:HD2	1.83	0.59
2:C:256:ASP:O	2:C:260:ARG:HG3	2.03	0.58
2:C:83:LEU:HD11	2:C:142:LYS:HD2	1.84	0.58
1:B:233:HIS:HD2	4:B:634:HOH:O	1.86	0.58
2:A:52:ILE:HD11	2:A:78:LEU:HD21	1.86	0.57
1:D:336:LEU:HD13	1:D:362:LEU:HD23	1.87	0.57
1:B:346:PRO:O	1:B:349:LYS:HG2	2.04	0.57
2:C:19:TYR:CD1	3:C:302:HHQ:I1	3.28	0.56
2:C:101:LEU:HB3	2:C:102:PRO:HD3	1.86	0.56
1:B:185:TYR:HA	1:B:188:GLU:OE2	2.07	0.55
2:C:293:VAL:CG1	2:C:294:PRO:HD2	2.37	0.55
2:A:36:ARG:NH2	2:A:75:LYS:CE	2.71	0.54
2:A:65:LYS:HG2	2:A:67:LEU:HD23	1.89	0.54
2:A:65:LYS:H	2:A:81:GLU:HG2	1.72	0.54
2:C:265:GLN:NE2	2:C:275:ILE:HD12	2.23	0.53
1:D:243:LEU:O	2:A:298:LEU:HD13	2.08	0.53
2:A:148:LEU:O	2:A:148:LEU:HG	2.08	0.53
1:B:395:HIS:HE1	1:B:427:PRO:O	1.90	0.53
2:A:266:MET:O	2:A:274:ARG:HD3	2.09	0.53
2:C:2:GLU:O	2:C:24:LYS:HE3	2.09	0.53
2:A:91:MET:HE3	2:A:196:MET:HA	1.90	0.52
2:A:36:ARG:HH22	2:A:75:LYS:CE	2.23	0.52
2:A:52:ILE:CD1	2:A:78:LEU:HD21	2.40	0.52
1:D:346:PRO:O	1:D:349:LYS:HG2	2.10	0.51
2:C:15:TYR:CB	2:C:35:ILE:HG12	2.40	0.51
1:D:326:ASN:HB3	1:D:329:VAL:HB	1.92	0.51
1:D:227:LEU:HD12	1:D:261:MET:HE3	1.92	0.51
2:A:91:MET:HG2	2:A:99:ILE:HD11	1.93	0.51
2:C:219:LEU:HA	2:C:245:ARG:HD3	1.93	0.50
2:A:38:ASP:OD1	2:A:39:THR:N	2.44	0.50
1:B:401:ALA:HB3	1:B:402:PRO:HD3	1.94	0.49
2:C:195:GLU:O	2:C:199:ARG:N	2.42	0.49
2:C:122:ARG:O	2:C:151:ALA:HA	2.12	0.49
2:A:296:LEU:C	2:A:296:LEU:HD12	2.38	0.49
1:B:185:TYR:O	1:B:188:GLU:CG	2.55	0.49
2:C:15:TYR:CD1	2:C:33:LYS:HD3	2.47	0.49
2:A:52:ILE:HG12	2:A:78:LEU:HD21	1.96	0.48
2:A:122:ARG:HD3	1:B:186:LEU:HD21	1.95	0.48
3:C:301[A]:HHQ:C2	4:C:403:HOH:O	2.61	0.48
1:D:395:HIS:CE1	1:D:427:PRO:HG2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:101:LEU:HB3	2:A:102:PRO:HD3	1.96	0.48
1:D:396:GLN:HE22	1:D:400:ARG:CZ	2.26	0.47
2:A:2:GLU:HG3	2:C:73:GLU:OE1	2.14	0.47
1:D:366:THR:HG23	1:D:427:PRO:HD3	1.96	0.47
2:C:163:VAL:HG23	2:C:164:VAL:H	1.80	0.47
1:B:185:TYR:CD1	1:B:188:GLU:OE2	2.60	0.47
2:C:15:TYR:HE2	2:C:47:THR:HB	1.80	0.47
2:A:203:PHE:CD2	2:A:215:ILE:HG12	2.50	0.46
2:C:124:LEU:HG	2:C:152:PHE:CD1	2.50	0.46
1:D:289:LYS:HE2	1:D:293:ARG:NH1	2.30	0.46
2:A:148:LEU:HD11	2:A:163:VAL:HG12	1.98	0.46
2:C:91:MET:CE	2:C:130:PRO:HB3	2.46	0.46
1:D:289:LYS:CE	1:D:293:ARG:NH1	2.79	0.45
2:A:52:ILE:HG12	2:A:78:LEU:CD2	2.46	0.45
1:B:183:HIS:HB2	1:B:317:GLN:HE22	1.82	0.45
1:D:322:GLN:O	1:D:323:GLN:C	2.59	0.45
1:D:327:CYS:HB3	1:D:419:HIS:NE2	2.32	0.45
2:C:157:ARG:HG3	2:C:159:TYR:CE1	2.51	0.45
1:D:388:LYS:O	1:D:389:PRO:C	2.59	0.45
2:A:36:ARG:NH1	2:A:75:LYS:HE2	2.31	0.45
2:A:223:ASP:H	2:A:226:VAL:HG12	1.82	0.45
2:C:252:VAL:O	2:C:253:PRO:C	2.60	0.45
2:A:248:PHE:HB3	2:A:260:ARG:HD2	1.99	0.45
2:A:148:LEU:HD21	2:A:164:VAL:H	1.82	0.45
2:A:52:ILE:CG1	2:A:78:LEU:HD21	2.47	0.44
1:B:185:TYR:C	1:B:188:GLU:HG2	2.39	0.44
2:C:41:THR:OG1	2:C:42:GLU:N	2.50	0.44
2:C:265:GLN:HE21	2:C:275:ILE:HD12	1.82	0.44
2:A:297:ARG:HA	2:A:297:ARG:HD2	1.56	0.44
1:D:196:LYS:HD2	1:D:196:LYS:HA	1.78	0.44
1:D:307:ALA:HB3	2:C:57:GLU:OE2	2.18	0.44
2:A:229:GLY:O	2:A:230:VAL:C	2.60	0.44
2:C:150:ARG:HD3	2:C:159:TYR:CD1	2.53	0.44
2:C:227:TRP:CE3	2:C:269:TYR:HB3	2.52	0.44
2:C:91:MET:HE1	2:C:130:PRO:CB	2.48	0.44
2:A:91:MET:CE	2:A:195:GLU:O	2.66	0.43
2:C:13:GLY:O	2:C:14:THR:C	2.60	0.43
2:A:84[B]:HIS:N	2:A:84[B]:HIS:ND1	2.65	0.43
1:D:401:ALA:HB3	1:D:402:PRO:HD3	2.00	0.43
2:C:91:MET:HE1	2:C:130:PRO:CG	2.49	0.43
2:C:252:VAL:HG11	2:C:255:LEU:HD22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:99:ILE:HG22	2:C:104:ILE:HG13	2.00	0.43
2:A:296:LEU:HD12	2:A:297:ARG:O	2.19	0.42
2:C:202:LEU:HD23	2:C:203:PHE:CE2	2.54	0.42
2:A:35:ILE:HB	2:A:76:LEU:HB3	2.02	0.42
2:C:247:ASP:C	2:C:249:SER:N	2.78	0.42
2:C:231:THR:HA	2:C:236:TYR:CD1	2.54	0.42
1:B:289:LYS:HE2	1:B:289:LYS:HB3	1.81	0.42
2:C:247:ASP:O	2:C:251:VAL:HG23	2.20	0.42
1:D:338:GLU:OE2	1:D:413:TYR:OH	2.36	0.41
2:A:64:VAL:HG21	3:A:303:HHQ:C2	2.50	0.41
2:A:55:LEU:HD23	2:A:55:LEU:HA	1.90	0.41
2:C:91:MET:HE2	2:C:130:PRO:HB3	2.02	0.41
2:A:49:ILE:HG23	1:B:306:LEU:HD12	2.02	0.41
2:A:72:THR:OG1	2:A:75:LYS:O	2.33	0.41
2:C:78:LEU:HD23	2:C:78:LEU:N	2.36	0.41
2:C:197:VAL:HG11	2:C:252:VAL:HG11	1.91	0.41
2:C:216:PHE:O	2:C:220:GLY:N	2.50	0.41
1:D:345:ASP:HA	1:D:346:PRO:HA	1.82	0.41
2:A:36:ARG:HH22	2:A:75:LYS:HE2	1.78	0.41
2:C:60:HIS:CG	2:C:61:PRO:CD	3.04	0.41
2:C:220:GLY:O	2:C:221:THR:C	2.63	0.41
1:D:388:LYS:HB3	1:D:389:PRO:HD3	2.03	0.41
2:A:121:HIS:C	2:A:122:ARG:HG3	2.46	0.41
1:B:345:ASP:HA	1:B:346:PRO:HA	1.81	0.41
2:C:281:LEU:HD23	2:C:281:LEU:HA	1.95	0.41
1:D:394:LEU:HD12	1:D:394:LEU:HA	1.83	0.40
2:A:9:LYS:HE3	2:A:17:VAL:HG13	2.03	0.40
2:C:9:LYS:HG3	2:C:17:VAL:CG1	2.51	0.40
1:B:398:TYR:CD2	1:B:426:PRO:HB3	2.56	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	B	261/268 (97%)	258 (99%)	3 (1%)	0	100	100
1	D	260/268 (97%)	252 (97%)	7 (3%)	1 (0%)	30	39
2	A	301/302 (100%)	291 (97%)	8 (3%)	2 (1%)	18	25
2	C	294/302 (97%)	280 (95%)	14 (5%)	0	100	100
All	All	1116/1140 (98%)	1081 (97%)	32 (3%)	3 (0%)	36	44

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	95	ALA
2	A	164	VAL
1	D	431	ASN

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	B	235/240 (98%)	232 (99%)	3 (1%)	61	74
1	D	234/240 (98%)	230 (98%)	4 (2%)	53	68
2	A	266/264 (101%)	258 (97%)	8 (3%)	36	51
2	C	261/264 (99%)	249 (95%)	12 (5%)	24	35
All	All	996/1008 (99%)	969 (97%)	27 (3%)	39	55

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	417	LYS
1	D	429	THR
1	D	431	ASN
1	D	432	VAL
2	A	35	ILE
2	A	47	THR
2	A	122	ARG
2	A	137	THR

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Mol	Chain	Res	Type
2	A	157	ARG
2	A	184	VAL
2	A	199	ARG
2	A	295	HIS
1	B	296	HIS
1	B	342	ILE
1	B	430	LEU
2	C	15	TYR
2	C	41	THR
2	C	46	SER
2	C	65	LYS
2	C	78	LEU
2	C	122	ARG
2	C	157	ARG
2	C	184	VAL
2	C	225	VAL
2	C	233	MET
2	C	245	ARG
2	C	287	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	179	HIS
1	D	395	HIS
1	D	396	GLN
1	D	406	GLN
1	D	415	ASN
1	D	431	ASN
2	A	85	GLN
2	A	211	GLN
2	A	246	GLN
1	B	183	HIS
1	B	254	GLN
1	B	317	GLN
1	B	378	GLN
1	B	395	HIS
1	B	419	HIS
2	C	59	ASN
2	C	74	ASN
2	C	265	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	TPO	C	160	2	8,10,11	0.76	0	10,14,16	1.25	2 (20%)
2	TPO	A	160	2	8,10,11	0.95	1 (12%)	10,14,16	1.00	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	TPO	C	160	2	-	1/9/11/13	-
2	TPO	A	160	2	-	1/9/11/13	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	160	TPO	P-OG1	2.32	1.63	1.59

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	160	TPO	P-OG1-CB	-2.57	116.33	123.33
2	C	160	TPO	O-C-CA	-2.08	119.42	124.77

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	160	TPO	O-C-CA-CB
2	C	160	TPO	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

12 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
3	HHQ	A	305	-	6,8,8	1.66	1 (16%)	2,10,10	3.14	1 (50%)
3	HHQ	A	303	-	6,8,8	1.35	1 (16%)	2,10,10	4.01	1 (50%)
3	HHQ	A	304	-	6,8,8	1.23	0	2,10,10	4.26	1 (50%)
3	HHQ	A	302	-	6,8,8	1.34	1 (16%)	2,10,10	3.66	1 (50%)
3	HHQ	D	501	-	6,8,8	1.47	1 (16%)	2,10,10	3.97	1 (50%)
3	HHQ	B	501	-	6,8,8	1.48	1 (16%)	2,10,10	4.07	1 (50%)
3	HHQ	B	502	-	6,8,8	1.39	1 (16%)	2,10,10	3.09	1 (50%)
3	HHQ	C	301[B]	-	6,8,8	1.15	0	2,10,10	4.24	1 (50%)
3	HHQ	C	301[A]	-	6,8,8	1.79	1 (16%)	2,10,10	2.83	1 (50%)
3	HHQ	C	303	-	6,8,8	1.81	1 (16%)	2,10,10	4.31	1 (50%)
3	HHQ	A	301	-	6,8,8	1.51	1 (16%)	2,10,10	3.30	1 (50%)
3	HHQ	C	302	-	6,8,8	1.46	1 (16%)	2,10,10	3.79	1 (50%)

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
3	HHQ	A	305	-	-	-	0/1/1/1
3	HHQ	A	303	-	-	-	0/1/1/1
3	HHQ	A	304	-	-	-	0/1/1/1
3	HHQ	A	302	-	-	-	0/1/1/1
3	HHQ	D	501	-	-	-	0/1/1/1
3	HHQ	B	501	-	-	-	0/1/1/1
3	HHQ	B	502	-	-	-	0/1/1/1
3	HHQ	C	301[B]	-	-	-	0/1/1/1
3	HHQ	C	301[A]	-	-	-	0/1/1/1
3	HHQ	C	303	-	-	-	0/1/1/1
3	HHQ	A	301	-	-	-	0/1/1/1
3	HHQ	C	302	-	-	-	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	301[A]	HHQ	O1-C1	3.38	1.26	1.22
3	C	303	HHQ	O1-C1	3.31	1.26	1.22
3	A	305	HHQ	O1-C1	2.97	1.26	1.22
3	A	301	HHQ	O1-C1	2.89	1.26	1.22
3	B	502	HHQ	O1-C1	2.64	1.25	1.22
3	D	501	HHQ	O1-C1	2.61	1.25	1.22
3	B	501	HHQ	O1-C1	2.57	1.25	1.22
3	C	302	HHQ	O1-C1	2.52	1.25	1.22
3	A	303	HHQ	C4-C5	-2.26	1.34	1.39
3	A	302	HHQ	O1-C1	2.07	1.25	1.22

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	303	HHQ	C4-C5-N1	-6.09	119.93	124.75
3	A	304	HHQ	C4-C5-N1	-6.02	119.99	124.75
3	C	301[B]	HHQ	C4-C5-N1	-5.96	120.03	124.75
3	B	501	HHQ	C4-C5-N1	-5.75	120.20	124.75
3	A	303	HHQ	C4-C5-N1	-5.68	120.26	124.75
3	D	501	HHQ	C4-C5-N1	-5.59	120.33	124.75
3	C	302	HHQ	C4-C5-N1	-5.34	120.52	124.75
3	A	302	HHQ	C4-C5-N1	-5.12	120.70	124.75
3	A	301	HHQ	C4-C5-N1	-4.64	121.08	124.75
3	A	305	HHQ	C4-C5-N1	-4.44	121.23	124.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	502	HHQ	C4-C5-N1	-4.34	121.32	124.75
3	C	301[A]	HHQ	C4-C5-N1	-3.94	121.64	124.75

There are no chirality outliers.

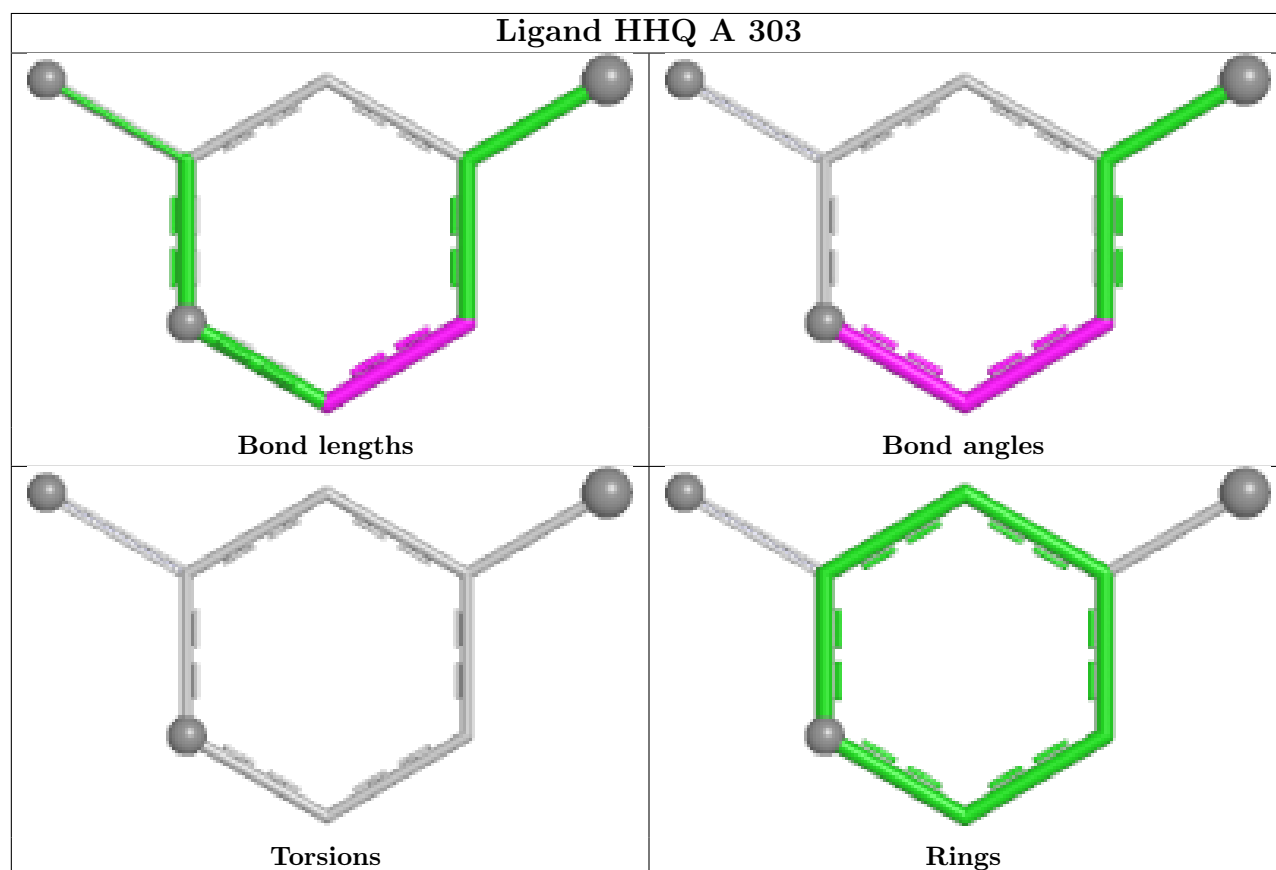
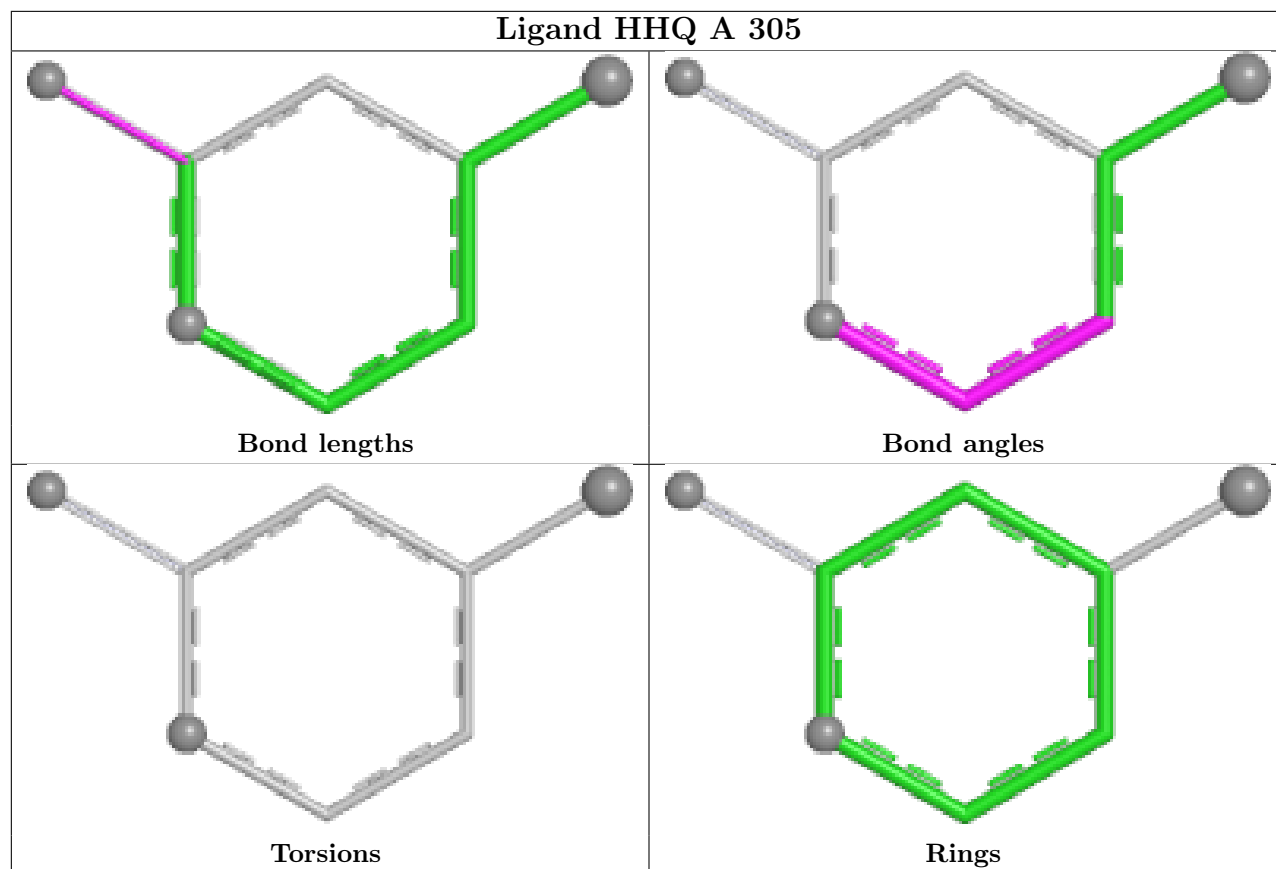
There are no torsion outliers.

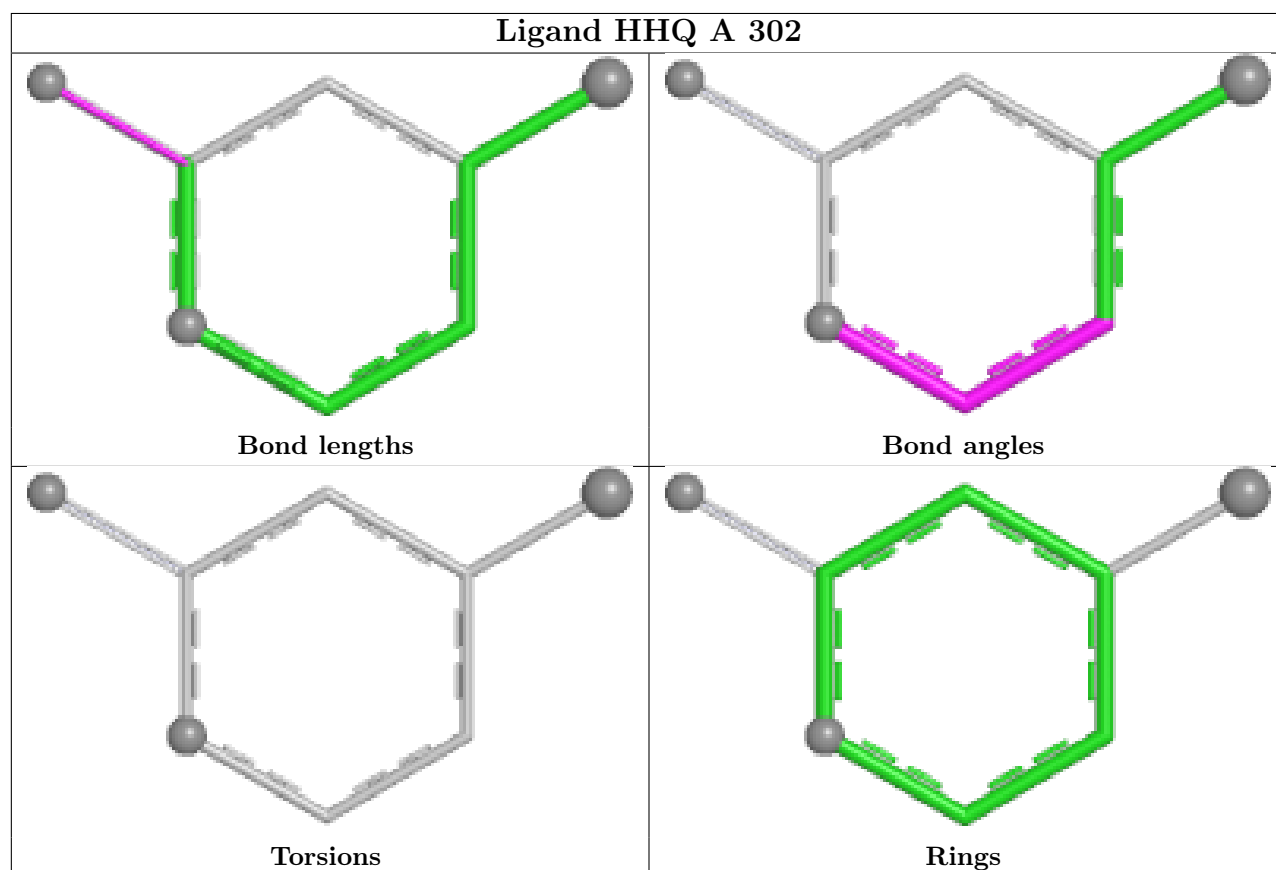
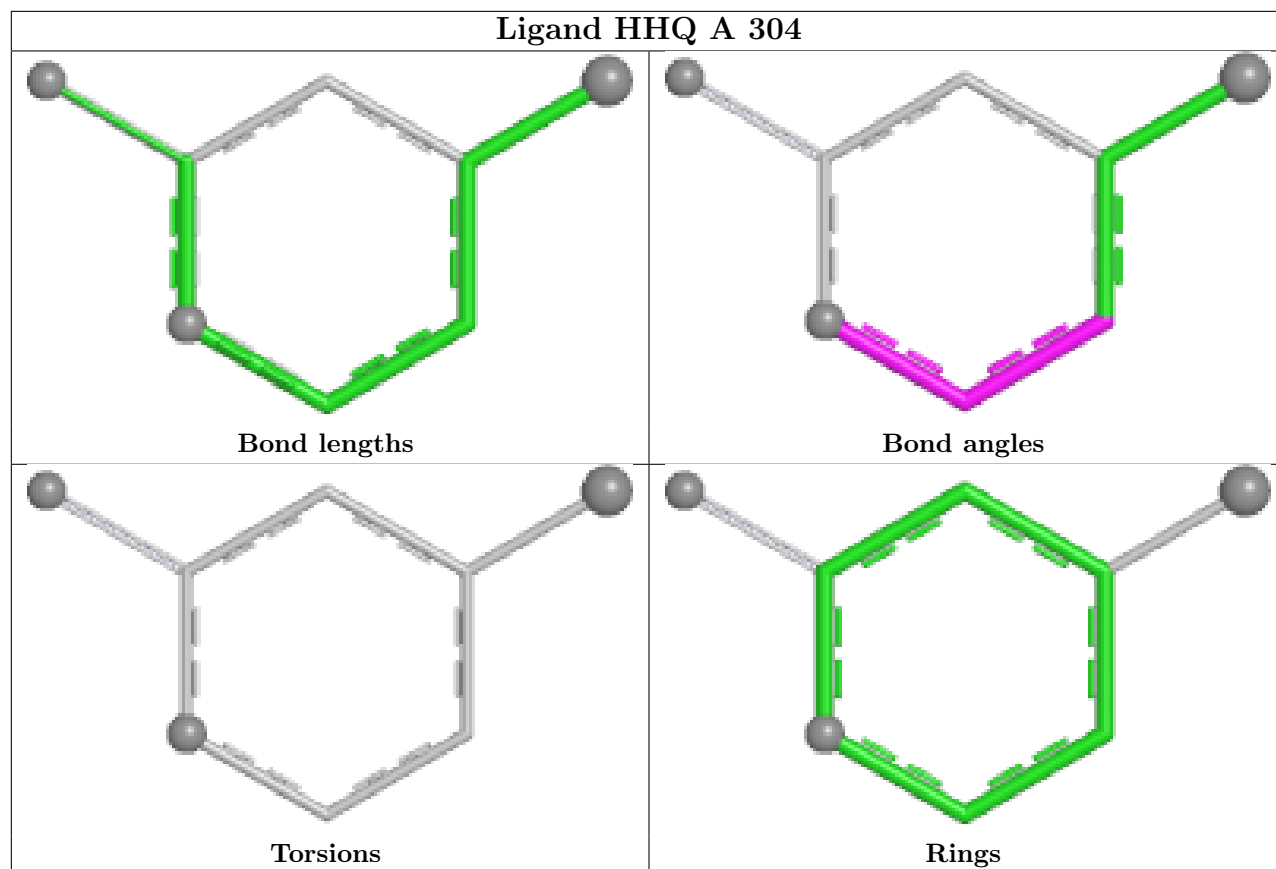
There are no ring outliers.

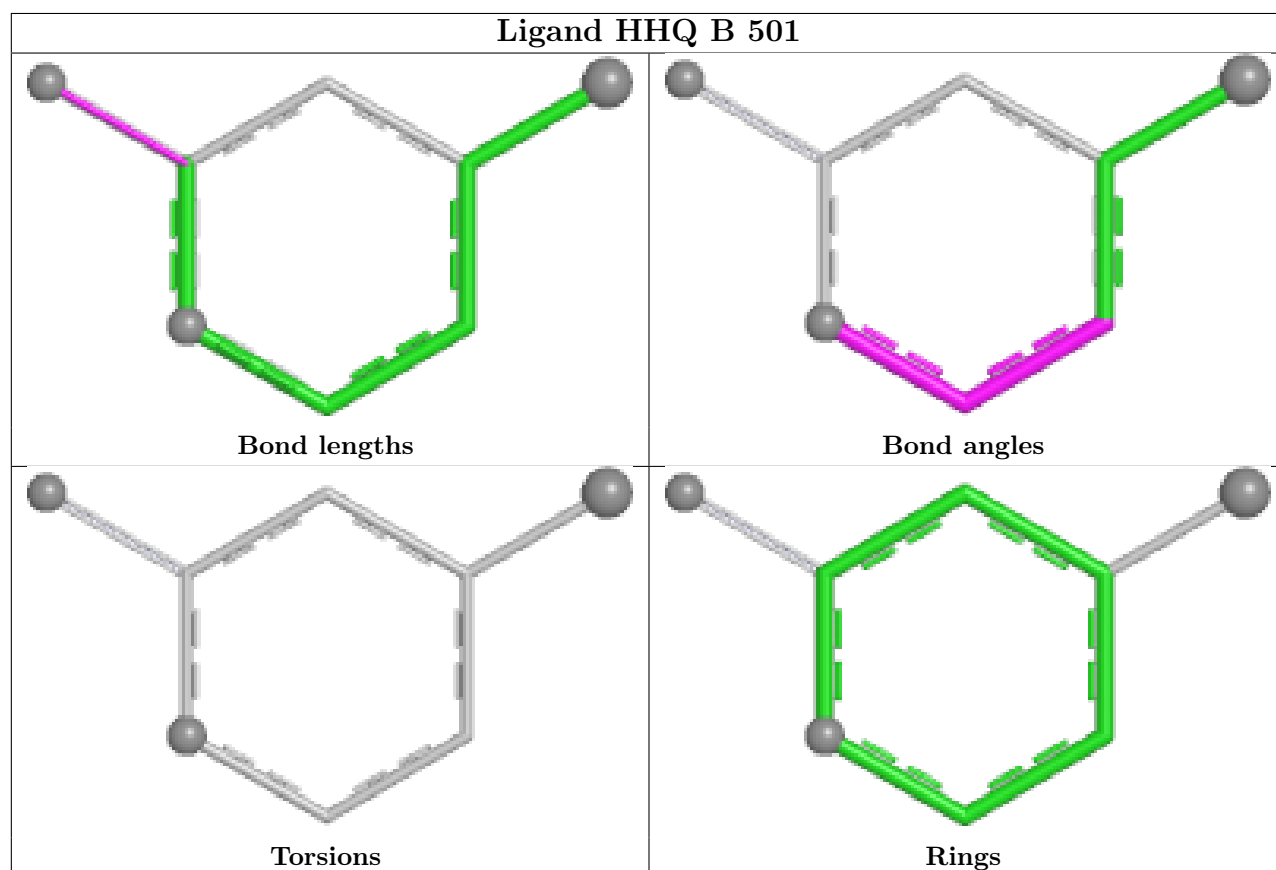
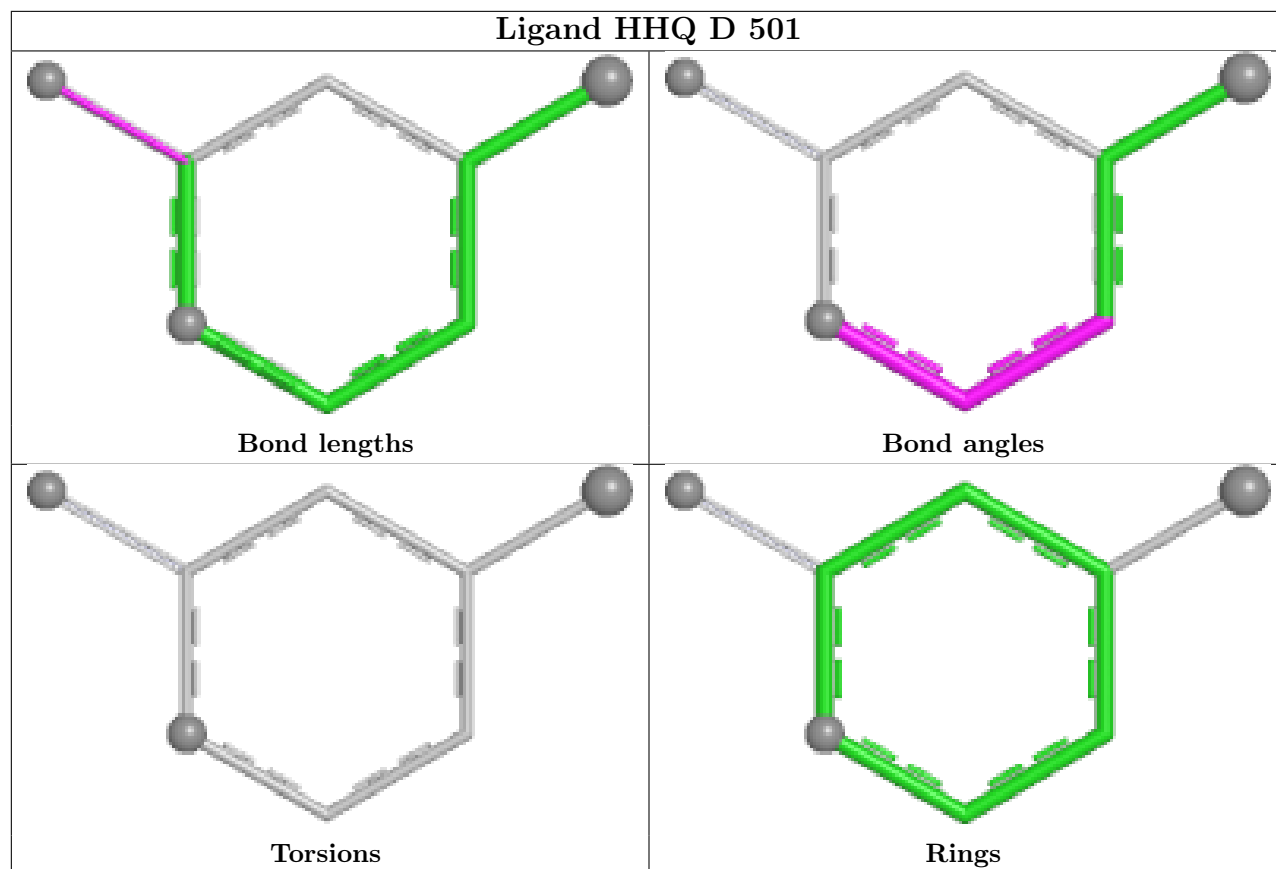
4 monomers are involved in 5 short contacts:

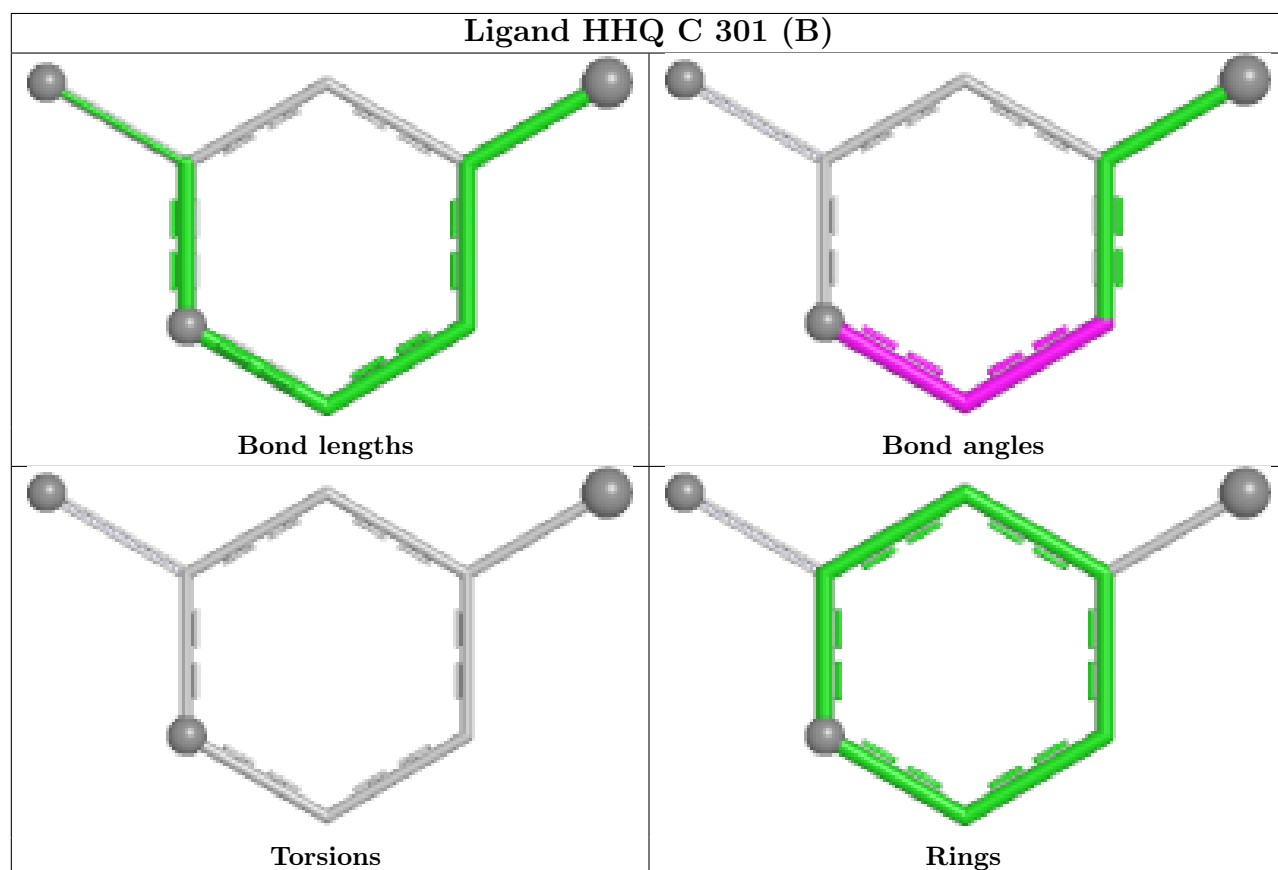
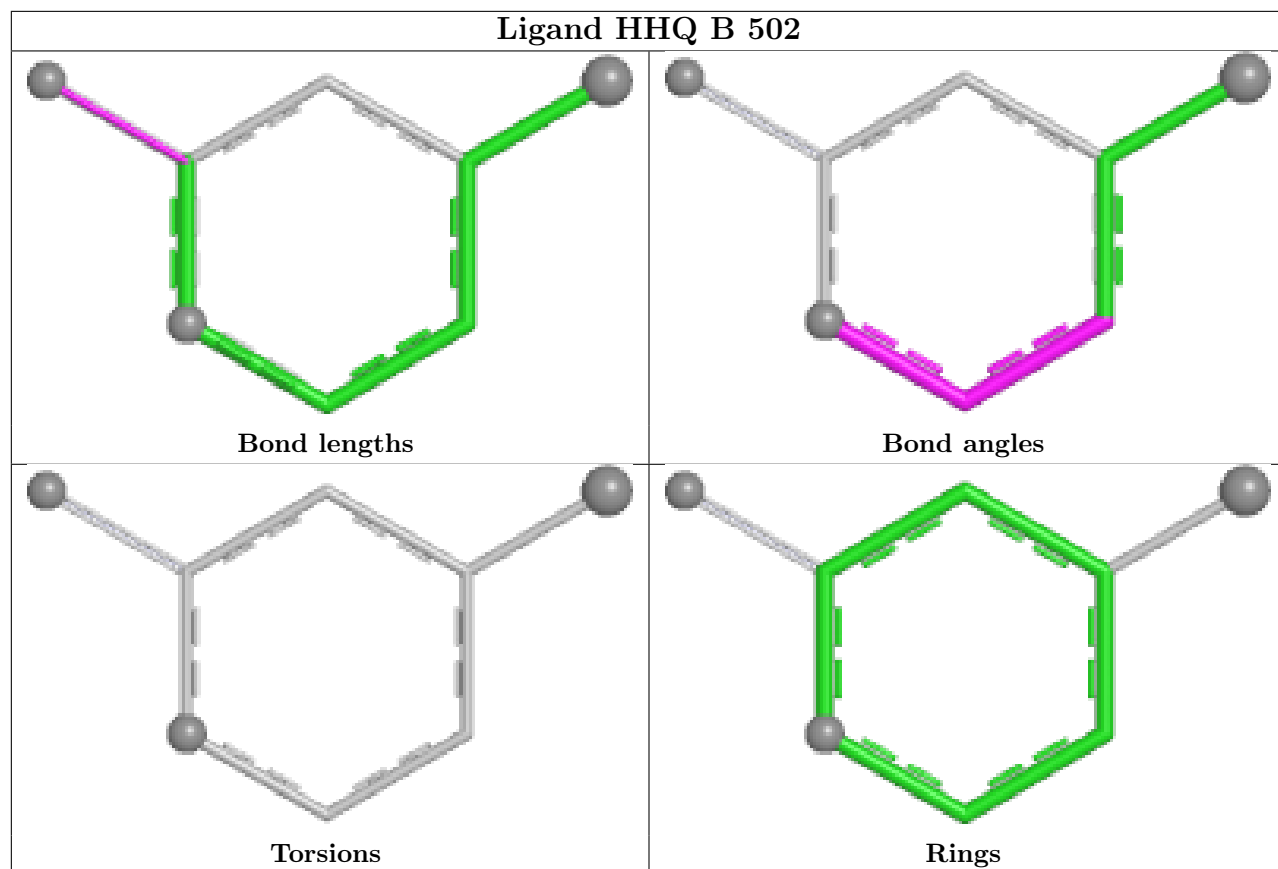
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	303	HHQ	2	0
3	C	301[A]	HHQ	1	0
3	C	303	HHQ	1	0
3	C	302	HHQ	1	0

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.

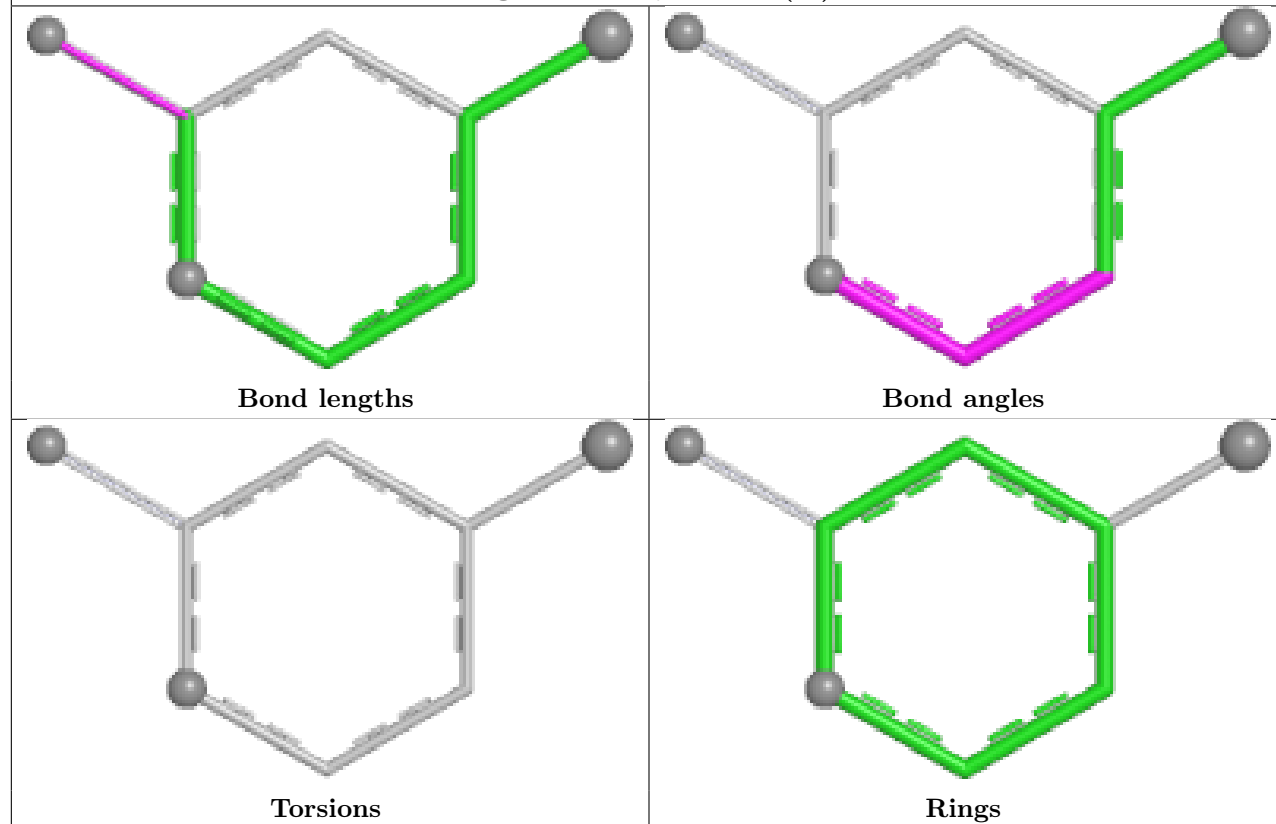




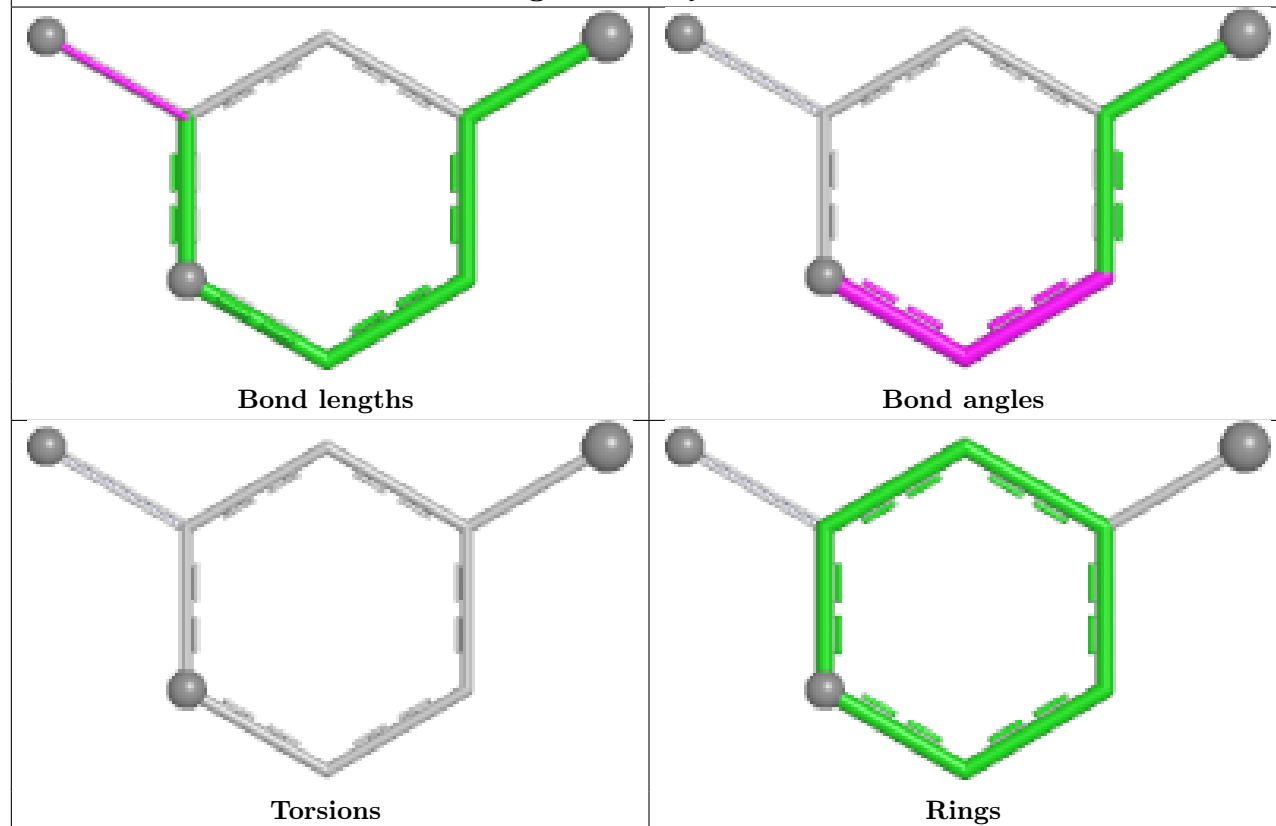


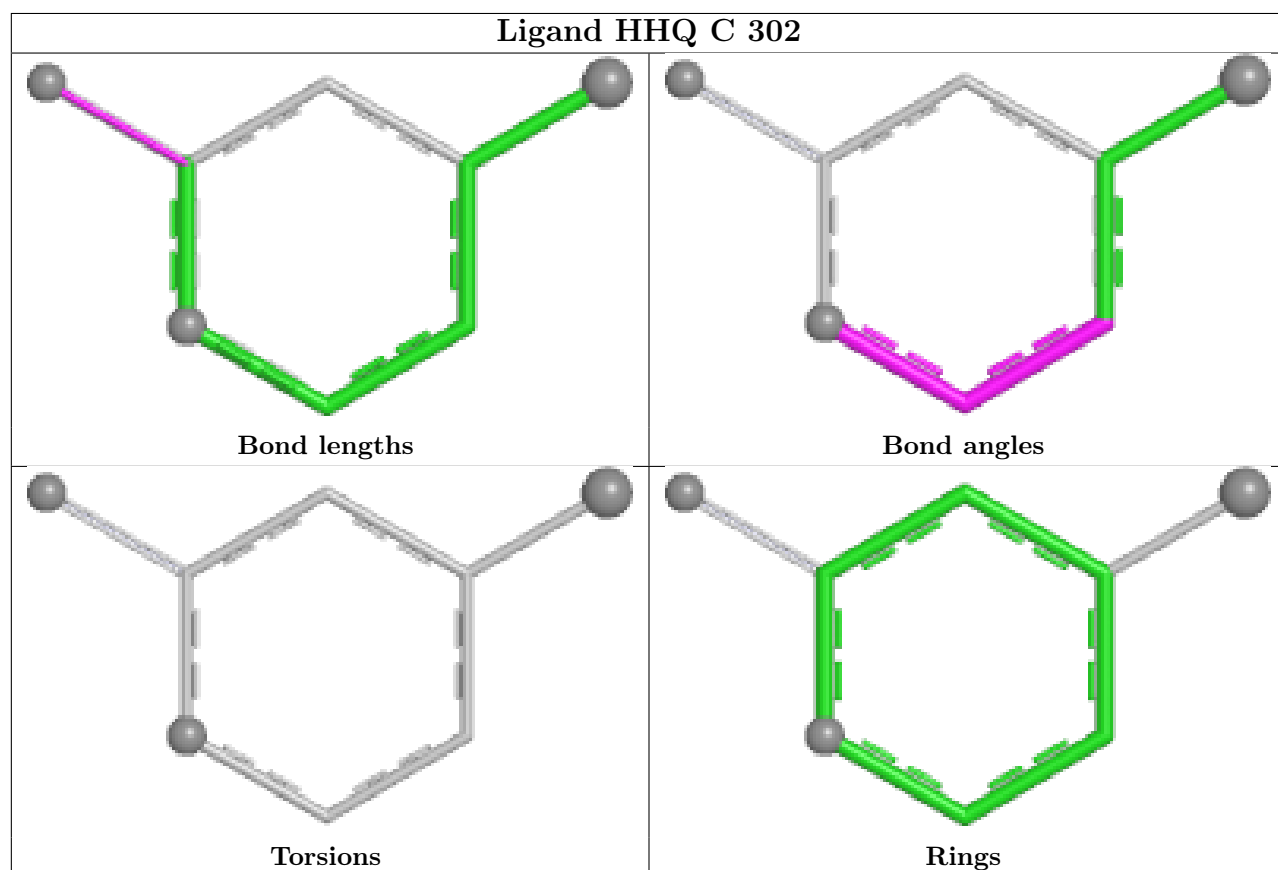
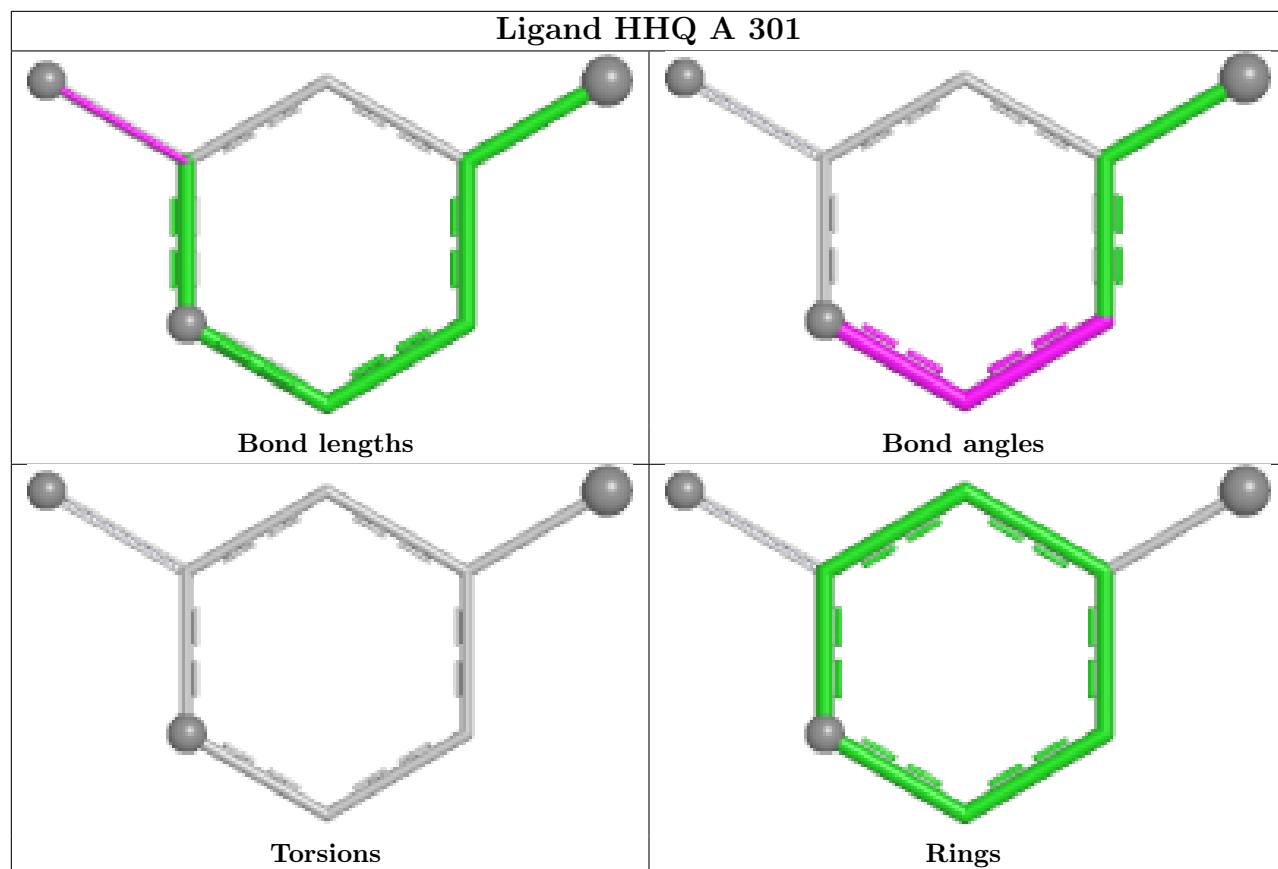


Ligand HHQ C 301 (A)



Ligand HHQ C 303





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	B	262/268 (97%)	-0.06	4 (1%) 72 73	28, 51, 77, 117	1 (0%)
1	D	262/268 (97%)	0.65	32 (12%) 8 8	39, 71, 120, 156	0
2	A	301/302 (99%)	0.26	28 (9%) 14 14	27, 48, 103, 149	2 (0%)
2	C	296/302 (98%)	0.55	24 (8%) 18 18	44, 67, 130, 148	0
All	All	1121/1140 (98%)	0.35	88 (7%) 18 18	27, 58, 120, 156	3 (0%)

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	291	LYS	5.7
2	A	296	LEU	5.2
2	A	93	ALA	5.2
1	D	432	VAL	4.8
2	C	244	ALA	4.6
2	C	241	PRO	4.6
2	A	96	LEU	4.5
1	D	384	LEU	4.4
2	C	243	TRP	4.4
2	A	294	PRO	4.3
2	A	298	LEU	4.3
2	A	72	THR	4.1
1	D	429	THR	4.0
2	A	292	PRO	4.0
2	A	94	SER	4.0
2	A	-2	PRO	4.0
2	C	222	PRO	3.8
2	C	217	ARG	3.7
2	C	238	PRO	3.7
1	D	391	LEU	3.6
1	D	324	PRO	3.6

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Mol	Chain	Res	Type	RSRZ
2	A	290	THR	3.6
2	A	97	THR	3.4
1	D	430	LEU	3.4
1	B	432	VAL	3.4
2	A	15	TYR	3.3
1	D	423	LEU	3.3
2	C	41	THR	3.2
1	D	424	LEU	3.2
2	A	92	ASP	3.2
1	D	387	LEU	3.2
2	A	295	HIS	3.2
2	A	95	ALA	3.1
2	C	226	VAL	3.1
1	D	392	LEU	3.0
2	C	227	TRP	3.0
2	C	242	LYS	3.0
2	C	246	GLN	3.0
2	A	293	VAL	3.0
2	C	293	VAL	3.0
1	B	188	GLU	2.9
2	C	225	VAL	2.9
2	C	14	THR	2.9
2	C	216	PHE	2.9
1	B	179	HIS	2.8
1	D	364	LEU	2.8
1	D	372	TRP	2.8
1	D	398	TYR	2.8
2	C	237	LYS	2.8
2	C	239	SER	2.7
2	C	101	LEU	2.7
2	A	297	ARG	2.6
2	A	17	VAL	2.6
2	A	148	LEU	2.6
1	D	373	PRO	2.5
1	D	323	GLN	2.5
1	D	319	PHE	2.5
1	D	431	ASN	2.5
1	B	374	GLU	2.4
1	D	320	LEU	2.4
1	D	426	PRO	2.4
2	A	-3	GLY	2.4
1	D	370	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	395	HIS	2.4
1	D	371	SER	2.4
1	D	360	PHE	2.4
2	A	14	THR	2.4
2	C	236	TYR	2.3
2	C	19	TYR	2.3
1	D	427	PRO	2.3
2	A	288	ASP	2.3
2	C	248	PHE	2.3
1	D	366	THR	2.2
2	C	240	PHE	2.2
2	A	22[A]	ARG	2.2
1	D	420	GLY	2.2
1	D	325	ALA	2.2
1	D	326	ASN	2.2
2	A	19	TYR	2.2
1	D	321	HIS	2.1
2	A	71	HIS	2.1
1	D	362	LEU	2.1
2	A	41	THR	2.1
1	D	368	THR	2.1
2	A	16	GLY	2.1
2	C	15	TYR	2.1
2	C	183	ALA	2.0
1	D	365	TYR	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	TPO	A	160	11/12	0.97	0.06	38,44,46,47	0
2	TPO	C	160	11/12	0.98	0.06	48,55,65,67	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands

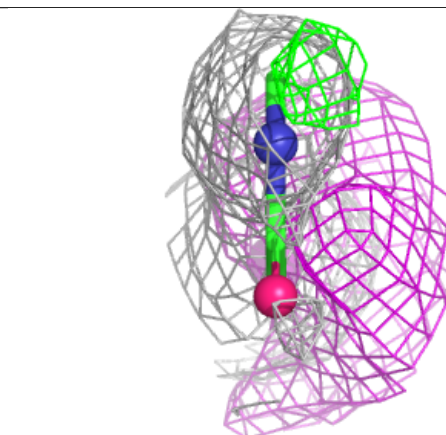
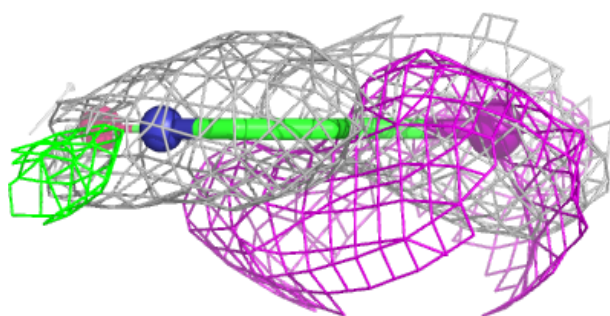
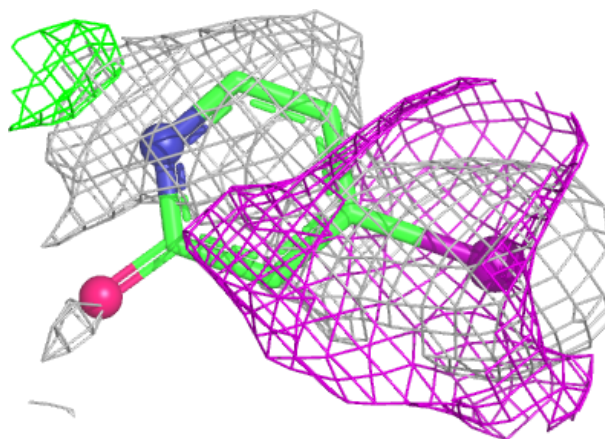
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	HHQ	C	303	8/8	0.80	0.22	89,108,120,146	0
3	HHQ	A	303	8/8	0.83	0.48	88,95,100,129	8
3	HHQ	D	501	8/8	0.89	0.23	120,136,146,152	0
3	HHQ	A	304	8/8	0.92	0.14	105,112,116,135	0
3	HHQ	A	302	8/8	0.92	0.38	72,78,90,103	8
3	HHQ	A	305	8/8	0.93	0.19	75,88,104,112	0
3	HHQ	C	301[B]	8/8	0.94	0.14	64,69,77,80	8
3	HHQ	C	301[A]	8/8	0.94	0.14	40,54,63,78	8
3	HHQ	C	302	8/8	0.95	0.12	103,106,109,121	0
3	HHQ	B	501	8/8	0.98	0.11	85,94,98,99	0
3	HHQ	A	301	8/8	0.99	0.08	63,67,68,69	0
3	HHQ	B	502	8/8	0.99	0.09	69,74,79,82	0

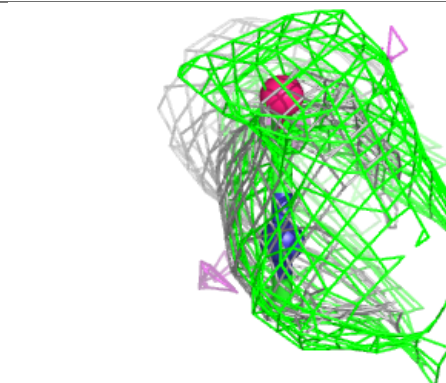
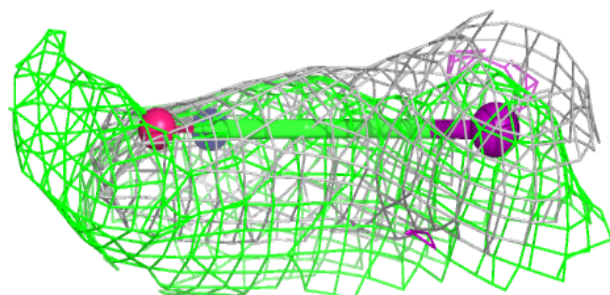
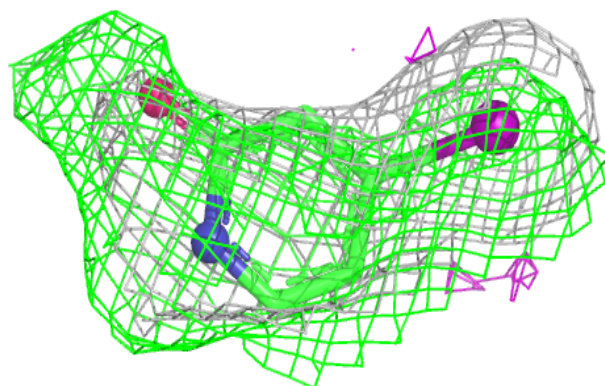
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around HHQ C 303:

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

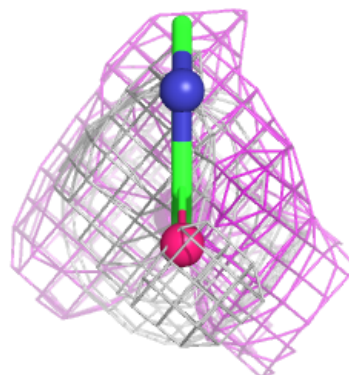
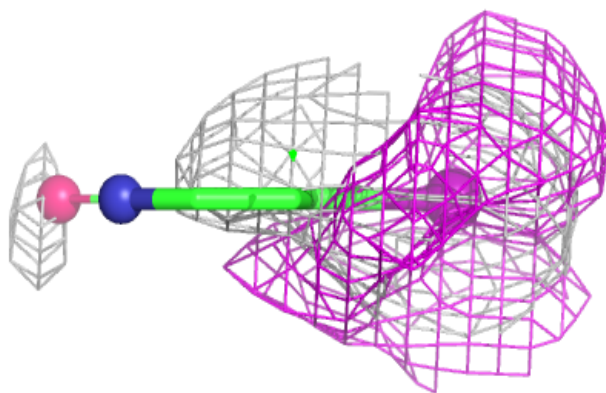
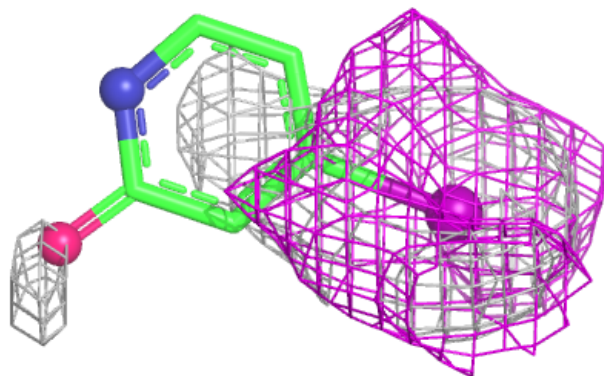
**Electron density around HHQ A 303:**

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



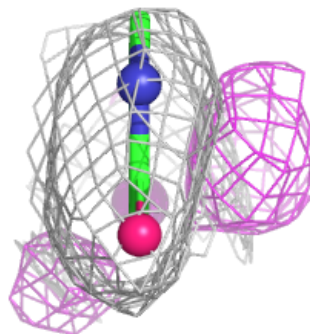
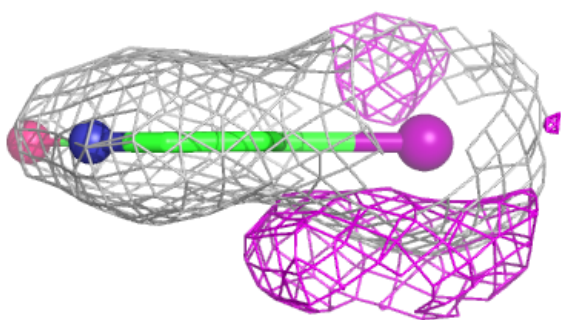
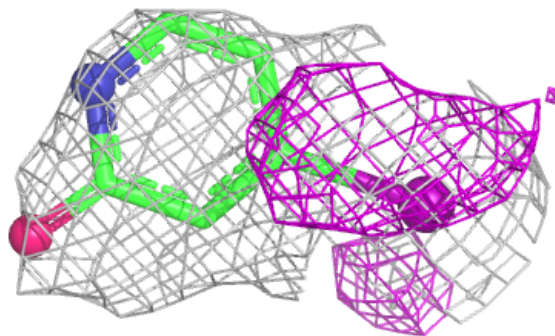
Electron density around HHQ D 501:

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



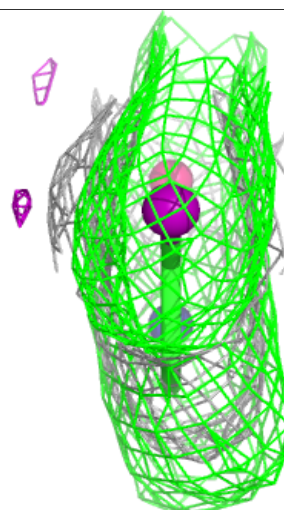
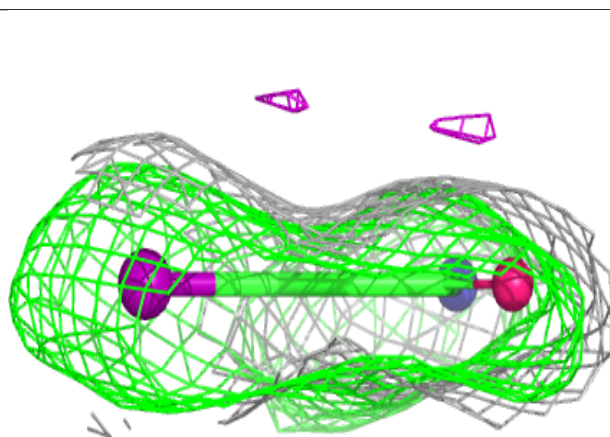
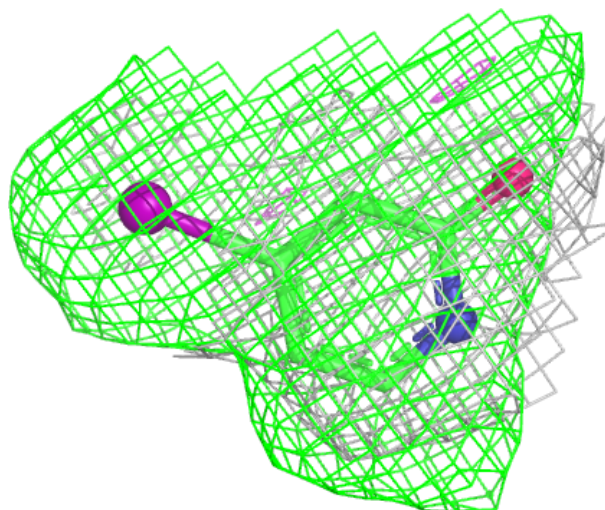
Electron density around HHQ A 304:

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



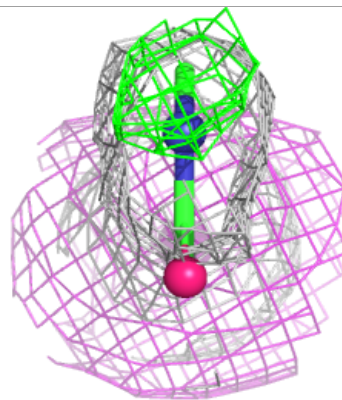
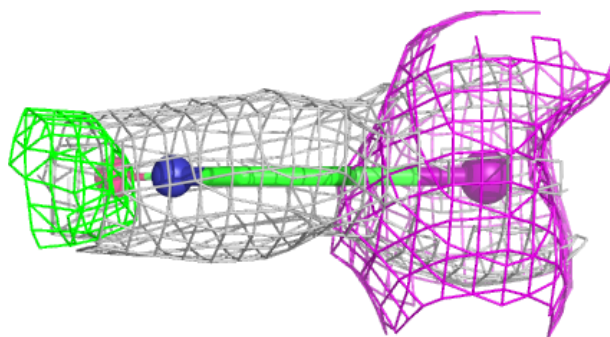
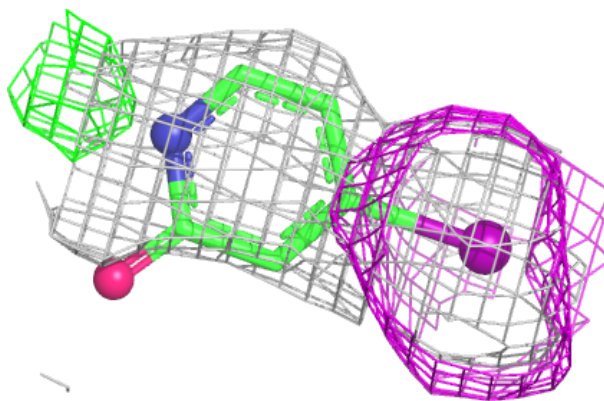
Electron density around HHQ A 302:

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



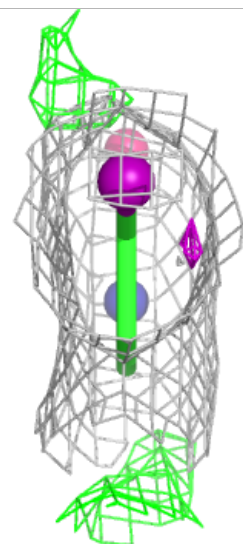
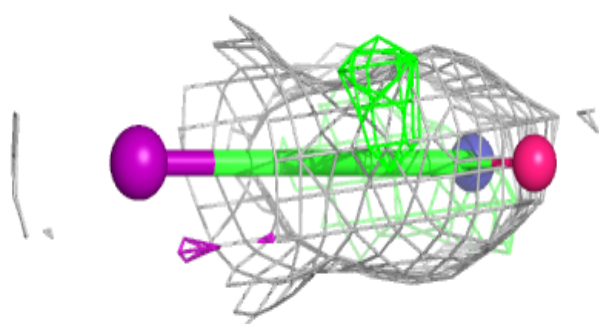
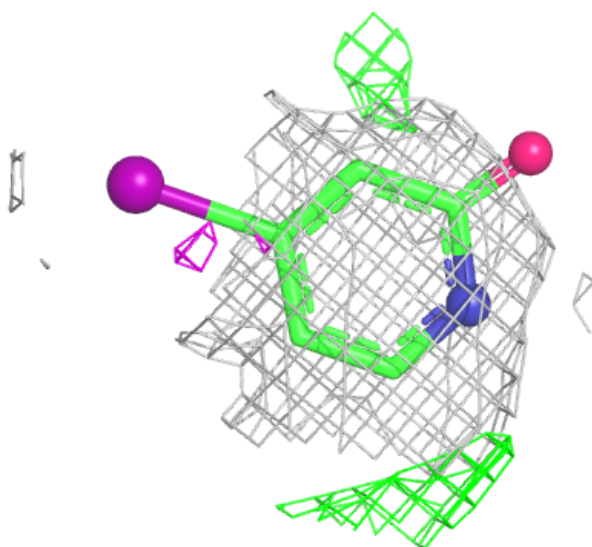
Electron density around HHQ A 305:

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



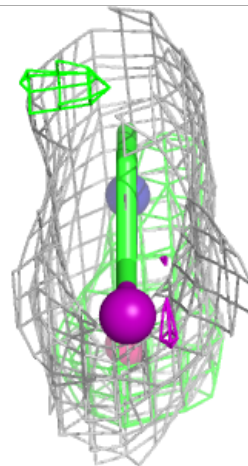
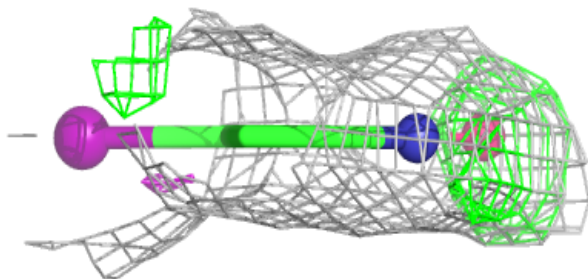
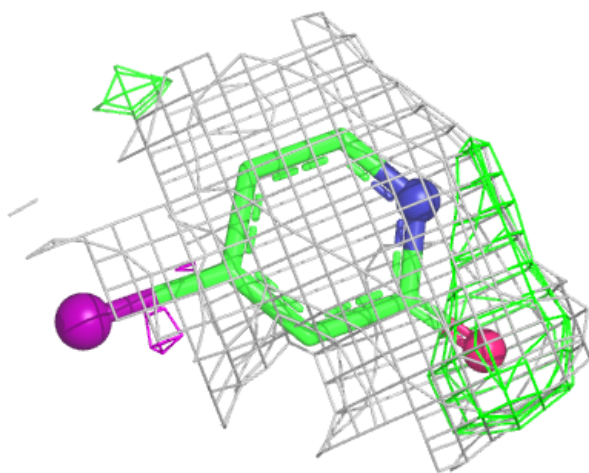
Electron density around HHQ C 301 (B):

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



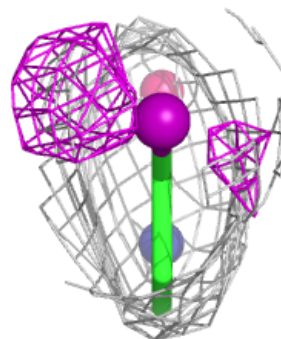
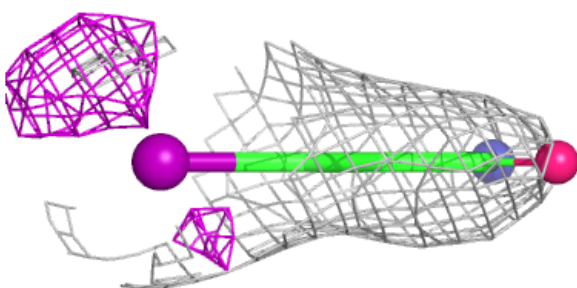
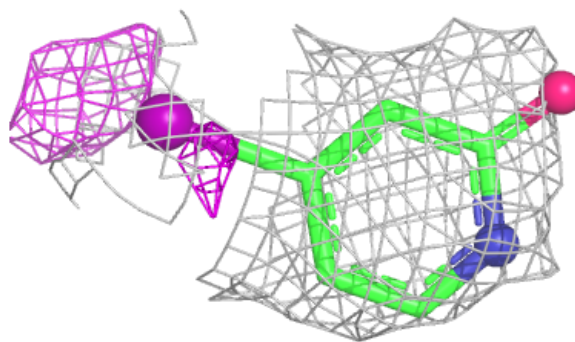
Electron density around HHQ C 301 (A):

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

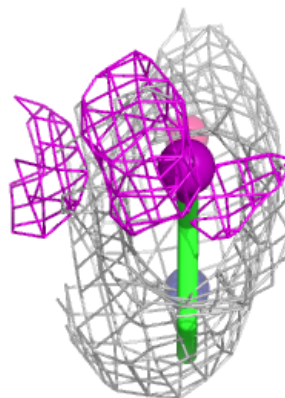
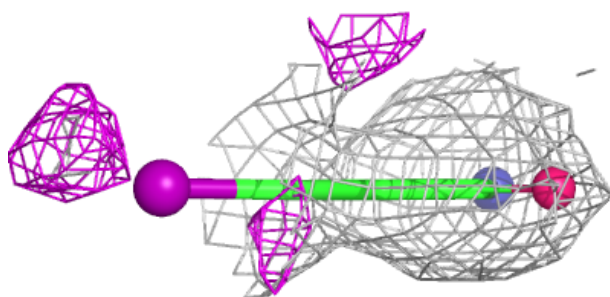
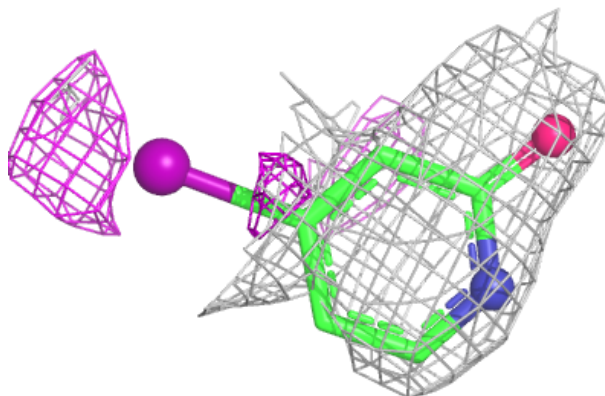


Electron density around HHQ C 302:

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

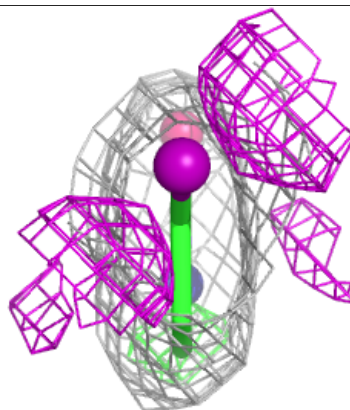
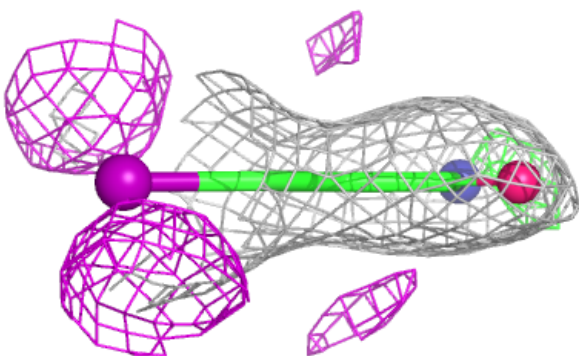
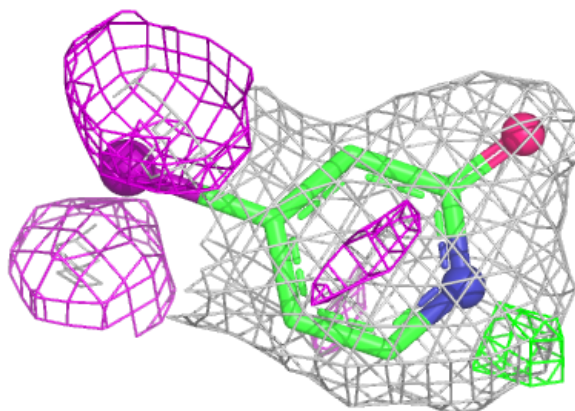
**Electron density around HHQ B 501:**

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

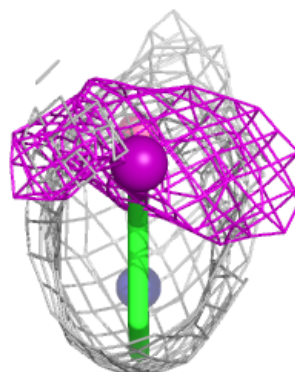
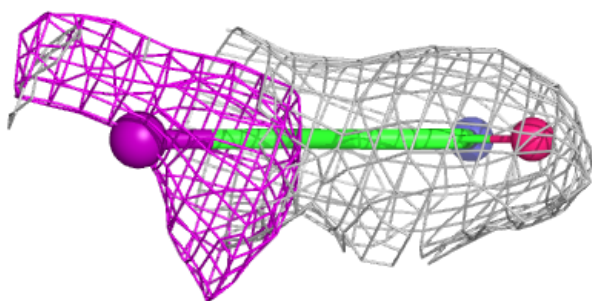
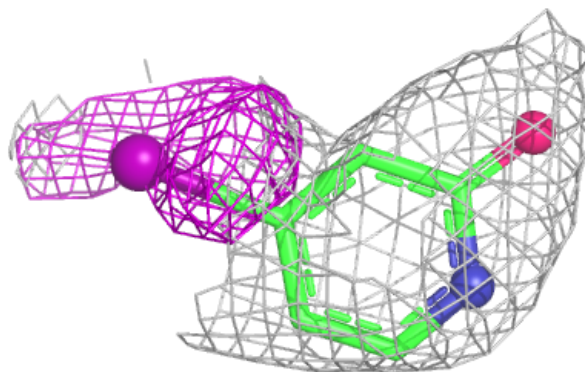


Electron density around HHQ A 301:

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

**Electron density around HHQ B 502:**

$2mF_o-DF_c$ (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.