



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 27, 2021 – 10:11 AM EDT

PDB ID : 6UVF
Title : Crystal structure of BCL-XL bound to compound 12: (R)-2-(3-([1,1'-Biphenyl]-4-carbonyl)-3-(4-methylbenzyl)ureido)-3-((cyclohexylmethyl)sulfonyl)propanoic acid
Authors : Roy, M.J.; Lessene, G.; Czabotar, P.E.
Deposited on : 2019-11-02
Resolution : 2.24 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

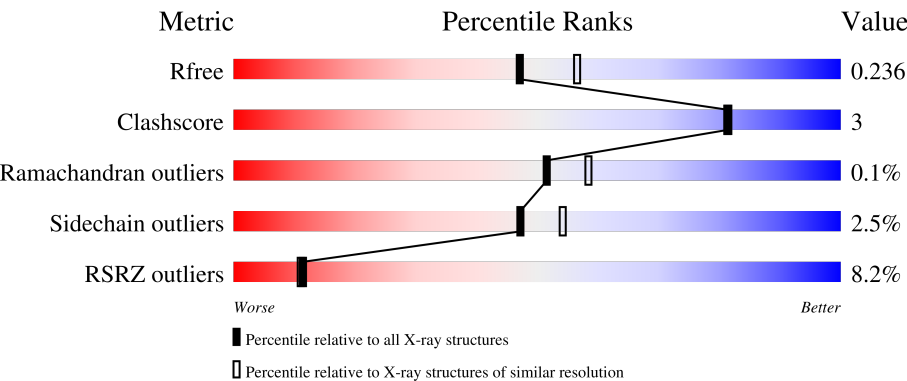
MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.18
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.18

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 2.24 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	2391 (2.26-2.22)
Clashscore	141614	2539 (2.26-2.22)
Ramachandran outliers	138981	2489 (2.26-2.22)
Sidechain outliers	138945	2490 (2.26-2.22)
RSRZ outliers	127900	2353 (2.26-2.22)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	158	<div><div>2%</div><div></div><div>84%</div><div>8%</div><div>8%</div></div>
1	B	158	<div><div>%</div><div></div><div>84%</div><div>7%</div><div>9%</div></div>
1	C	158	<div><div>3%</div><div></div><div>84%</div><div>6%</div><div>10%</div></div>
1	D	158	<div><div>2%</div><div></div><div>83%</div><div>8%</div><div>9%</div></div>
1	E	158	<div><div>21%</div><div></div><div>81%</div><div>7%</div><div>12%</div></div>

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Mol	Chain	Length	Quality of chain
1	F	158	<div><div>%</div><div><div></div><div>82%</div><div>6%</div><div>11%</div></div></div>
1	G	158	<div><div>8%</div><div><div></div><div>77%</div><div>10%</div><div>12%</div></div></div>
1	H	158	<div><div>4%</div><div><div></div><div>82%</div><div>6%</div><div>10%</div></div></div>
1	I	158	<div><div>6%</div><div><div></div><div>81%</div><div>6%</div><div>13%</div></div></div>
1	J	158	<div><div>11%</div><div><div></div><div>82%</div><div>9%</div><div>9%</div></div></div>
1	K	158	<div><div>15%</div><div><div></div><div>87%</div><div>6%</div><div>7%</div></div></div>
1	L	158	<div><div>16%</div><div><div></div><div>80%</div><div>9%</div><div>11%</div></div></div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14260 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 Bcl-2-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	145	Total	C	N	O	S	0	0	0
			1149	736	190	218	5			
1	B	144	Total	C	N	O	S	0	0	0
			1160	742	195	218	5			
1	C	142	Total	C	N	O	S	0	0	0
			1137	727	192	213	5			
1	D	144	Total	C	N	O	S	0	0	0
			1160	742	195	218	5			
1	E	139	Total	C	N	O	S	0	0	0
			1079	690	180	204	5			
1	F	140	Total	C	N	O	S	0	0	0
			1122	719	188	211	4			
1	G	139	Total	C	N	O	S	0	0	0
			1100	706	180	210	4			
1	H	142	Total	C	N	O	S	0	0	0
			1111	708	188	211	4			
1	I	138	Total	C	N	O	S	0	0	0
			1103	709	183	207	4			
1	J	144	Total	C	N	O	S	0	0	0
			1118	718	180	215	5			
1	K	147	Total	C	N	O	S	0	0	0
			1111	708	189	211	3			
1	L	140	Total	C	N	O	S	0	0	0
			1095	701	184	205	5			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	expression tag	UNP Q07817
A	-4	PRO	-	expression tag	UNP Q07817
A	-3	LEU	-	expression tag	UNP Q07817
A	-2	GLY	-	expression tag	UNP Q07817
A	-1	SER	-	expression tag	UNP Q07817

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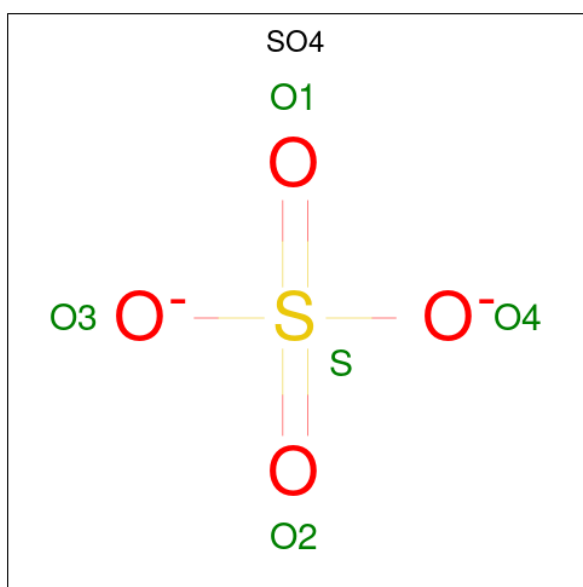
Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	GLY	-	expression tag	UNP Q07817
B	-4	PRO	-	expression tag	UNP Q07817
B	-3	LEU	-	expression tag	UNP Q07817
B	-2	GLY	-	expression tag	UNP Q07817
B	-1	SER	-	expression tag	UNP Q07817
C	-5	GLY	-	expression tag	UNP Q07817
C	-4	PRO	-	expression tag	UNP Q07817
C	-3	LEU	-	expression tag	UNP Q07817
C	-2	GLY	-	expression tag	UNP Q07817
C	-1	SER	-	expression tag	UNP Q07817
D	-5	GLY	-	expression tag	UNP Q07817
D	-4	PRO	-	expression tag	UNP Q07817
D	-3	LEU	-	expression tag	UNP Q07817
D	-2	GLY	-	expression tag	UNP Q07817
D	-1	SER	-	expression tag	UNP Q07817
E	-4	GLY	-	expression tag	UNP Q07817
E	-3	PRO	-	expression tag	UNP Q07817
E	-2	LEU	-	expression tag	UNP Q07817
E	-1	GLY	-	expression tag	UNP Q07817
E	0	SER	-	expression tag	UNP Q07817
F	-4	GLY	-	expression tag	UNP Q07817
F	-3	PRO	-	expression tag	UNP Q07817
F	-2	LEU	-	expression tag	UNP Q07817
F	-1	GLY	-	expression tag	UNP Q07817
F	0	SER	-	expression tag	UNP Q07817
G	-4	GLY	-	expression tag	UNP Q07817
G	-3	PRO	-	expression tag	UNP Q07817
G	-2	LEU	-	expression tag	UNP Q07817
G	-1	GLY	-	expression tag	UNP Q07817
G	0	SER	-	expression tag	UNP Q07817
H	-5	GLY	-	expression tag	UNP Q07817
H	-4	PRO	-	expression tag	UNP Q07817
H	-3	LEU	-	expression tag	UNP Q07817
H	-2	GLY	-	expression tag	UNP Q07817
H	-1	SER	-	expression tag	UNP Q07817
I	-4	GLY	-	expression tag	UNP Q07817
I	-3	PRO	-	expression tag	UNP Q07817
I	-2	LEU	-	expression tag	UNP Q07817
I	-1	GLY	-	expression tag	UNP Q07817
I	0	SER	-	expression tag	UNP Q07817
J	-5	GLY	-	expression tag	UNP Q07817
J	-4	PRO	-	expression tag	UNP Q07817

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-3	LEU	-	expression tag	UNP Q07817
J	-2	GLY	-	expression tag	UNP Q07817
J	-1	SER	-	expression tag	UNP Q07817
K	-5	GLY	-	expression tag	UNP Q07817
K	-4	PRO	-	expression tag	UNP Q07817
K	-3	LEU	-	expression tag	UNP Q07817
K	-2	GLY	-	expression tag	UNP Q07817
K	-1	SER	-	expression tag	UNP Q07817
L	-5	GLY	-	expression tag	UNP Q07817
L	-4	PRO	-	expression tag	UNP Q07817
L	-3	LEU	-	expression tag	UNP Q07817
L	-2	GLY	-	expression tag	UNP Q07817
L	-1	SER	-	expression tag	UNP Q07817

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



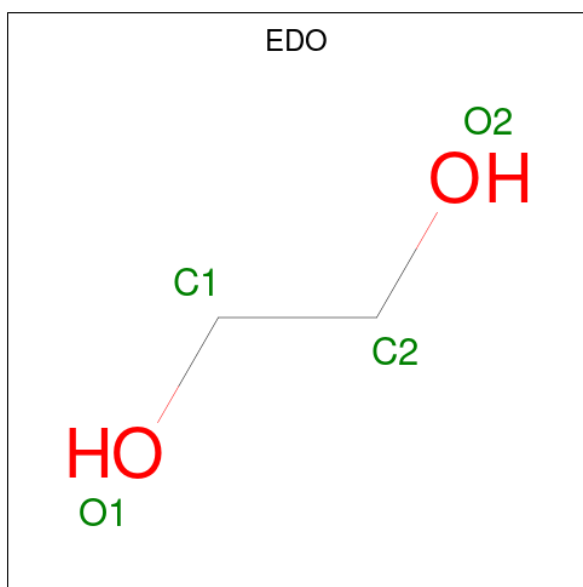
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

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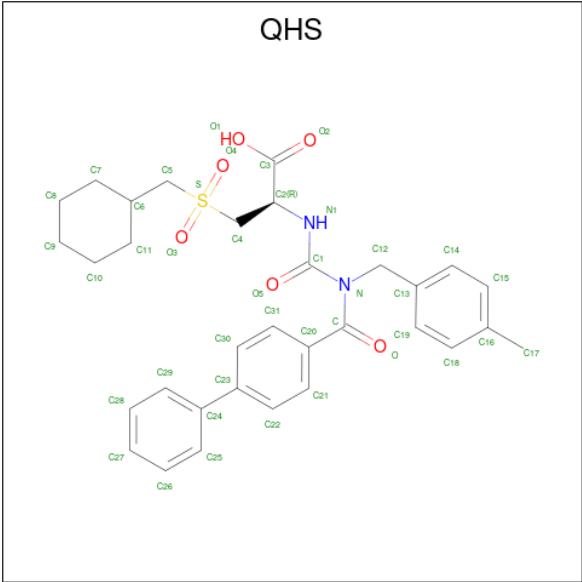
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		
2	G	1	Total	O	S	0	0
			5	4	1		
2	H	1	Total	O	S	0	0
			5	4	1		
2	I	1	Total	O	S	0	0
			5	4	1		
2	I	1	Total	O	S	0	0
			5	4	1		
2	J	1	Total	O	S	0	0
			5	4	1		
2	K	1	Total	O	S	0	0
			5	4	1		
2	K	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		
3	H	1	Total	C	O	0	0
			4	2	2		
3	J	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is (R)-2-(3-([1,1'-Biphenyl]-4-carbonyl)-3-(4-methylbenzyl)ureido)-3-((cyclohexylmethyl)sulfonyl)propanoic acid (three-letter code: QHS) (formula: C₃₂H₃₆N₂O₆S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			41	32	2	6	1		
4	B	1	Total	C	N	O	S	0	0
			41	32	2	6	1		
4	C	1	Total	C	N	O	S	0	0
			41	32	2	6	1		
4	D	1	Total	C	N	O	S	0	0
			41	32	2	6	1		
4	E	1	Total	C	N	O	S	0	0
			41	32	2	6	1		
4	F	1	Total	C	N	O	S	0	0
			41	32	2	6	1		
4	G	1	Total	C	N	O	S	0	0
			41	32	2	6	1		
4	H	1	Total	C	N	O	S	0	0
			41	32	2	6	1		
4	I	1	Total	C	N	O	S	0	0
			41	32	2	6	1		
4	J	1	Total	C	N	O	S	0	0
			41	32	2	6	1		
4	K	1	Total	C	N	O	S	0	0
			41	32	2	6	1		
4	L	1	Total	C	N	O	S	0	0
			41	32	2	6	1		

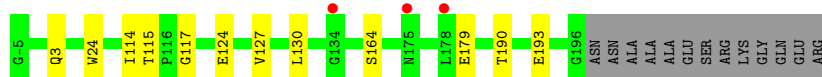
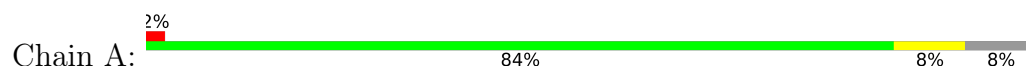
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	24	Total 24	O 24	0	0
5	B	48	Total 48	O 48	0	0
5	C	10	Total 10	O 10	0	0
5	D	29	Total 29	O 29	0	0
5	E	5	Total 5	O 5	0	0
5	F	23	Total 23	O 23	0	0
5	G	4	Total 4	O 4	0	0
5	H	14	Total 14	O 14	0	0
5	I	12	Total 12	O 12	0	0
5	J	7	Total 7	O 7	0	0
5	K	8	Total 8	O 8	0	0
5	L	1	Total 1	O 1	0	0

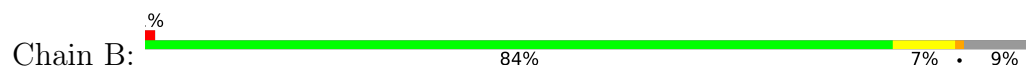
3 Residue-property plots [i](#)

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.

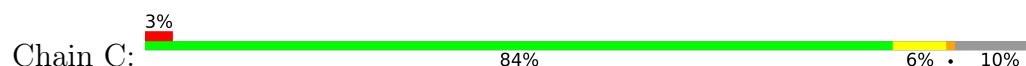
- Molecule 1: Bcl-2-like protein 1



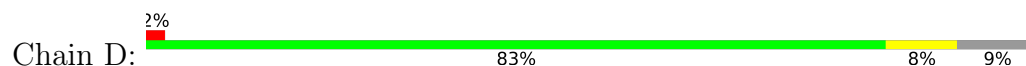
- Molecule 1: Bcl-2-like protein 1



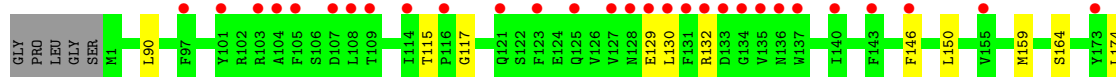
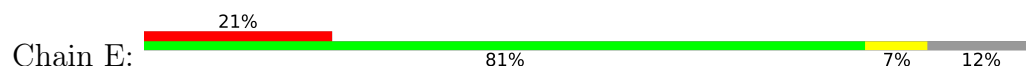
- Molecule 1: Bcl-2-like protein 1

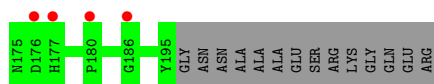


- Molecule 1: Bcl-2-like protein 1

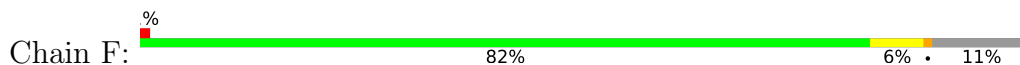


- Molecule 1: Bcl-2-like protein 1

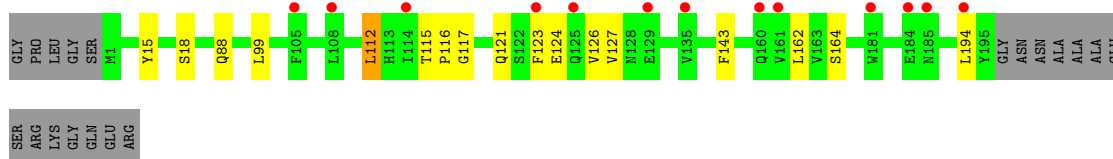




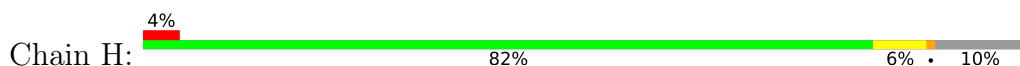
- Molecule 1: Bcl-2-like protein 1



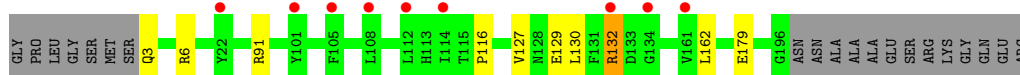
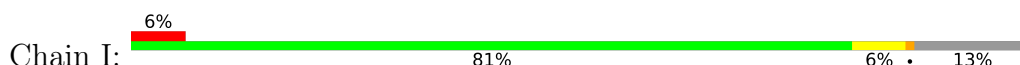
- Molecule 1: Bcl-2-like protein 1



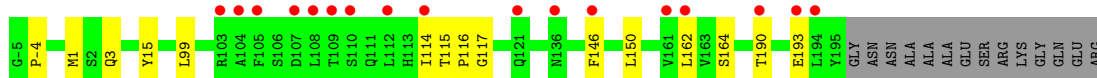
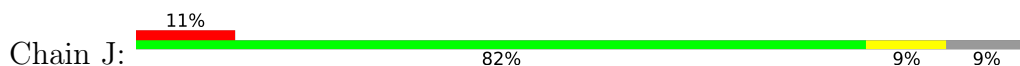
- Molecule 1: Bcl-2-like protein 1



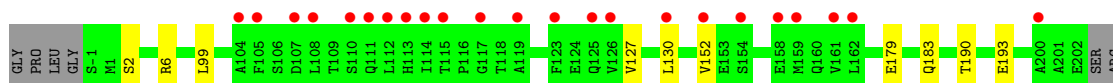
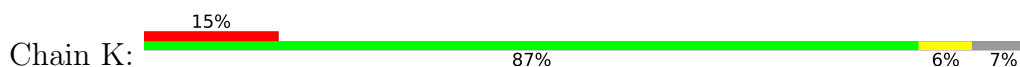
- Molecule 1: Bcl-2-like protein 1



- Molecule 1: Bcl-2-like protein 1

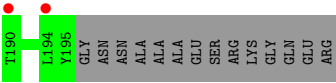
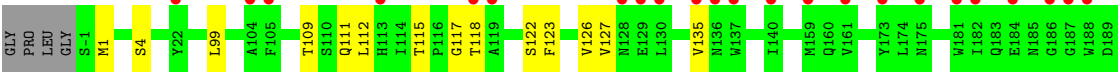
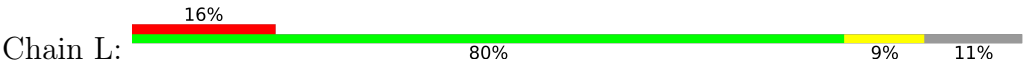


- Molecule 1: Bcl-2-like protein 1



LYS
GLY
GLN
GLU
ARG

● Molecule 1: Bcl-2-like protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	92.39Å 104.65Å 110.08Å 90.00° 110.99° 90.00°	Depositor
Resolution (Å)	47.52 – 2.24 47.52 – 2.24	Depositor EDS
% Data completeness (in resolution range)	99.5 (47.52-2.24) 99.5 (47.52-2.24)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.66 (at 2.24Å)	Xtriage
Refinement program	BUSTER	Depositor
R, R_{free}	0.200 , 0.227 0.206 , 0.236	Depositor DCC
R_{free} test set	4655 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	49.1	Xtriage
Anisotropy	0.315	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 54.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14260	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.31% 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: QHS, SO4, EDO

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	0.53	0/1177	0.62	0/1595
1	B	0.62	0/1189	0.62	0/1609
1	C	0.53	0/1165	0.59	0/1577
1	D	0.55	0/1189	0.61	0/1609
1	E	0.50	0/1105	0.63	0/1501
1	F	0.56	0/1150	0.59	0/1559
1	G	0.52	0/1127	0.62	0/1530
1	H	0.57	0/1139	0.62	0/1546
1	I	0.53	0/1130	0.63	0/1532
1	J	0.51	0/1146	0.62	0/1557
1	K	0.53	0/1139	0.63	0/1552
1	L	0.50	0/1122	0.62	0/1522
All	All	0.54	0/13778	0.62	0/18689

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

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	1149	0	1090	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1160	0	1109	7	0
1	C	1137	0	1081	8	0
1	D	1160	0	1109	11	0
1	E	1079	0	995	6	0
1	F	1122	0	1061	5	0
1	G	1100	0	1025	10	0
1	H	1111	0	1021	7	0
1	I	1103	0	1042	6	0
1	J	1118	0	1034	11	0
1	K	1111	0	983	6	0
1	L	1095	0	1019	4	0
2	A	10	0	0	0	0
2	B	15	0	0	0	0
2	C	15	0	0	0	0
2	D	15	0	0	0	0
2	E	10	0	0	0	0
2	F	10	0	0	0	0
2	G	5	0	0	0	0
2	H	5	0	0	0	0
2	I	10	0	0	0	0
2	J	5	0	0	0	0
2	K	10	0	0	0	0
3	A	4	0	6	1	0
3	B	4	0	6	0	0
3	C	4	0	6	2	0
3	D	8	0	12	2	0
3	H	4	0	6	0	0
3	J	4	0	6	0	0
4	A	41	0	0	1	0
4	B	41	0	0	0	0
4	C	41	0	0	0	0
4	D	41	0	0	0	0
4	E	41	0	0	0	0
4	F	41	0	0	0	0
4	G	41	0	0	0	0
4	H	41	0	0	0	0
4	I	41	0	0	0	0
4	J	41	0	0	0	0
4	K	41	0	0	0	0
4	L	41	0	0	0	0
5	A	24	0	0	0	0
5	B	48	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	10	0	0	0	0
5	D	29	0	0	0	0
5	E	5	0	0	0	0
5	F	23	0	0	0	0
5	G	4	0	0	0	0
5	H	14	0	0	0	0
5	I	12	0	0	0	0
5	J	7	0	0	0	0
5	K	8	0	0	0	0
5	L	1	0	0	0	0
All	All	14260	0	12611	69	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (69) 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:G:164:SER:HB3	1:K:2:SER:HB3	1.56	0.85
1:A:179:GLU:HG2	1:B:1:MET:SD	2.25	0.77
1:G:164:SER:CB	1:K:2:SER:HB3	2.15	0.77
1:C:114:ILE:HG22	1:C:162:LEU:HD13	1.72	0.70
1:J:114:ILE:HG12	1:J:162:LEU:HD13	1.75	0.68
1:C:179:GLU:HG3	1:D:5:ASN:HD21	1.57	0.68
1:I:129:GLU:HA	1:I:132:ARG:HE	1.60	0.66
1:A:3:GLN:HE22	1:J:3:GLN:HA	1.60	0.66
1:L:112:LEU:HB2	1:L:126:VAL:HG21	1.77	0.65
1:D:2:SER:HB3	1:E:164:SER:CB	2.28	0.63
1:D:139:ARG:HE	3:D:304:EDO:H22	1.68	0.59
1:I:116:PRO:HA	1:I:162:LEU:HD21	1.84	0.59
1:A:190:THR:HA	1:A:193:GLU:HG2	1.84	0.59
1:J:190:THR:HA	1:J:193:GLU:HG2	1.86	0.58
1:D:2:SER:HB3	1:E:164:SER:HB3	1.86	0.58
1:B:2:SER:HB2	1:J:164:SER:HB3	1.86	0.58
1:H:3:GLN:O	1:H:7:GLU:HB2	2.04	0.57
1:C:114:ILE:HD11	1:C:150:LEU:HD13	1.86	0.57
1:D:135:VAL:CG2	1:H:184:GLU:HG2	2.34	0.57
1:C:95:ASP:HA	3:C:304:EDO:H11	1.86	0.56
1:K:190:THR:HA	1:K:193:GLU:HG2	1.88	0.56
1:B:2:SER:HB2	1:J:164:SER:CB	2.38	0.54
1:I:179:GLU:HG2	1:J:1:MET:SD	2.48	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:139:ARG:NE	3:D:304:EDO:H22	2.24	0.53
1:D:127:VAL:O	1:D:130:LEU:HB2	2.09	0.53
1:B:114:ILE:HD12	1:B:169:TRP:HZ3	1.75	0.52
1:E:90:LEU:HD22	1:F:12:PHE:CD2	2.45	0.52
1:B:168:ALA:HB1	1:J:-4:PRO:HB2	1.91	0.52
1:H:2:SER:O	1:H:6:ARG:HB2	2.09	0.52
1:A:115:THR:HG23	1:A:117:GLY:H	1.76	0.51
1:C:115:THR:HG23	1:C:117:GLY:H	1.75	0.51
1:F:116:PRO:HA	1:F:162:LEU:HD21	1.93	0.51
1:G:115:THR:HG23	1:G:117:GLY:H	1.76	0.51
1:G:121:GLN:HA	1:G:124:GLU:HG2	1.92	0.51
1:A:164:SER:HB2	1:I:3:GLN:HG3	1.93	0.50
1:E:115:THR:HG23	1:E:117:GLY:H	1.77	0.50
1:C:116:PRO:HA	1:C:162:LEU:HD21	1.92	0.50
1:J:115:THR:HG23	1:J:117:GLY:H	1.77	0.50
1:G:116:PRO:HA	1:G:162:LEU:HD21	1.94	0.49
1:C:179:GLU:OE2	1:D:1:MET:HB3	2.13	0.48
1:F:114:ILE:HD11	1:F:150:LEU:HD13	1.95	0.48
1:E:129:GLU:HA	1:E:132:ARG:HG3	1.96	0.48
1:L:115:THR:HG23	1:L:117:GLY:H	1.78	0.47
1:D:3:GLN:HG2	1:F:6:ARG:HH22	1.79	0.47
1:G:112:LEU:HB2	1:G:126:VAL:HG21	1.95	0.47
1:L:123:PHE:O	1:L:127:VAL:HG23	2.14	0.47
1:B:116:PRO:HA	1:B:162:LEU:HD21	1.96	0.46
1:J:146:PHE:CZ	1:J:150:LEU:HD11	2.50	0.46
1:K:179:GLU:CD	1:L:1:MET:HG2	2.36	0.46
1:H:2:SER:HB3	1:K:6:ARG:HH12	1.80	0.46
1:A:24:TRP:HE1	3:A:303:EDO:H12	1.81	0.46
1:A:127:VAL:O	1:A:130:LEU:HB3	2.15	0.46
1:H:116:PRO:HA	1:H:162:LEU:HD21	1.97	0.45
1:K:127:VAL:O	1:K:130:LEU:HB3	2.16	0.45
1:D:114:ILE:HD12	1:D:169:TRP:HZ3	1.81	0.45
1:B:127:VAL:O	1:B:130:LEU:HB3	2.18	0.44
1:F:127:VAL:O	1:F:130:LEU:HB3	2.18	0.44
1:I:127:VAL:O	1:I:130:LEU:HB3	2.18	0.43
1:J:116:PRO:HA	1:J:162:LEU:HD21	2.00	0.43
1:G:123:PHE:O	1:G:127:VAL:HG12	2.20	0.42
1:D:116:PRO:HA	1:D:162:LEU:HD21	2.00	0.42
1:G:15:TYR:HB2	1:H:91:ARG:CZ	2.50	0.42
1:G:18:SER:HB2	1:G:88:GLN:HG2	2.01	0.42
1:C:98:GLU:HB2	3:C:304:EDO:H22	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:127:VAL:HG21	1:G:143:PHE:HD1	1.86	0.41
4:A:304:QHS:O	4:A:304:QHS:N1	2.54	0.41
1:E:146:PHE:O	1:E:150:LEU:HG	2.20	0.40
1:I:91:ARG:CZ	1:J:15:TYR:HB2	2.52	0.40
1:H:186:GLY:HA3	1:H:190:THR:HG21	2.04	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	143/158 (90%)	143 (100%)	0	0	100	100
1	B	142/158 (90%)	141 (99%)	1 (1%)	0	100	100
1	C	140/158 (89%)	140 (100%)	0	0	100	100
1	D	142/158 (90%)	141 (99%)	1 (1%)	0	100	100
1	E	137/158 (87%)	134 (98%)	2 (2%)	1 (1%)	22	20
1	F	138/158 (87%)	138 (100%)	0	0	100	100
1	G	137/158 (87%)	135 (98%)	2 (2%)	0	100	100
1	H	140/158 (89%)	138 (99%)	2 (1%)	0	100	100
1	I	136/158 (86%)	135 (99%)	1 (1%)	0	100	100
1	J	142/158 (90%)	141 (99%)	1 (1%)	0	100	100
1	K	145/158 (92%)	145 (100%)	0	0	100	100
1	L	138/158 (87%)	136 (99%)	2 (1%)	0	100	100
All	All	1680/1896 (89%)	1667 (99%)	12 (1%)	1 (0%)	51	58

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	159	MET

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	119/131 (91%)	117 (98%)	2 (2%)	60	68
1	B	122/131 (93%)	118 (97%)	4 (3%)	38	43
1	C	118/131 (90%)	116 (98%)	2 (2%)	60	68
1	D	122/131 (93%)	121 (99%)	1 (1%)	81	87
1	E	107/131 (82%)	105 (98%)	2 (2%)	57	64
1	F	116/131 (88%)	113 (97%)	3 (3%)	46	52
1	G	112/131 (86%)	109 (97%)	3 (3%)	44	51
1	H	111/131 (85%)	107 (96%)	4 (4%)	35	39
1	I	113/131 (86%)	111 (98%)	2 (2%)	59	66
1	J	113/131 (86%)	112 (99%)	1 (1%)	78	84
1	K	103/131 (79%)	100 (97%)	3 (3%)	42	48
1	L	110/131 (84%)	103 (94%)	7 (6%)	17	14
All	All	1366/1572 (87%)	1332 (98%)	34 (2%)	47	54

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

Mol	Chain	Res	Type
1	A	114	ILE
1	A	124	GLU
1	B	1	MET
1	B	99	LEU
1	B	184	GLU
1	B	193	GLU
1	C	99	LEU
1	C	179	GLU
1	D	-3	LEU
1	E	130	LEU

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Mol	Chain	Res	Type
1	E	174	LEU
1	F	2	SER
1	F	6	ARG
1	F	99	LEU
1	G	99	LEU
1	G	112	LEU
1	G	194	LEU
1	H	-1	SER
1	H	2	SER
1	H	6	ARG
1	H	132	ARG
1	I	6	ARG
1	I	132	ARG
1	J	99	LEU
1	K	99	LEU
1	K	152	VAL
1	K	183	GLN
1	L	4	SER
1	L	99	LEU
1	L	109	THR
1	L	111	GLN
1	L	118	THR
1	L	122	SER
1	L	135	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	C	128	ASN
1	D	5	ASN
1	F	88	GLN
1	G	185	ASN
1	H	3	GLN
1	I	3	GLN
1	K	175	ASN
1	L	113	HIS

5.3.3 RNA ⓘ

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](#)

41 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	SO4	A	302	-	4,4,4	0.43	0	6,6,6	0.15	0
4	QHS	H	303	-	39,44,44	0.91	1 (2%)	51,61,61	0.50	1 (1%)
2	SO4	J	301	-	4,4,4	0.09	0	6,6,6	0.13	0
4	QHS	E	303	-	39,44,44	0.72	1 (2%)	51,61,61	0.38	0
4	QHS	G	302	-	39,44,44	0.70	1 (2%)	51,61,61	0.51	1 (1%)
2	SO4	D	303	-	4,4,4	0.17	0	6,6,6	0.07	0
2	SO4	B	301	-	4,4,4	0.16	0	6,6,6	0.24	0
2	SO4	D	302	-	4,4,4	0.22	0	6,6,6	0.22	0
2	SO4	H	301	-	4,4,4	0.11	0	6,6,6	0.20	0
4	QHS	I	303	-	39,44,44	0.63	1 (2%)	51,61,61	0.31	0
2	SO4	D	301	-	4,4,4	0.17	0	6,6,6	0.20	0
2	SO4	C	302	-	4,4,4	0.34	0	6,6,6	0.10	0
2	SO4	E	301	-	4,4,4	0.14	0	6,6,6	0.16	0
3	EDO	H	302	-	3,3,3	0.72	0	2,2,2	0.09	0
2	SO4	I	302	-	4,4,4	0.19	0	6,6,6	0.07	0
2	SO4	C	303	-	4,4,4	0.11	0	6,6,6	0.12	0
2	SO4	I	301	-	4,4,4	0.14	0	6,6,6	0.15	0
4	QHS	K	303	-	39,44,44	0.94	1 (2%)	51,61,61	0.49	1 (1%)
4	QHS	L	301	-	39,44,44	1.48	1 (2%)	51,61,61	0.75	1 (1%)
3	EDO	B	304	-	3,3,3	0.40	0	2,2,2	0.55	0
4	QHS	F	303	-	39,44,44	1.13	1 (2%)	51,61,61	0.62	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	K	302	-	4,4,4	0.27	0	6,6,6	0.13	0
3	EDO	A	303	-	3,3,3	1.08	0	2,2,2	0.41	0
3	EDO	J	302	-	3,3,3	1.10	0	2,2,2	0.50	0
3	EDO	D	304	-	3,3,3	0.57	0	2,2,2	0.34	0
2	SO4	F	301	-	4,4,4	0.20	0	6,6,6	0.09	0
2	SO4	B	302	-	4,4,4	0.22	0	6,6,6	0.16	0
2	SO4	B	303	-	4,4,4	0.32	0	6,6,6	0.21	0
3	EDO	C	304	-	3,3,3	0.66	0	2,2,2	0.50	0
2	SO4	K	301	-	4,4,4	0.23	0	6,6,6	0.11	0
4	QHS	C	305	-	39,44,44	0.65	1 (2%)	51,61,61	0.41	0
2	SO4	G	301	-	4,4,4	0.17	0	6,6,6	0.16	0
2	SO4	A	301	-	4,4,4	0.14	0	6,6,6	0.16	0
2	SO4	C	301	-	4,4,4	0.26	0	6,6,6	0.17	0
4	QHS	B	305	-	39,44,44	1.37	1 (2%)	51,61,61	0.65	1 (1%)
4	QHS	D	306	-	39,44,44	0.98	1 (2%)	51,61,61	0.44	0
2	SO4	F	302	-	4,4,4	0.38	0	6,6,6	0.08	0
4	QHS	A	304	-	39,44,44	1.74	1 (2%)	51,61,61	0.67	1 (1%)
4	QHS	J	303	-	39,44,44	1.06	1 (2%)	51,61,61	0.47	1 (1%)
2	SO4	E	302	-	4,4,4	0.30	0	6,6,6	0.23	0
3	EDO	D	305	-	3,3,3	0.74	0	2,2,2	0.23	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
4	QHS	H	303	-	-	6/34/46/46	0/4/4/4
4	QHS	E	303	-	-	6/34/46/46	0/4/4/4
4	QHS	G	302	-	-	7/34/46/46	0/4/4/4
4	QHS	I	303	-	-	8/34/46/46	0/4/4/4
3	EDO	H	302	-	-	0/1/1/1	-
4	QHS	L	301	-	-	12/34/46/46	0/4/4/4
3	EDO	B	304	-	-	0/1/1/1	-
4	QHS	F	303	-	-	4/34/46/46	0/4/4/4
3	EDO	J	302	-	-	0/1/1/1	-
3	EDO	A	303	-	-	1/1/1/1	-
3	EDO	D	304	-	-	0/1/1/1	-
3	EDO	C	304	-	-	1/1/1/1	-
4	QHS	C	305	-	-	9/34/46/46	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	QHS	B	305	-	-	5/34/46/46	0/4/4/4
4	QHS	D	306	-	-	6/34/46/46	0/4/4/4
4	QHS	A	304	-	-	8/34/46/46	0/4/4/4
4	QHS	J	303	-	-	5/34/46/46	0/4/4/4
4	QHS	K	303	-	-	8/34/46/46	0/4/4/4
3	EDO	D	305	-	-	1/1/1/1	-

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	304	QHS	C4-C2	10.48	1.61	1.53
4	L	301	QHS	C4-C2	9.08	1.60	1.53
4	B	305	QHS	C4-C2	8.26	1.59	1.53
4	F	303	QHS	C4-C2	6.41	1.58	1.53
4	J	303	QHS	C4-C2	5.85	1.57	1.53
4	D	306	QHS	C4-C2	5.50	1.57	1.53
4	K	303	QHS	C4-C2	5.24	1.57	1.53
4	H	303	QHS	C4-C2	5.21	1.57	1.53
4	G	302	QHS	C4-C2	3.49	1.56	1.53
4	E	303	QHS	C4-C2	3.48	1.56	1.53
4	C	305	QHS	C4-C2	3.38	1.56	1.53
4	I	303	QHS	C4-C2	2.70	1.55	1.53

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L	301	QHS	C2-C4-S	4.16	124.22	114.56
4	A	304	QHS	C2-C4-S	2.53	120.43	114.56
4	K	303	QHS	C2-C4-S	2.48	120.31	114.56
4	J	303	QHS	C2-C4-S	2.40	120.13	114.56
4	H	303	QHS	C2-C4-S	2.36	120.05	114.56
4	G	302	QHS	C2-C4-S	2.20	119.67	114.56
4	B	305	QHS	C21-C20-C	2.18	125.81	120.29

There are no chirality outliers.

All (87) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	304	QHS	C2-C4-S-O3
4	D	306	QHS	S-C5-C6-C11

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Mol	Chain	Res	Type	Atoms
4	K	303	QHS	C2-C4-S-C5
4	L	301	QHS	C2-C4-S-C5
4	L	301	QHS	C2-C4-S-O3
4	L	301	QHS	S-C5-C6-C7
4	L	301	QHS	C20-C-N-C1
4	L	301	QHS	O-C-N-C1
3	A	303	EDO	O1-C1-C2-O2
3	D	305	EDO	O1-C1-C2-O2
4	C	305	QHS	S-C5-C6-C7
4	C	305	QHS	S-C5-C6-C11
4	D	306	QHS	S-C5-C6-C7
4	I	303	QHS	S-C5-C6-C7
4	I	303	QHS	S-C5-C6-C11
4	J	303	QHS	S-C5-C6-C7
4	K	303	QHS	S-C5-C6-C7
4	K	303	QHS	S-C5-C6-C11
4	I	303	QHS	C30-C23-C24-C29
4	L	301	QHS	C20-C-N-C12
4	L	301	QHS	O-C-N-C12
4	D	306	QHS	O-C-N-C1
4	E	303	QHS	O-C-N-C1
4	K	303	QHS	O-C-N-C1
4	A	304	QHS	C30-C23-C24-C29
4	A	304	QHS	C2-C4-S-C5
4	G	302	QHS	C6-C5-S-O4
4	K	303	QHS	C20-C-N-C1
4	C	305	QHS	N1-C2-C4-S
4	D	306	QHS	N1-C2-C4-S
4	G	302	QHS	N1-C2-C4-S
4	H	303	QHS	N1-C2-C4-S
4	L	301	QHS	C13-C12-N-C1
4	E	303	QHS	S-C5-C6-C11
4	J	303	QHS	O5-C1-N-C12
4	A	304	QHS	C2-C4-S-O4
4	J	303	QHS	N1-C1-N-C12
4	L	301	QHS	C2-C4-S-O4
4	L	301	QHS	N1-C1-N-C12
4	D	306	QHS	O-C-N-C12
4	E	303	QHS	O-C-N-C12
4	G	302	QHS	O-C-N-C12
4	I	303	QHS	O-C-N-C12
4	K	303	QHS	O-C-N-C12

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Mol	Chain	Res	Type	Atoms
4	C	305	QHS	N1-C1-N-C
4	C	305	QHS	O5-C1-N-C
4	I	303	QHS	C22-C23-C24-C29
4	C	305	QHS	C13-C12-N-C1
4	A	304	QHS	O-C-N-C1
4	B	305	QHS	O-C-N-C1
4	C	305	QHS	O-C-N-C1
4	F	303	QHS	O-C-N-C1
4	G	302	QHS	O-C-N-C1
4	H	303	QHS	O-C-N-C1
4	I	303	QHS	O-C-N-C1
4	G	302	QHS	C6-C5-S-C4
4	I	303	QHS	C30-C23-C24-C25
4	H	303	QHS	N-C1-N1-C2
4	B	305	QHS	C2-C4-S-C5
4	A	304	QHS	C20-C-N-C12
4	A	304	QHS	O-C-N-C12
4	B	305	QHS	C20-C-N-C12
4	B	305	QHS	O-C-N-C12
4	C	305	QHS	O-C-N-C12
4	D	306	QHS	C20-C-N-C12
4	E	303	QHS	C20-C-N-C12
4	F	303	QHS	C20-C-N-C12
4	F	303	QHS	O-C-N-C12
4	G	302	QHS	C20-C-N-C12
4	H	303	QHS	C20-C-N-C12
4	H	303	QHS	O-C-N-C12
4	I	303	QHS	C20-C-N-C12
4	K	303	QHS	C20-C-N-C12
4	K	303	QHS	C30-C23-C24-C29
4	A	304	QHS	C20-C-N-C1
4	B	305	QHS	C20-C-N-C1
4	C	305	QHS	C20-C-N-C1
4	E	303	QHS	C20-C-N-C1
4	F	303	QHS	C20-C-N-C1
4	G	302	QHS	C20-C-N-C1
4	H	303	QHS	C20-C-N-C1
4	J	303	QHS	C20-C-N-C1
4	E	303	QHS	N1-C2-C4-S
4	L	301	QHS	C30-C23-C24-C29
3	C	304	EDO	O1-C1-C2-O2
4	J	303	QHS	N1-C1-N-C

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Mol	Chain	Res	Type	Atoms
4	L	301	QHS	O5-C1-N-C12

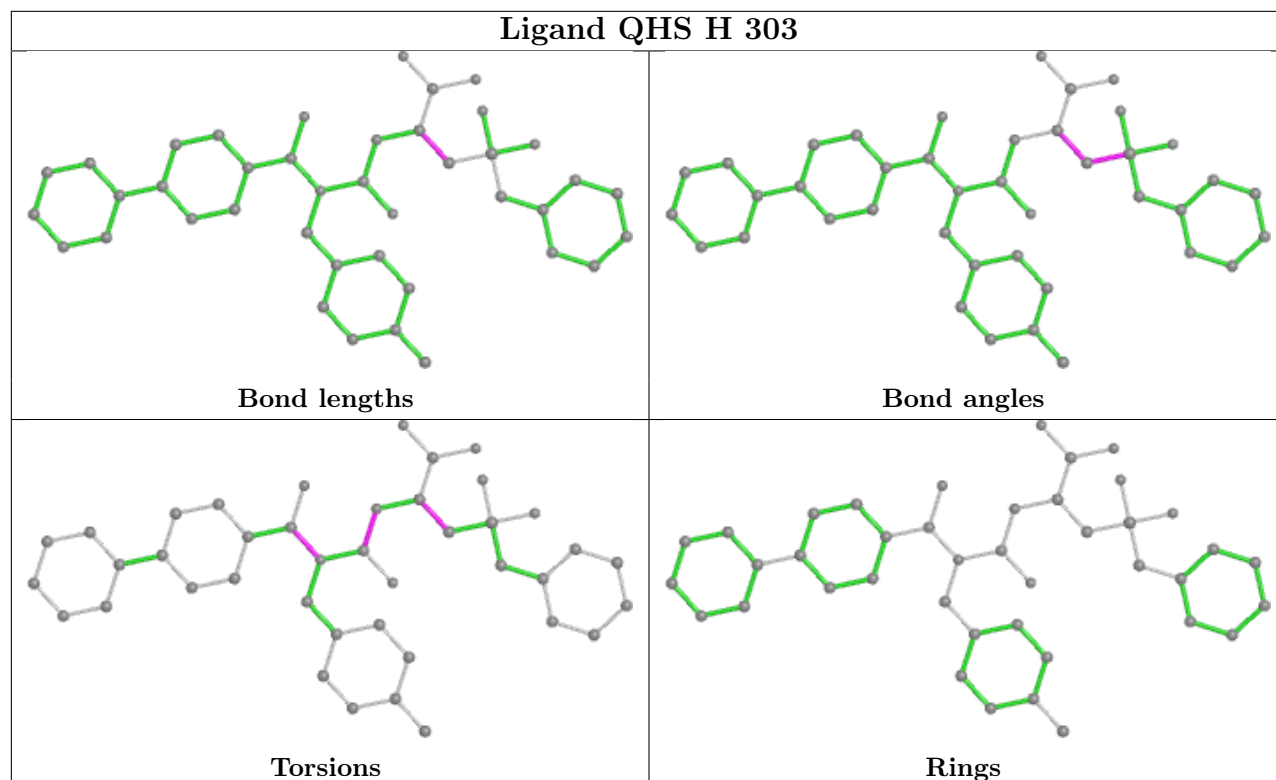
There are no ring outliers.

4 monomers are involved in 6 short contacts:

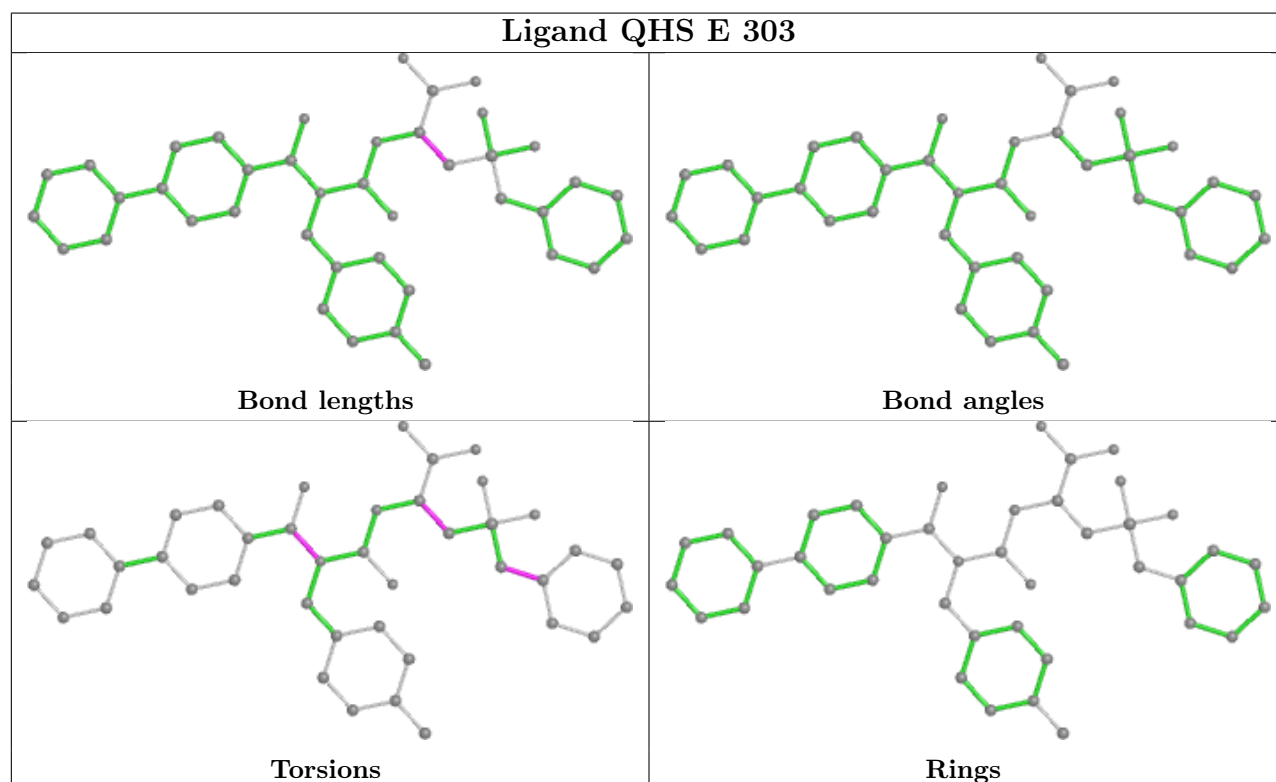
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	303	EDO	1	0
3	D	304	EDO	2	0
3	C	304	EDO	2	0
4	A	304	QHS	1	0

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.

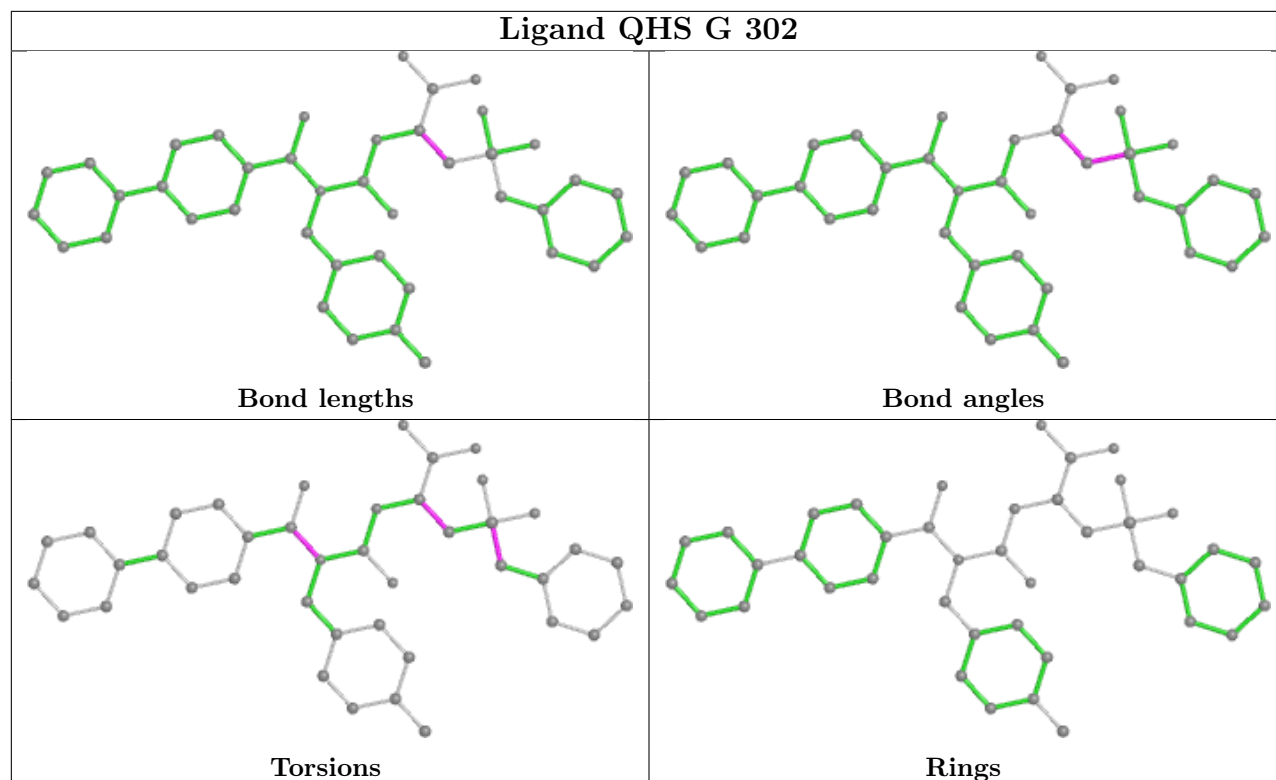
Ligand QHS H 303



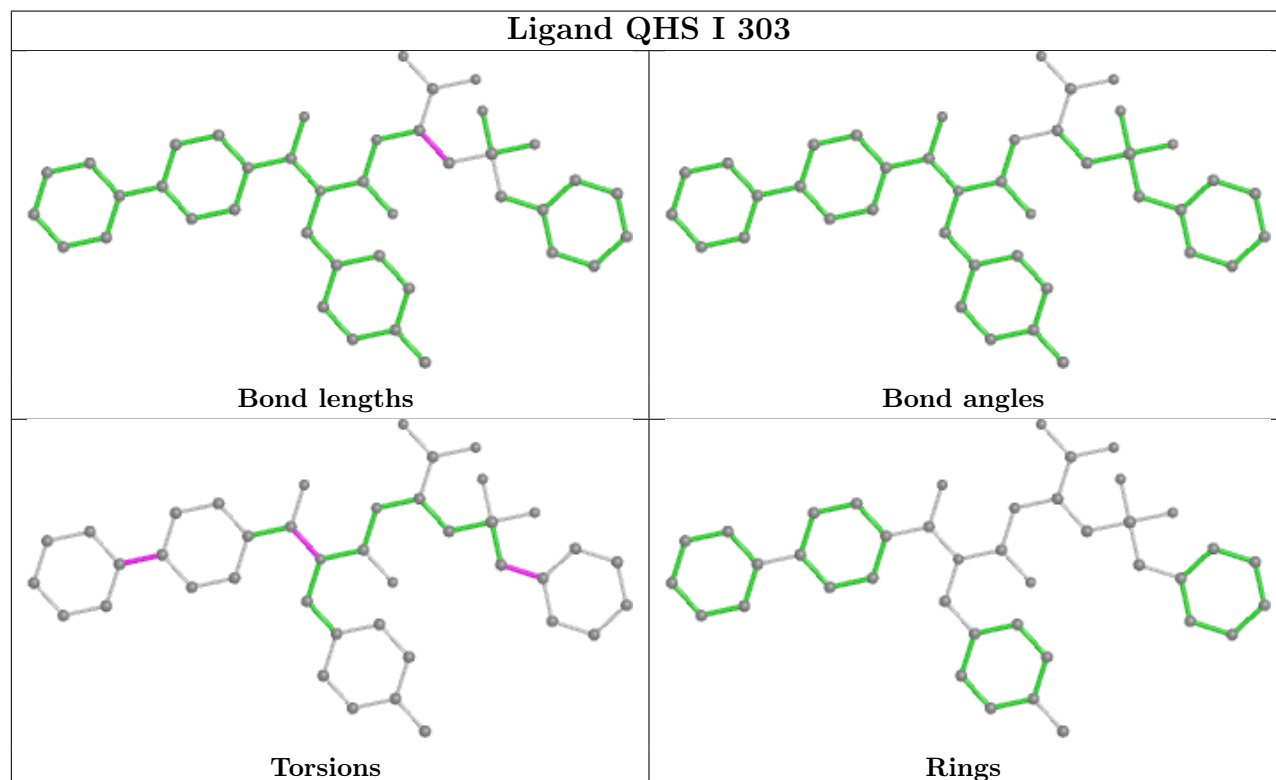
Ligand QHS E 303



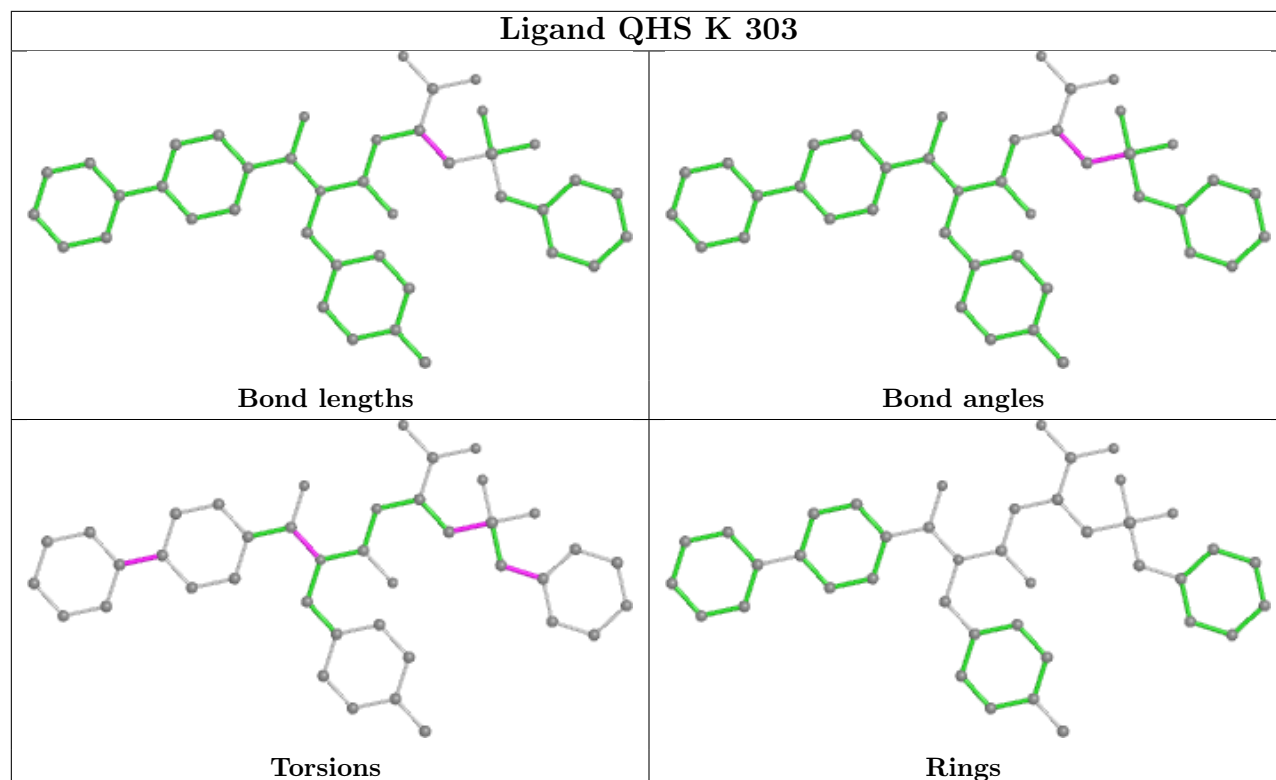
Ligand QHS G 302



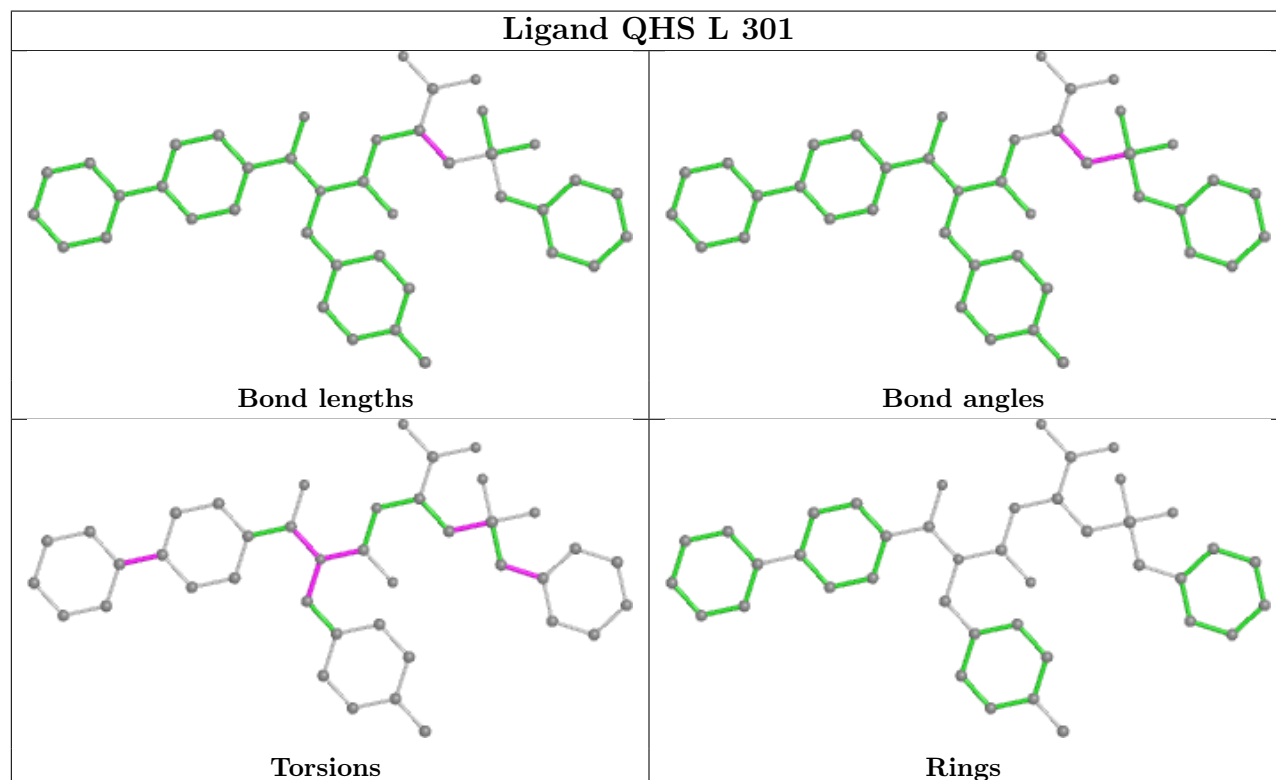
Ligand QHS I 303



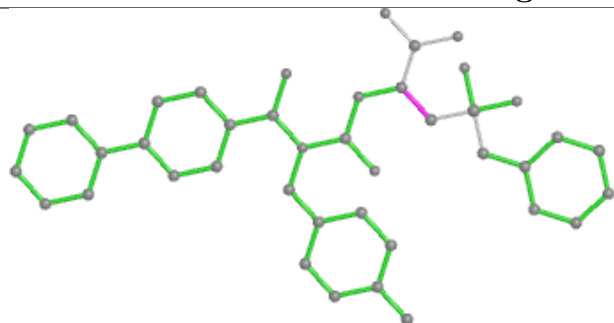
Ligand QHS K 303



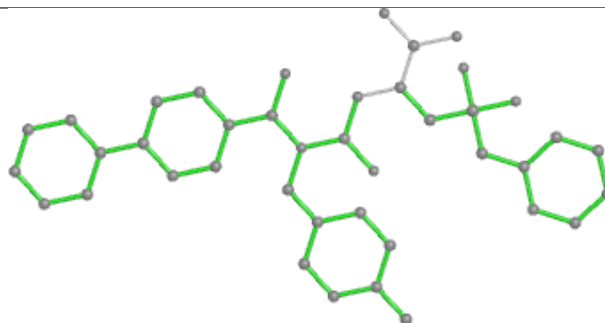
Ligand QHS L 301



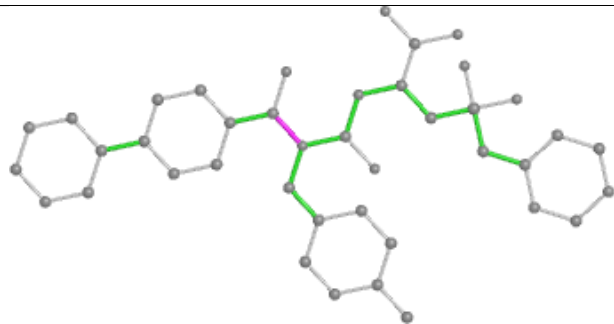
Ligand QHS F 303



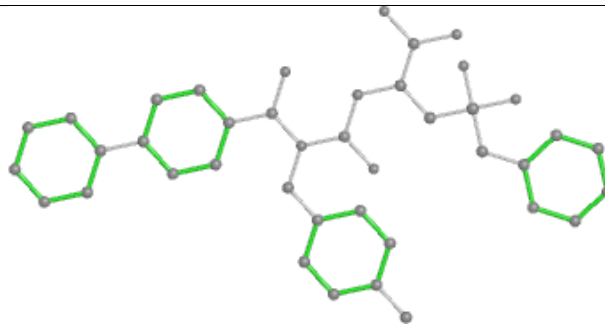
Bond lengths



Bond angles

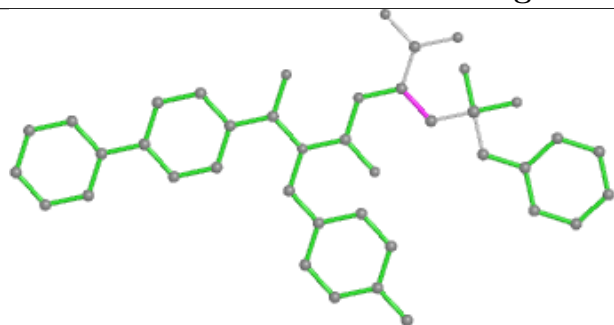


Torsions

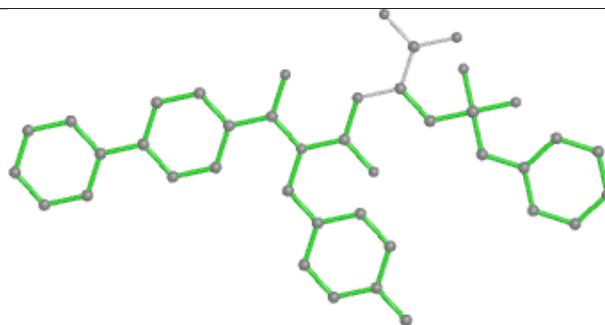


Rings

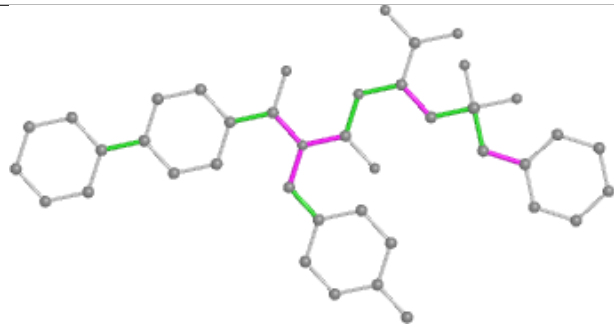
Ligand QHS C 305



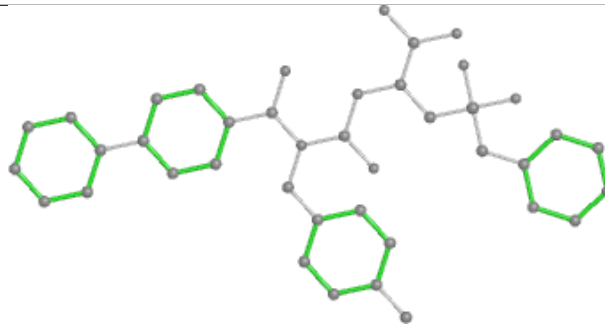
Bond lengths



Bond angles

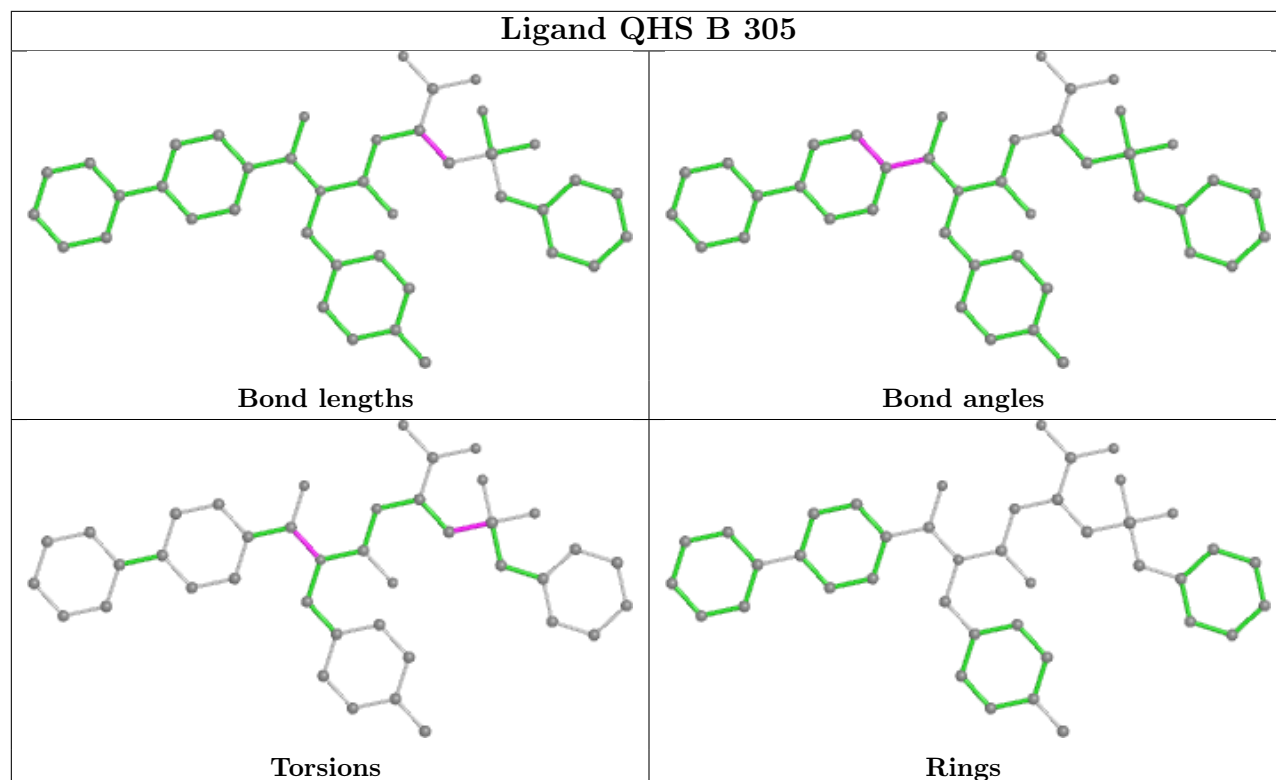


Torsions

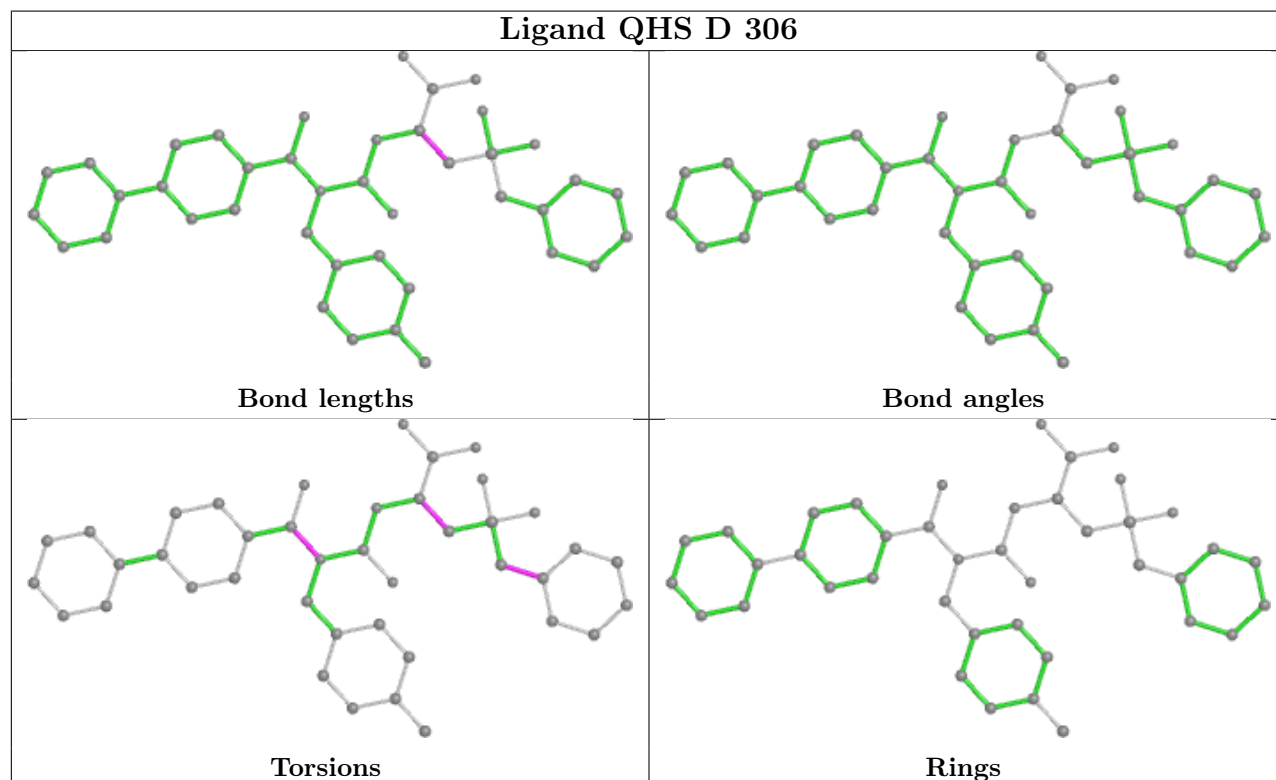


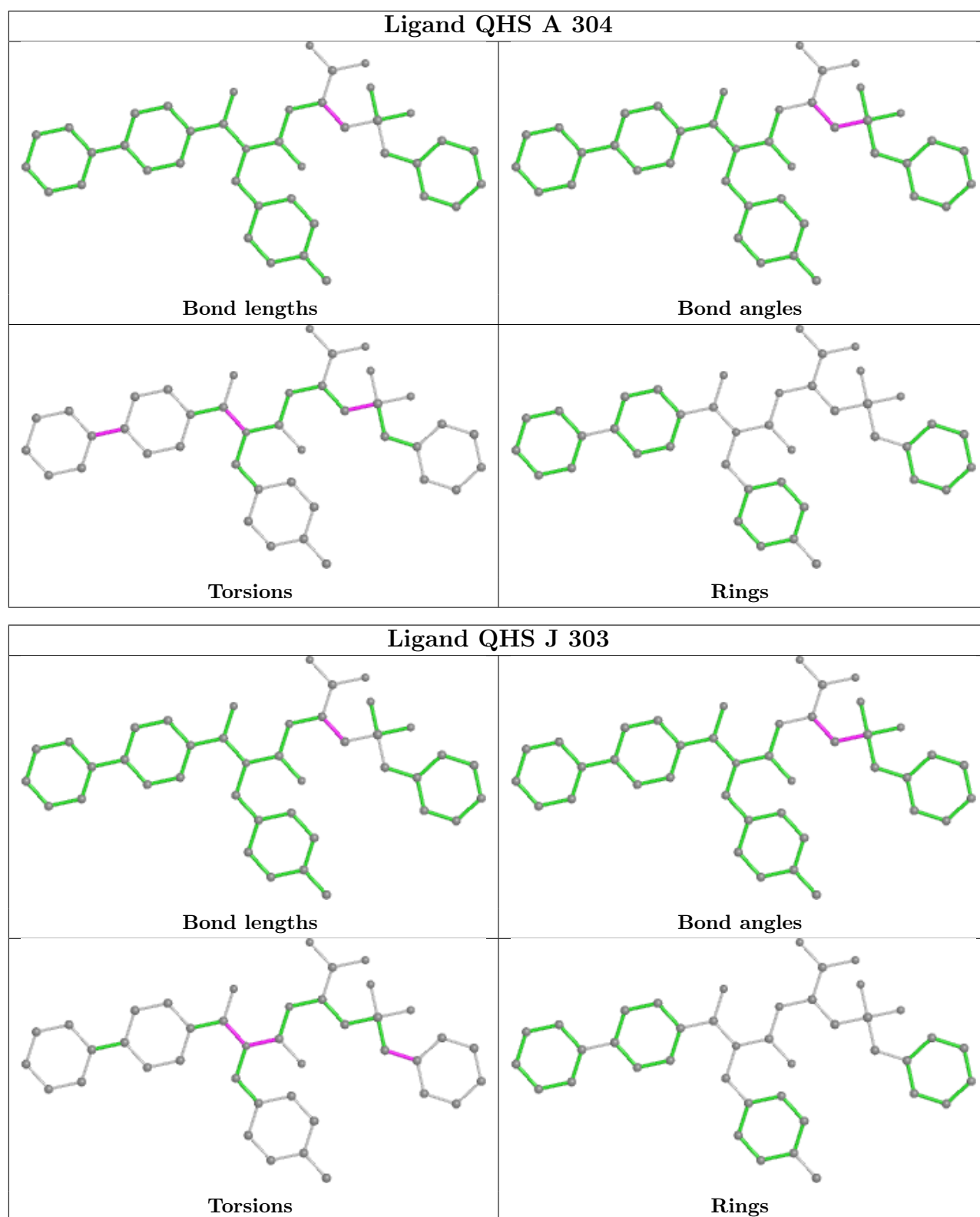
Rings

Ligand QHS B 305



Ligand QHS D 306





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	145/158 (91%)	0.22	3 (2%) 63 65	34, 60, 90, 96	0
1	B	144/158 (91%)	0.07	2 (1%) 75 76	33, 45, 76, 88	0
1	C	142/158 (89%)	0.30	5 (3%) 44 43	36, 70, 105, 114	0
1	D	144/158 (91%)	0.21	3 (2%) 63 65	36, 52, 93, 108	0
1	E	139/158 (87%)	1.25	33 (23%) 0 0	39, 93, 127, 148	0
1	F	140/158 (88%)	0.21	1 (0%) 87 87	37, 57, 89, 118	0
1	G	139/158 (87%)	0.60	13 (9%) 8 8	42, 86, 126, 141	0
1	H	142/158 (89%)	0.24	6 (4%) 36 35	43, 69, 106, 119	0
1	I	138/158 (87%)	0.40	9 (6%) 18 18	43, 70, 113, 125	0
1	J	144/158 (91%)	0.67	17 (11%) 4 3	50, 82, 129, 137	0
1	K	147/158 (93%)	0.86	23 (15%) 2 1	44, 85, 127, 146	0
1	L	140/158 (88%)	0.92	25 (17%) 1 1	57, 91, 121, 135	0
All	All	1704/1896 (89%)	0.49	140 (8%) 11 11	33, 70, 118, 148	0

All (140) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	114	ILE	10.7
1	E	130	LEU	8.9
1	E	105	PHE	7.3
1	K	115	THR	7.2
1	G	105	PHE	6.5
1	J	110	SER	6.1
1	E	107	ASP	5.6
1	E	173	TYR	5.5
1	E	134	GLY	5.5
1	K	113	HIS	5.4
1	J	105	PHE	5.1

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Mol	Chain	Res	Type	RSRZ
1	E	108	LEU	4.8
1	K	162	LEU	4.8
1	I	105	PHE	4.8
1	J	108	LEU	4.6
1	L	187	GLY	4.6
1	K	108	LEU	4.6
1	C	114	ILE	4.5
1	E	186	GLY	4.5
1	E	97	PHE	4.4
1	B	-3	LEU	4.4
1	E	135	VAL	4.3
1	L	182	ILE	4.2
1	G	123	PHE	4.2
1	L	188	TRP	4.1
1	K	123	PHE	4.1
1	G	108	LEU	4.1
1	K	161	VAL	4.1
1	L	135	VAL	4.0
1	I	108	LEU	4.0
1	K	112	LEU	4.0
1	E	104	ALA	3.9
1	L	161	VAL	3.9
1	K	104	ALA	3.9
1	I	112	LEU	3.9
1	H	1	MET	3.9
1	C	194	LEU	3.8
1	L	175	ASN	3.8
1	E	132	ARG	3.7
1	I	114	ILE	3.7
1	J	103	ARG	3.7
1	G	114	ILE	3.7
1	E	125	GLN	3.7
1	K	125	GLN	3.6
1	H	114	ILE	3.6
1	E	114	ILE	3.5
1	L	181	TRP	3.5
1	L	173	TYR	3.4
1	E	128	ASN	3.4
1	J	190	THR	3.4
1	E	123	PHE	3.4
1	L	128	ASN	3.4
1	E	109	THR	3.3

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Mol	Chain	Res	Type	RSRZ
1	L	136	ASN	3.3
1	D	-3	LEU	3.3
1	E	127	VAL	3.3
1	E	136	ASN	3.3
1	L	194	LEU	3.3
1	K	158	GLU	3.3
1	J	114	ILE	3.2
1	E	180	PRO	3.2
1	H	-1	SER	3.2
1	L	186	GLY	3.2
1	E	177	HIS	3.2
1	A	134	GLY	3.2
1	J	107	ASP	3.2
1	K	154	SER	3.1
1	L	130	LEU	3.1
1	E	121	GLN	3.1
1	E	133	ASP	3.1
1	L	118	THR	3.1
1	G	194	LEU	3.1
1	H	194	LEU	3.0
1	J	194	LEU	3.0
1	H	-2	GLY	3.0
1	G	181	TRP	3.0
1	G	135	VAL	3.0
1	L	22	TYR	2.9
1	K	107	ASP	2.9
1	E	131	PHE	2.9
1	G	161	VAL	2.9
1	L	140	ILE	2.8
1	K	105	PHE	2.8
1	I	161	VAL	2.8
1	L	184	GLU	2.7
1	K	110	SER	2.7
1	J	109	THR	2.7
1	F	3	GLN	2.7
1	G	184	GLU	2.6
1	E	146	PHE	2.6
1	L	190	THR	2.6
1	I	101	TYR	2.6
1	J	112	LEU	2.6
1	J	104	ALA	2.6
1	C	186	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	E	155	VAL	2.6
1	K	152	VAL	2.5
1	G	125	GLN	2.5
1	L	137	TRP	2.5
1	L	159	MET	2.5
1	J	121	GLN	2.5
1	L	129	GLU	2.5
1	L	105	PHE	2.5
1	J	162	LEU	2.5
1	K	130	LEU	2.5
1	E	137	TRP	2.5
1	E	101	TYR	2.4
1	H	3	GLN	2.4
1	I	134	GLY	2.4
1	D	194	LEU	2.4
1	B	1	MET	2.4
1	K	159	MET	2.4
1	J	161	VAL	2.4
1	K	126	VAL	2.4
1	C	-2	GLY	2.3
1	G	185	ASN	2.3
1	L	113	HIS	2.3
1	G	129	GLU	2.3
1	L	119	ALA	2.3
1	E	143	PHE	2.3
1	J	193	GLU	2.3
1	K	119	ALA	2.3
1	L	104	ALA	2.3
1	J	136	ASN	2.2
1	K	117	GLY	2.2
1	I	22	TYR	2.2
1	E	129	GLU	2.2
1	E	176	ASP	2.2
1	K	200	ALA	2.2
1	I	132	ARG	2.1
1	C	132	ARG	2.1
1	J	146	PHE	2.1
1	E	103	ARG	2.1
1	D	-4	PRO	2.1
1	E	140	ILE	2.1
1	G	160	GLN	2.1
1	A	178	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	175	ASN	2.1
1	E	116	PRO	2.0
1	K	111	GLN	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	SO4	D	303	5/5	0.51	0.28	181,181,182,182	0
2	SO4	F	302	5/5	0.64	0.21	127,127,130,130	0
3	EDO	A	303	4/4	0.67	0.36	57,60,63,63	0
2	SO4	F	301	5/5	0.69	0.16	152,152,153,153	0
2	SO4	K	302	5/5	0.70	0.23	138,138,139,140	0
2	SO4	E	301	5/5	0.76	0.31	156,156,157,157	0
2	SO4	A	302	5/5	0.79	0.16	124,126,127,127	0
2	SO4	D	302	5/5	0.79	0.33	146,147,148,148	0
4	QHS	L	301	41/41	0.81	0.37	112,126,147,148	0
4	QHS	E	303	41/41	0.82	0.39	87,111,117,121	0
2	SO4	B	303	5/5	0.83	0.20	113,114,119,121	0
4	QHS	J	303	41/41	0.83	0.30	92,112,123,126	0
3	EDO	J	302	4/4	0.83	0.20	53,56,56,58	0
2	SO4	I	302	5/5	0.84	0.19	155,155,155,156	0
2	SO4	J	301	5/5	0.84	0.21	151,151,151,152	0
2	SO4	B	302	5/5	0.86	0.13	120,122,122,123	0
2	SO4	H	301	5/5	0.87	0.12	139,140,140,141	0
3	EDO	C	304	4/4	0.87	0.25	53,57,60,61	0
2	SO4	C	303	5/5	0.88	0.25	139,141,142,143	0
3	EDO	D	305	4/4	0.88	0.12	55,57,61,65	0

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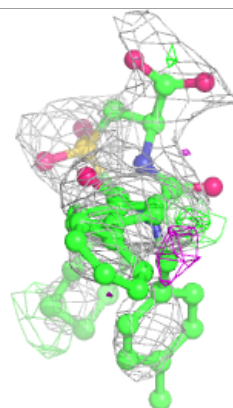
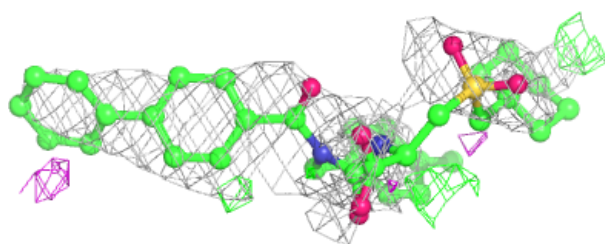
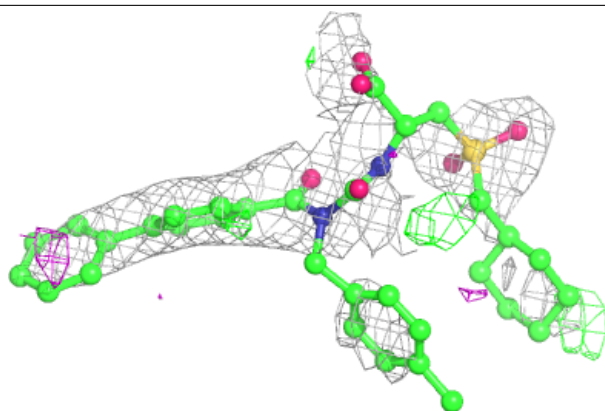
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	SO4	A	301	5/5	0.89	0.23	119,120,121,123	0
3	EDO	D	304	4/4	0.90	0.16	61,61,64,70	0
2	SO4	C	302	5/5	0.90	0.12	118,121,123,124	0
4	QHS	G	302	41/41	0.91	0.31	88,97,118,120	0
2	SO4	K	301	5/5	0.91	0.21	135,136,138,138	0
4	QHS	K	303	41/41	0.91	0.20	67,91,100,102	0
2	SO4	C	301	5/5	0.91	0.17	129,130,130,131	0
4	QHS	I	303	41/41	0.92	0.24	54,72,96,100	0
2	SO4	B	301	5/5	0.93	0.18	115,115,119,119	0
4	QHS	A	304	41/41	0.93	0.27	50,70,88,97	0
2	SO4	G	301	5/5	0.94	0.14	122,123,124,124	0
3	EDO	B	304	4/4	0.95	0.36	63,64,64,65	0
3	EDO	H	302	4/4	0.95	0.25	69,70,70,71	0
2	SO4	E	302	5/5	0.95	0.19	128,129,130,130	0
2	SO4	D	301	5/5	0.95	0.12	117,118,119,120	0
4	QHS	C	305	41/41	0.95	0.21	64,73,94,100	0
4	QHS	D	306	41/41	0.95	0.17	44,63,82,85	0
4	QHS	F	303	41/41	0.96	0.13	42,48,67,71	0
4	QHS	H	303	41/41	0.96	0.12	44,55,77,82	0
2	SO4	I	301	5/5	0.97	0.11	110,111,112,112	0
4	QHS	B	305	41/41	0.97	0.12	33,50,62,66	0

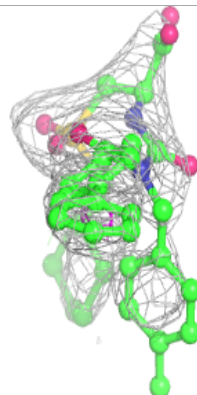
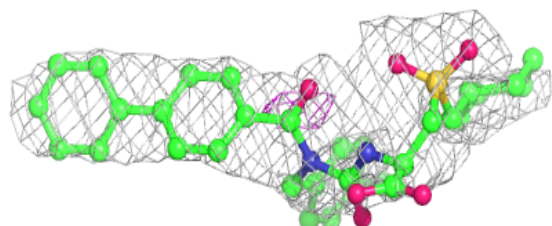
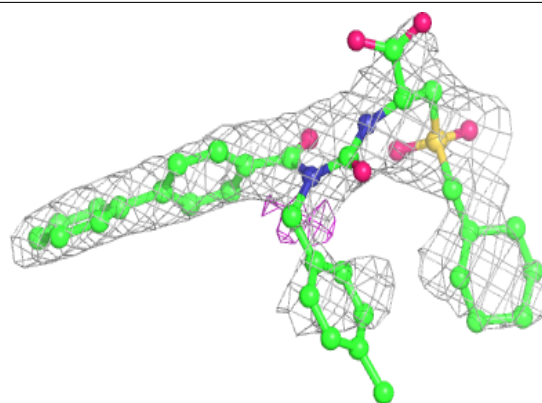
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around QHS L 301:

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

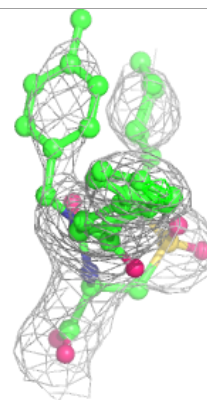
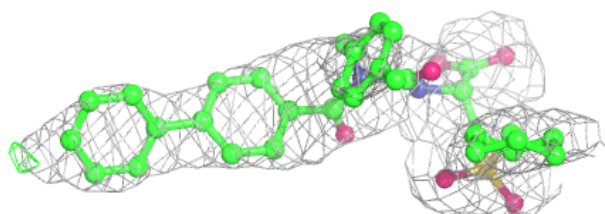
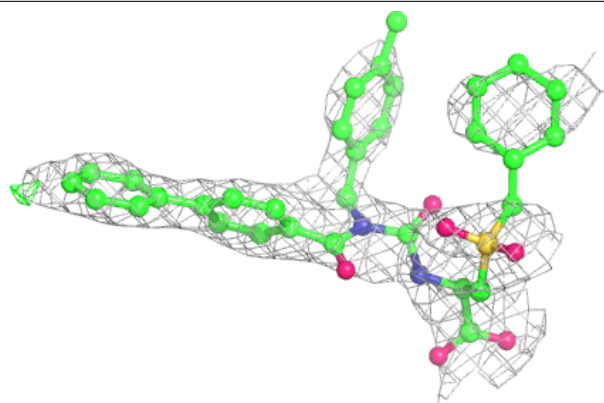
**Electron density around QHS E 303:**

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

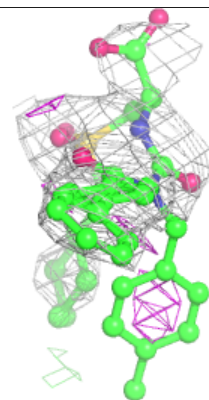
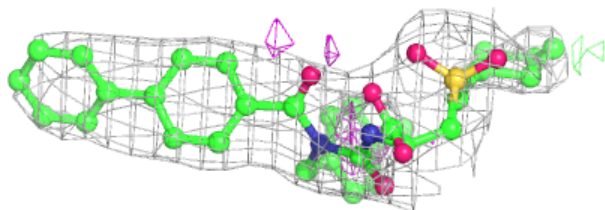
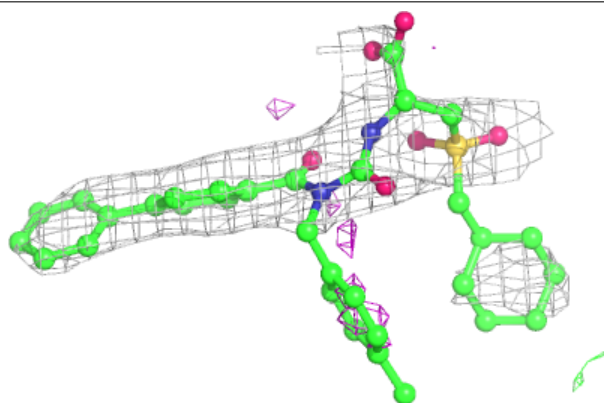


Electron density around QHS J 303:

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

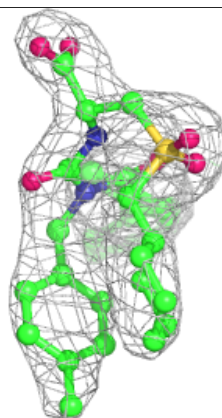
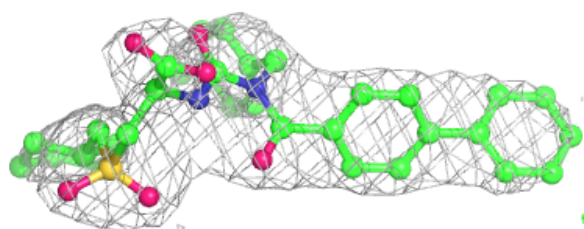
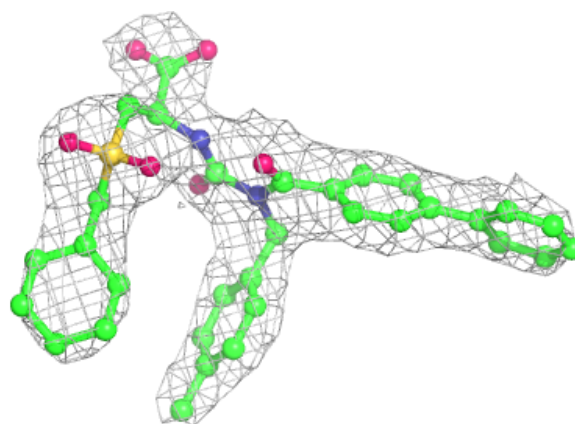
**Electron density around QHS G 302:**

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

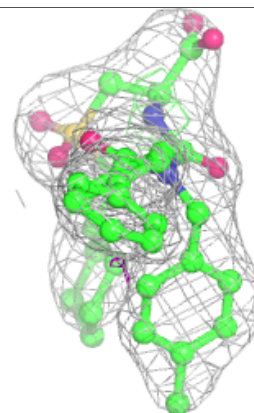
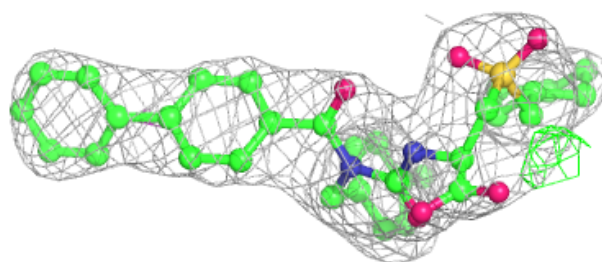
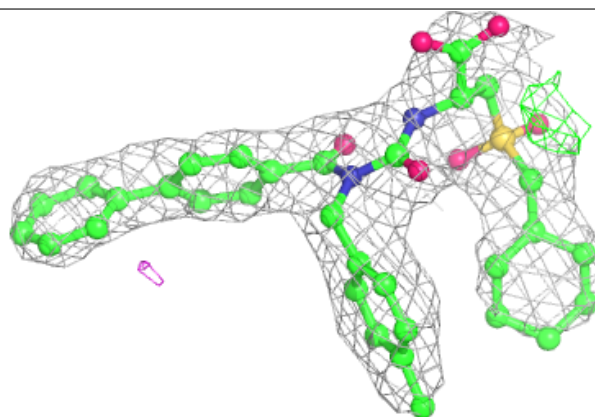


Electron density around QHS K 303:

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

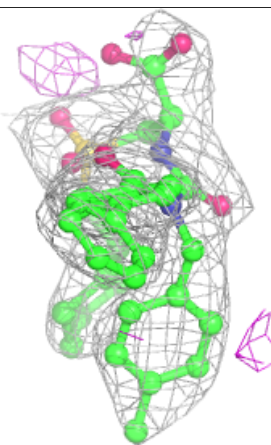
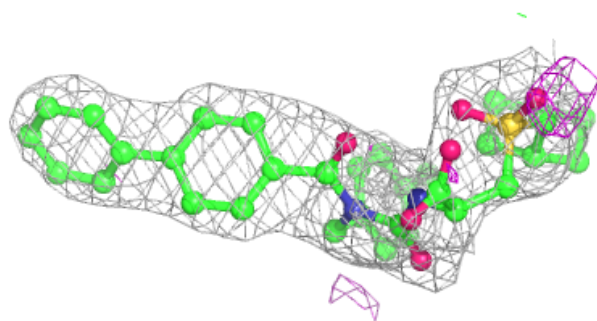
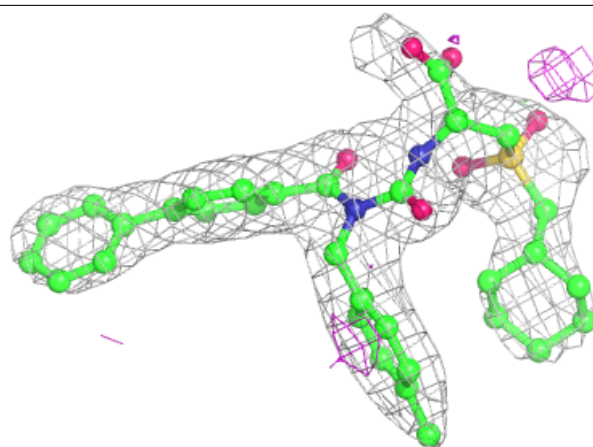
**Electron density around QHS I 303:**

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

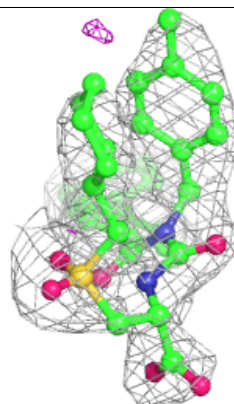
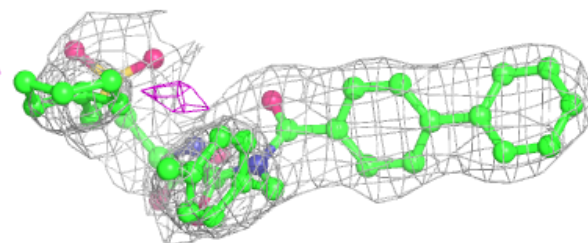
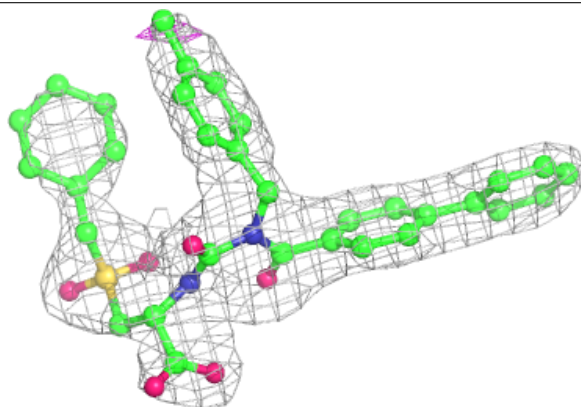


Electron density around QHS A 304:

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

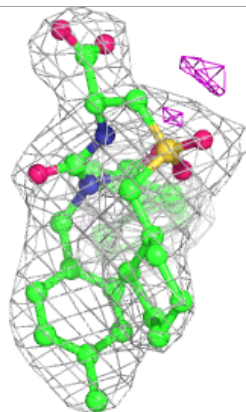
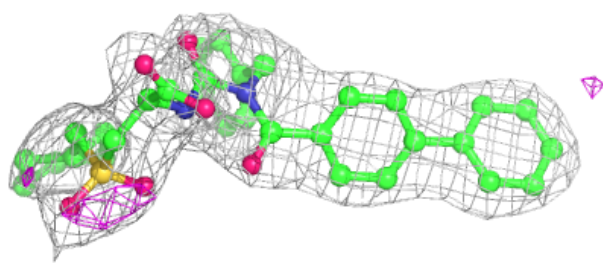
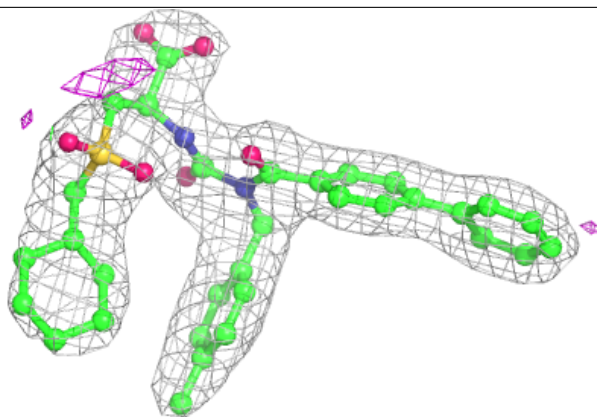
**Electron density around QHS C 305:**

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

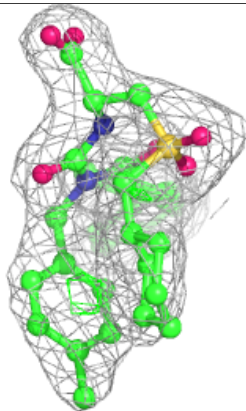
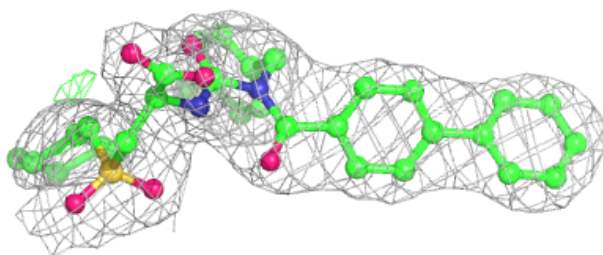
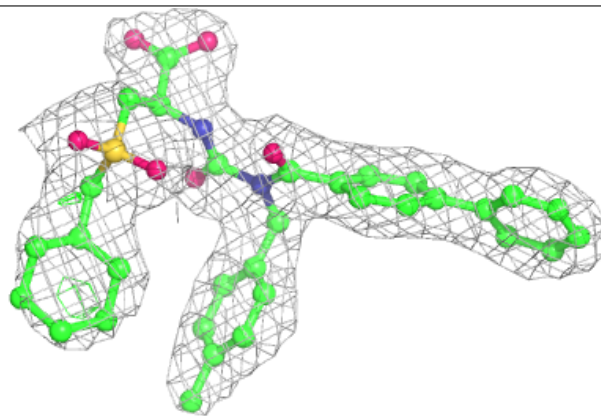


Electron density around QHS D 306:

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

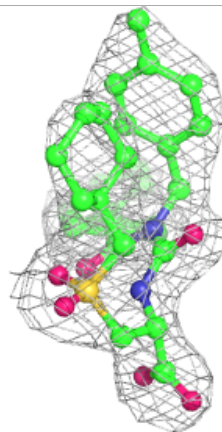
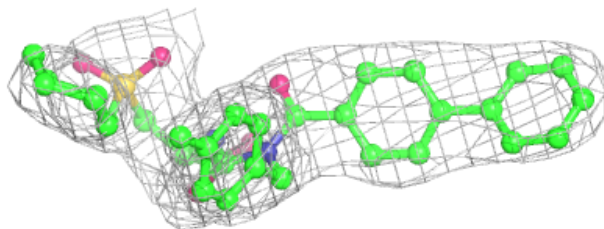
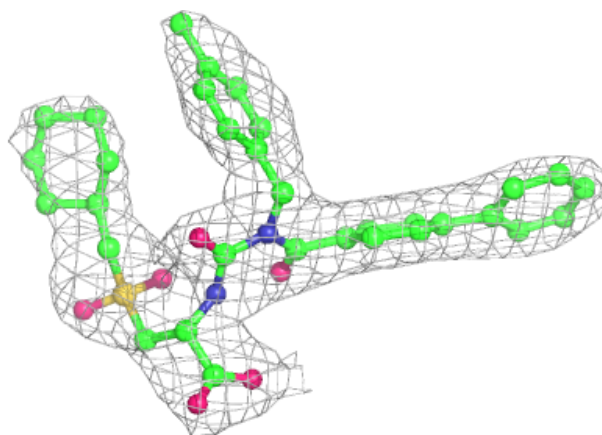
**Electron density around QHS F 303:**

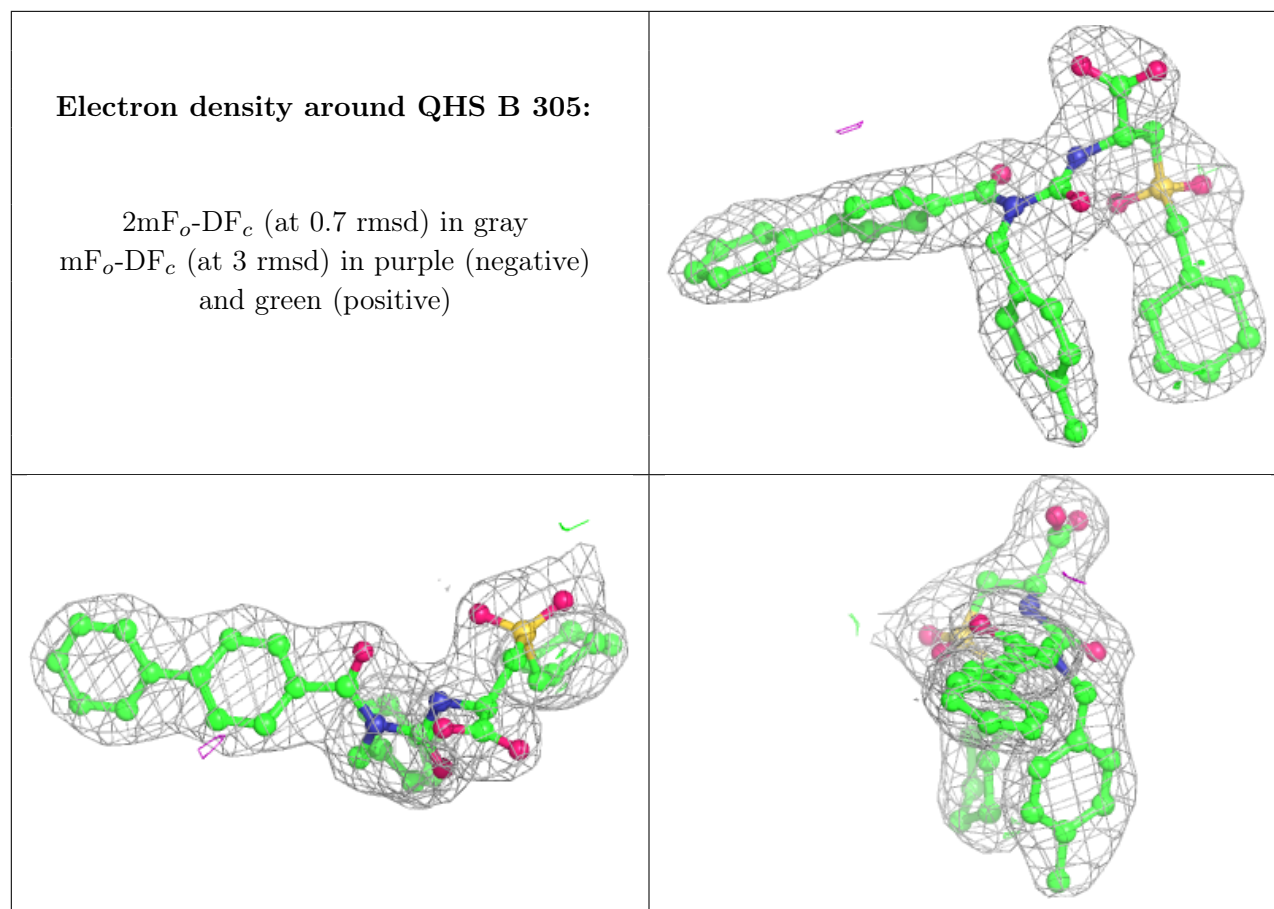
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around QHS H 303:

$2mF_o-DF_c$ (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.