



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 11:46 AM UTC

PDB ID : 7NDV / pdb\_00007ndv  
Title : X-ray structure of acetylcholine-binding protein (AChBP) in complex with FL001888.  
Authors : Cederfelt, D.; Boronat, P.; Dobritsch, D.; Hennig, S.; Fitzgerald, E.A.; de Esch, I.J.P.; Danielson, U.H.  
Deposited on : 2021-02-02  
Resolution : 1.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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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)  
Xtrriage (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

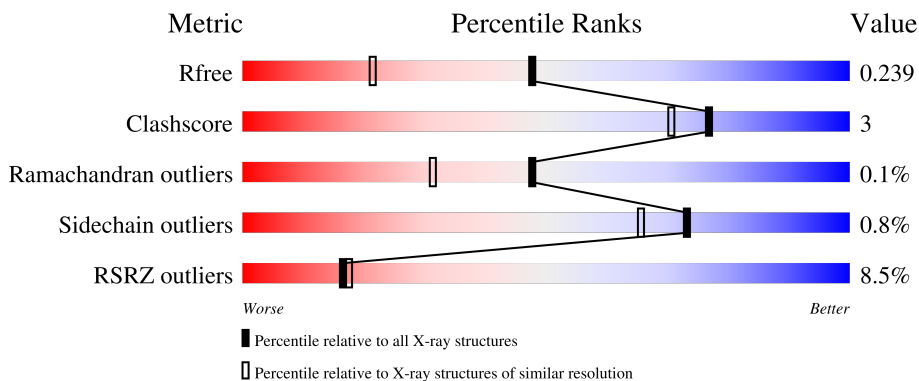
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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.



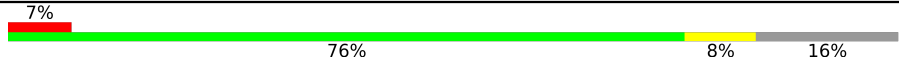
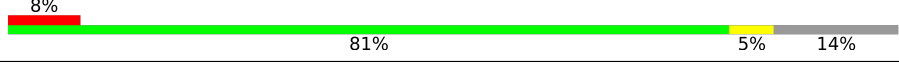



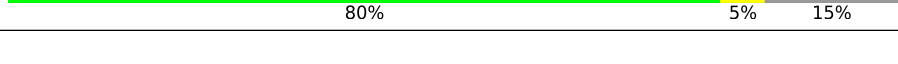
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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  $\geq 3$ , 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	237	 5% 79% 5% 15%
1	B	237	 16% 81% 5% 14%
1	C	237	 9% 78% 6% 15%
1	D	237	 6% 81% 5% 14%

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Mol	Chain	Length	Quality of chain
1	E	237	
1	F	237	
1	G	237	
1	H	237	
1	I	237	
1	J	237	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 17801 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Acetylcholine-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	202	Total 1631	C 1024	N 279	O 323	S 5	0	4	0
1	B	205	Total 1644	C 1031	N 282	O 326	S 5	0	1	0
1	C	201	Total 1606	C 1007	N 275	O 319	S 5	0	0	0
1	D	203	Total 1630	C 1021	N 280	O 324	S 5	0	2	0
1	E	200	Total 1618	C 1015	N 280	O 318	S 5	0	2	0
1	F	204	Total 1639	C 1027	N 279	O 328	S 5	0	2	0
1	G	210	Total 1703	C 1068	N 292	O 338	S 5	0	5	0
1	H	212	Total 1705	C 1068	N 290	O 342	S 5	0	4	0
1	I	203	Total 1645	C 1033	N 284	O 323	S 5	0	4	0
1	J	201	Total 1613	C 1013	N 275	O 320	S 5	0	1	0

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	230	GLY	-	expression tag	UNP P58154
A	231	SER	-	expression tag	UNP P58154
A	232	HIS	-	expression tag	UNP P58154
A	233	HIS	-	expression tag	UNP P58154
A	234	HIS	-	expression tag	UNP P58154
A	235	HIS	-	expression tag	UNP P58154
A	236	HIS	-	expression tag	UNP P58154
A	237	HIS	-	expression tag	UNP P58154
B	230	GLY	-	expression tag	UNP P58154

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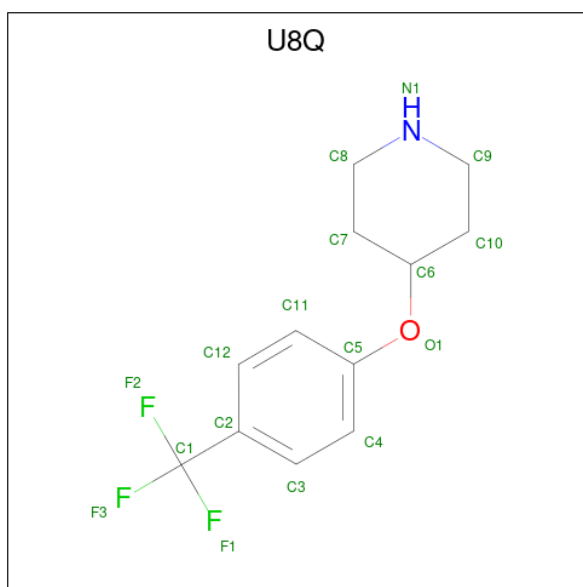
Chain	Residue	Modelled	Actual	Comment	Reference
B	231	SER	-	expression tag	UNP P58154
B	232	HIS	-	expression tag	UNP P58154
B	233	HIS	-	expression tag	UNP P58154
B	234	HIS	-	expression tag	UNP P58154
B	235	HIS	-	expression tag	UNP P58154
B	236	HIS	-	expression tag	UNP P58154
B	237	HIS	-	expression tag	UNP P58154
C	230	GLY	-	expression tag	UNP P58154
C	231	SER	-	expression tag	UNP P58154
C	232	HIS	-	expression tag	UNP P58154
C	233	HIS	-	expression tag	UNP P58154
C	234	HIS	-	expression tag	UNP P58154
C	235	HIS	-	expression tag	UNP P58154
C	236	HIS	-	expression tag	UNP P58154
C	237	HIS	-	expression tag	UNP P58154
D	230	GLY	-	expression tag	UNP P58154
D	231	SER	-	expression tag	UNP P58154
D	232	HIS	-	expression tag	UNP P58154
D	233	HIS	-	expression tag	UNP P58154
D	234	HIS	-	expression tag	UNP P58154
D	235	HIS	-	expression tag	UNP P58154
D	236	HIS	-	expression tag	UNP P58154
D	237	HIS	-	expression tag	UNP P58154
E	230	GLY	-	expression tag	UNP P58154
E	231	SER	-	expression tag	UNP P58154
E	232	HIS	-	expression tag	UNP P58154
E	233	HIS	-	expression tag	UNP P58154
E	234	HIS	-	expression tag	UNP P58154
E	235	HIS	-	expression tag	UNP P58154
E	236	HIS	-	expression tag	UNP P58154
E	237	HIS	-	expression tag	UNP P58154
F	230	GLY	-	expression tag	UNP P58154
F	231	SER	-	expression tag	UNP P58154
F	232	HIS	-	expression tag	UNP P58154
F	233	HIS	-	expression tag	UNP P58154
F	234	HIS	-	expression tag	UNP P58154
F	235	HIS	-	expression tag	UNP P58154
F	236	HIS	-	expression tag	UNP P58154
F	237	HIS	-	expression tag	UNP P58154
G	230	GLY	-	expression tag	UNP P58154
G	231	SER	-	expression tag	UNP P58154
G	232	HIS	-	expression tag	UNP P58154

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Chain	Residue	Modelled	Actual	Comment	Reference
G	233	HIS	-	expression tag	UNP P58154
G	234	HIS	-	expression tag	UNP P58154
G	235	HIS	-	expression tag	UNP P58154
G	236	HIS	-	expression tag	UNP P58154
G	237	HIS	-	expression tag	UNP P58154
H	230	GLY	-	expression tag	UNP P58154
H	231	SER	-	expression tag	UNP P58154
H	232	HIS	-	expression tag	UNP P58154
H	233	HIS	-	expression tag	UNP P58154
H	234	HIS	-	expression tag	UNP P58154
H	235	HIS	-	expression tag	UNP P58154
H	236	HIS	-	expression tag	UNP P58154
H	237	HIS	-	expression tag	UNP P58154
I	230	GLY	-	expression tag	UNP P58154
I	231	SER	-	expression tag	UNP P58154
I	232	HIS	-	expression tag	UNP P58154
I	233	HIS	-	expression tag	UNP P58154
I	234	HIS	-	expression tag	UNP P58154
I	235	HIS	-	expression tag	UNP P58154
I	236	HIS	-	expression tag	UNP P58154
I	237	HIS	-	expression tag	UNP P58154
J	230	GLY	-	expression tag	UNP P58154
J	231	SER	-	expression tag	UNP P58154
J	232	HIS	-	expression tag	UNP P58154
J	233	HIS	-	expression tag	UNP P58154
J	234	HIS	-	expression tag	UNP P58154
J	235	HIS	-	expression tag	UNP P58154
J	236	HIS	-	expression tag	UNP P58154
J	237	HIS	-	expression tag	UNP P58154

- Molecule 2 is 4-[4-(trifluoromethyl)phenoxy]piperidine (CCD ID: U8Q) (formula: C<sub>12</sub>H<sub>14</sub>F<sub>3</sub>NO) (labeled as "Ligand of Interest" by depositor).



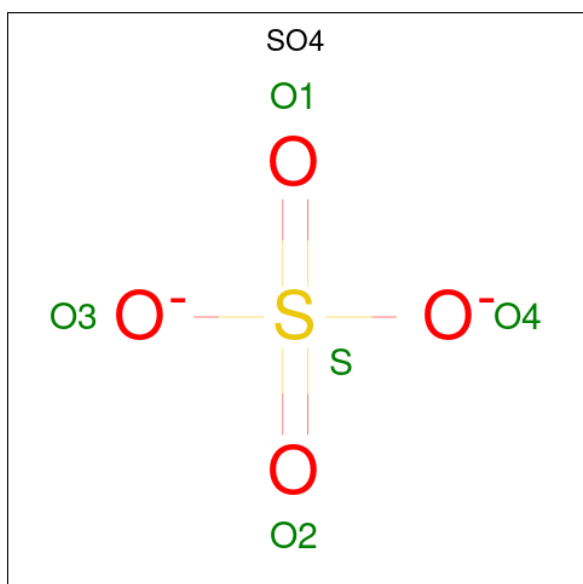
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	F	N	O		
2	A	1	Total	C	F	N	O	0	0
			17	12	3	1	1		
2	C	1	Total	C	F	N	O	0	0
			17	12	3	1	1		
2	D	1	Total	C	F	N	O	0	0
			17	12	3	1	1		
2	E	1	Total	C	F	N	O	0	0
			17	12	3	1	1		
2	F	1	Total	C	F	N	O	0	0
			17	12	3	1	1		
2	F	1	Total	C	F	N	O	0	0
			17	12	3	1	1		
2	G	1	Total	C	F	N	O	0	0
			17	12	3	1	1		
2	H	1	Total	C	F	N	O	0	0
			17	12	3	1	1		
2	I	1	Total	C	F	N	O	0	0
			17	12	3	1	1		

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	1	Total O S 5 4 1	0	0
4	G	1	Total O S 5 4 1	0	0
4	H	1	Total O S 5 4 1	0	0
4	J	1	Total O S 5 4 1	0	0

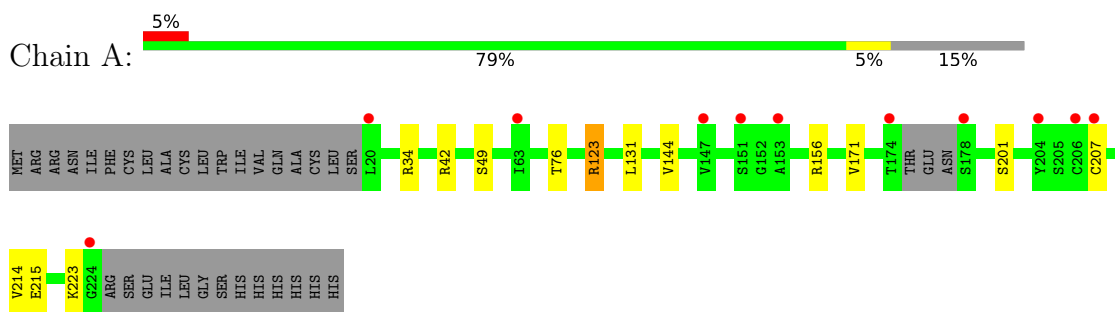
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	94	Total O 94 94	0	0
5	B	79	Total O 79 79	0	0
5	C	72	Total O 73 73	0	1
5	D	97	Total O 99 99	0	2
5	E	96	Total O 96 96	0	0
5	F	131	Total O 131 131	0	0
5	G	144	Total O 146 146	0	2
5	H	169	Total O 170 170	0	1
5	I	122	Total O 124 124	0	2
5	J	111	Total O 112 112	0	1

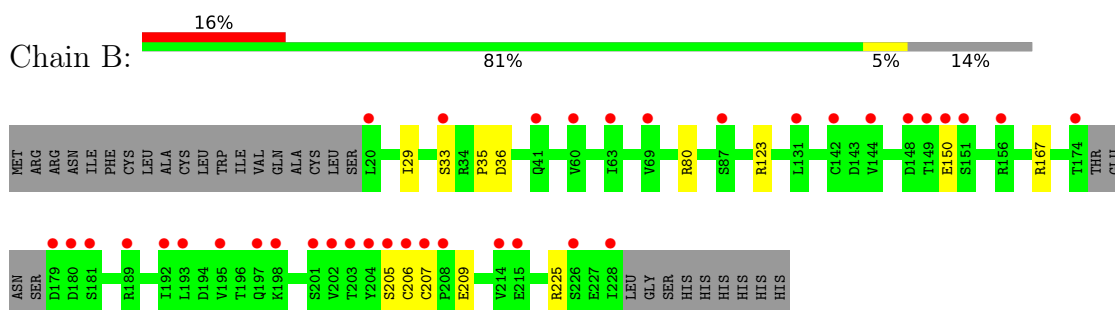
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

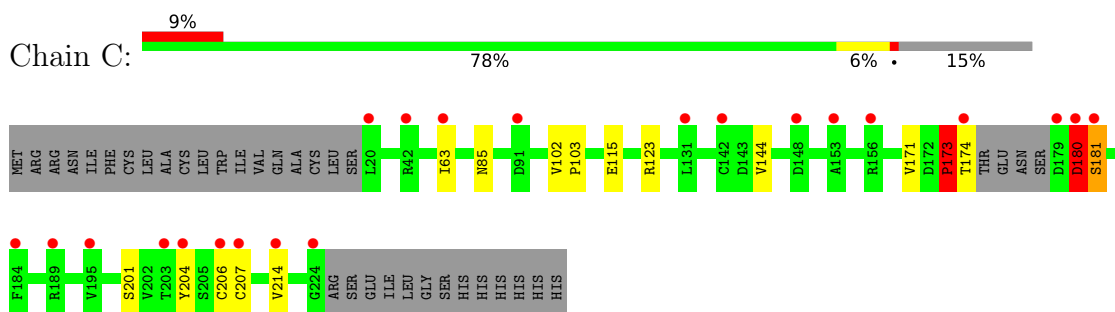
- Molecule 1: Acetylcholine-binding protein



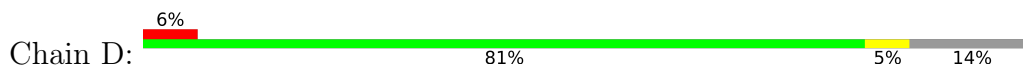
- Molecule 1: Acetylcholine-binding protein

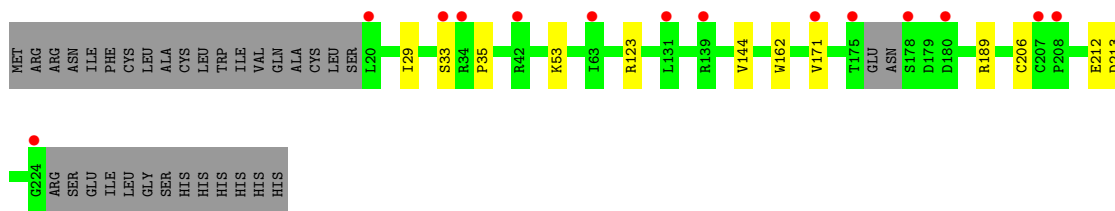


- Molecule 1: Acetylcholine-binding protein

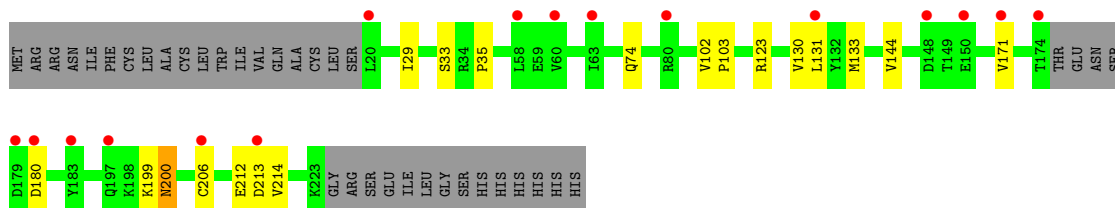
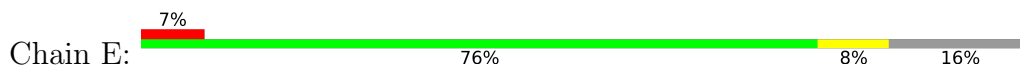


- Molecule 1: Acetylcholine-binding protein

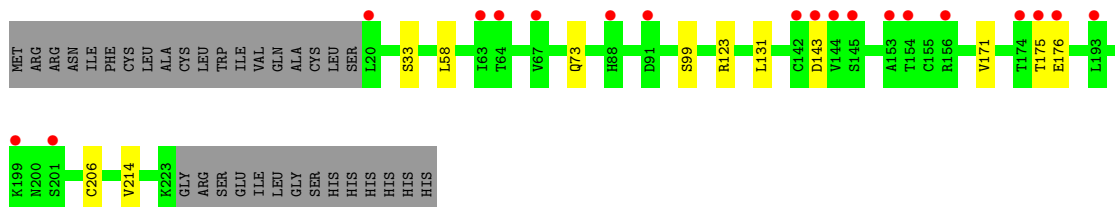
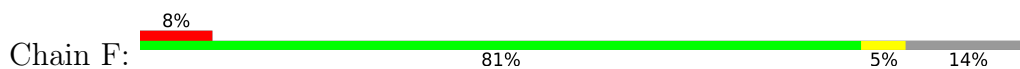




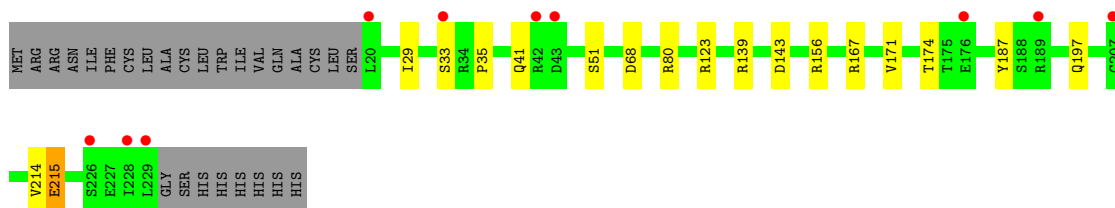
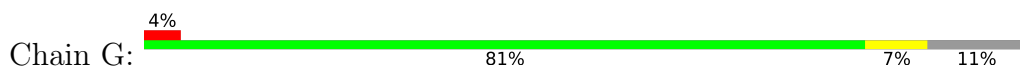
- Molecule 1: Acetylcholine-binding protein



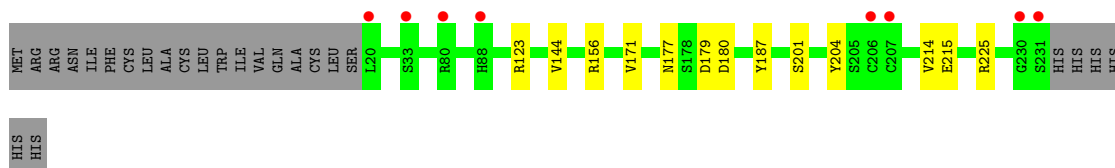
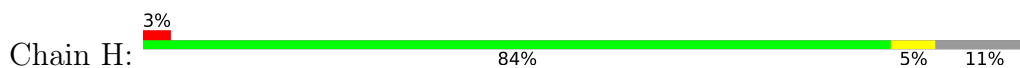
- Molecule 1: Acetylcholine-binding protein



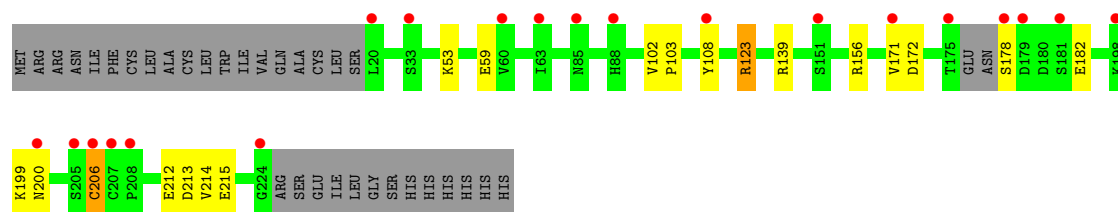
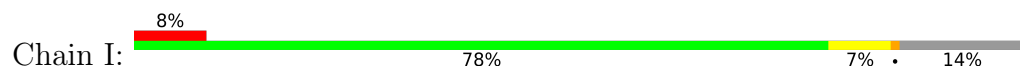
- Molecule 1: Acetylcholine-binding protein



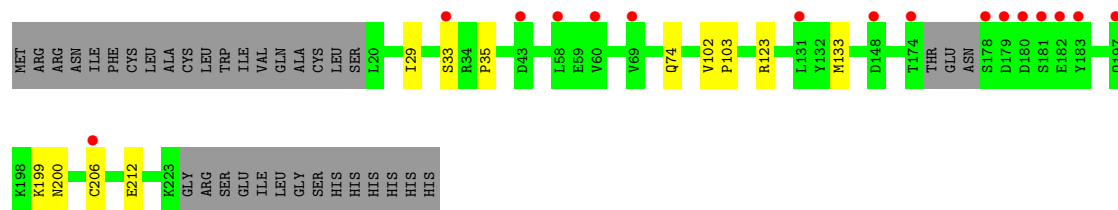
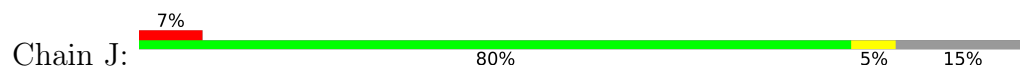
- Molecule 1: Acetylcholine-binding protein



- Molecule 1: Acetylcholine-binding protein



- Molecule 1: Acetylcholine-binding protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.68Å 121.27Å 239.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.27 – 1.70 48.27 – 1.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.27-1.70) 100.0 (48.27-1.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.17 (at 1.70Å)	Xtrriage
Refinement program	REFMAC 5.8.0238	Depositor
R, $R_{free}$	0.205 , 0.233 0.213 , 0.239	Depositor DCC
$R_{free}$ test set	12236 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.8	Xtrriage
Anisotropy	0.107	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 34.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	17801	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 35.19 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.0682e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: U8Q, SO4, NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.98	0/1678	1.15	1/2289 (0.0%)
1	B	0.98	0/1682	1.16	1/2293 (0.0%)
1	C	1.00	1/1641 (0.1%)	1.16	2/2238 (0.1%)
1	D	0.97	0/1671	1.14	0/2278
1	E	1.00	1/1659 (0.1%)	1.19	3/2261 (0.1%)
1	F	1.04	0/1681	1.21	1/2296 (0.0%)
1	G	1.03	0/1754	1.18	2/2393 (0.1%)
1	H	1.03	0/1753	1.22	3/2392 (0.1%)
1	I	0.99	0/1692	1.14	0/2306
1	J	1.02	0/1651	1.17	1/2252 (0.0%)
All	All	1.01	2/16862 (0.0%)	1.17	14/22998 (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	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	I	0	1
1	J	0	1
All	All	0	7

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	173	PRO	C-O	-5.55	1.16	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	200	ASN	C-O	-5.23	1.17	1.24

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	123	ARG	CG-CD-NE	-8.81	92.61	112.00
1	E	123	ARG	CG-CD-NE	-8.78	92.69	112.00
1	H	123	ARG	CG-CD-NE	-8.57	93.14	112.00
1	B	123	ARG	CG-CD-NE	-8.45	93.40	112.00
1	G	123	ARG	CG-CD-NE	-7.38	95.76	112.00

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	206	CYS	Peptide
1	C	206	CYS	Peptide
1	D	206	CYS	Peptide
1	E	206	CYS	Peptide
1	F	206	CYS	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1631	0	1591	12	0
1	B	1644	0	1596	6	0
1	C	1606	0	1552	10	1
1	D	1630	0	1583	9	0
1	E	1618	0	1576	11	0
1	F	1639	0	1588	6	0
1	G	1703	0	1668	15	0
1	H	1705	0	1660	6	0
1	I	1645	0	1613	13	0
1	J	1613	0	1566	10	0
2	A	17	0	0	0	0
2	C	17	0	0	1	0

*Continued on next page...*

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	17	0	0	1	0
2	E	17	0	0	0	0
2	F	34	0	0	0	0
2	G	17	0	0	0	0
2	H	17	0	0	0	0
2	I	17	0	0	4	0
3	A	14	0	13	0	0
3	B	14	0	13	0	0
3	C	14	0	13	1	0
3	F	14	0	13	0	0
3	H	14	0	13	1	1
4	D	5	0	0	0	0
4	G	5	0	0	1	0
4	H	5	0	0	0	0
4	J	5	0	0	0	0
5	A	94	0	0	3	0
5	B	79	0	0	1	0
5	C	73	0	0	2	0
5	D	99	0	0	0	0
5	E	96	0	0	0	0
5	F	131	0	0	2	0
5	G	146	0	0	2	0
5	H	170	0	0	0	0
5	I	124	0	0	1	0
5	J	112	0	0	0	0
All	All	17801	0	16058	94	1

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.

The worst 5 of 94 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:I:200:ASN:HB3	1:I:213:ASP:OD1	1.57	1.05
1:E:171:VAL:HG12	1:E:214:VAL:HG23	1.44	0.96
1:I:171:VAL:HG12	1:I:214:VAL:HG23	1.50	0.93
1:E:200:ASN:HB2	1:E:213:ASP:OD1	1.69	0.91
1:C:171:VAL:HG12	1:C:214:VAL:HG23	1.58	0.84

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:180:ASP:O	3:H:302:NAG:O3[4_455]	2.17	0.03

### 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	202/237 (85%)	200 (99%)	2 (1%)	0	100	100
1	B	202/237 (85%)	200 (99%)	2 (1%)	0	100	100
1	C	197/237 (83%)	194 (98%)	1 (0%)	2 (1%)	12	3
1	D	201/237 (85%)	200 (100%)	1 (0%)	0	100	100
1	E	198/237 (84%)	197 (100%)	1 (0%)	0	100	100
1	F	204/237 (86%)	200 (98%)	4 (2%)	0	100	100
1	G	213/237 (90%)	211 (99%)	2 (1%)	0	100	100
1	H	214/237 (90%)	211 (99%)	3 (1%)	0	100	100
1	I	203/237 (86%)	201 (99%)	2 (1%)	0	100	100
1	J	198/237 (84%)	197 (100%)	1 (0%)	0	100	100
All	All	2032/2370 (86%)	2011 (99%)	19 (1%)	2 (0%)	48	31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	181	SER
1	C	173	PRO

#### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	192/220 (87%)	187 (97%)	5 (3%)	40	23
1	B	192/220 (87%)	190 (99%)	2 (1%)	68	58
1	C	187/220 (85%)	183 (98%)	4 (2%)	47	30
1	D	191/220 (87%)	190 (100%)	1 (0%)	81	76
1	E	189/220 (86%)	189 (100%)	0	100	100
1	F	193/220 (88%)	192 (100%)	1 (0%)	81	76
1	G	201/220 (91%)	201 (100%)	0	100	100
1	H	201/220 (91%)	200 (100%)	1 (0%)	81	76
1	I	193/220 (88%)	192 (100%)	1 (0%)	81	76
1	J	189/220 (86%)	188 (100%)	1 (0%)	81	76
All	All	1928/2200 (88%)	1912 (99%)	16 (1%)	73	65

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	123	ARG
1	H	201	SER
1	C	180	ASP
1	F	131	LEU
1	C	123	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	120	GLN
1	J	200	ASN
1	F	41	GLN
1	G	41	GLN
1	G	88	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

18 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	U8Q	G	301	-	18,18,18	0.42	0	23,25,25	2.74	4 (17%)
3	NAG	B	301	1	14,14,15	0.67	0	17,19,21	1.62	2 (11%)
2	U8Q	I	301	-	18,18,18	0.37	0	23,25,25	0.84	1 (4%)
3	NAG	F	302	1	14,14,15	0.51	0	17,19,21	1.23	2 (11%)
4	SO4	G	302	-	4,4,4	0.25	0	6,6,6	0.20	0
2	U8Q	F	301	-	18,18,18	0.30	0	23,25,25	2.83	3 (13%)
4	SO4	J	301	-	4,4,4	0.28	0	6,6,6	0.08	0
3	NAG	A	302	1	14,14,15	0.69	0	17,19,21	1.33	2 (11%)
2	U8Q	A	301	-	18,18,18	0.36	0	23,25,25	0.87	1 (4%)
2	U8Q	C	301	-	18,18,18	0.35	0	23,25,25	0.78	1 (4%)
2	U8Q	D	301	-	18,18,18	0.47	0	23,25,25	0.89	1 (4%)
3	NAG	C	302	1	14,14,15	0.72	0	17,19,21	1.59	2 (11%)
2	U8Q	F	303	-	18,18,18	0.49	0	23,25,25	1.32	4 (17%)
2	U8Q	H	301	-	18,18,18	0.44	0	23,25,25	2.65	3 (13%)
2	U8Q	E	301	-	18,18,18	0.33	0	23,25,25	0.35	0
4	SO4	D	302	-	4,4,4	0.29	0	6,6,6	0.15	0
4	SO4	H	303	-	4,4,4	0.24	0	6,6,6	0.16	0
3	NAG	H	302	1	14,14,15	0.79	0	17,19,21	1.72	3 (17%)

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	U8Q	G	301	-	-	4/10/18/18	0/2/2/2
3	NAG	B	301	1	-	0/6/23/26	0/1/1/1
2	U8Q	I	301	-	-	0/10/18/18	1/2/2/2
3	NAG	F	302	1	-	0/6/23/26	0/1/1/1
2	U8Q	F	301	-	-	0/10/18/18	1/2/2/2
3	NAG	A	302	1	-	1/6/23/26	0/1/1/1
2	U8Q	A	301	-	-	2/10/18/18	0/2/2/2
2	U8Q	C	301	-	-	2/10/18/18	0/2/2/2
2	U8Q	D	301	-	-	1/10/18/18	1/2/2/2
3	NAG	C	302	1	-	0/6/23/26	0/1/1/1
2	U8Q	F	303	-	-	3/10/18/18	0/2/2/2
2	U8Q	H	301	-	-	2/10/18/18	1/2/2/2
2	U8Q	E	301	-	-	0/10/18/18	0/2/2/2
3	NAG	H	302	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	301	U8Q	C5-O1-C6	12.42	141.65	119.18
2	G	301	U8Q	C5-O1-C6	11.76	140.45	119.18
2	H	301	U8Q	C5-O1-C6	11.56	140.09	119.18
3	H	302	NAG	C1-O5-C5	5.25	119.23	112.19
3	C	302	NAG	C1-O5-C5	5.09	119.01	112.19

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	G	301	U8Q	C10-C6-O1-C5
2	H	301	U8Q	C10-C6-O1-C5
2	F	303	U8Q	C11-C5-O1-C6
2	G	301	U8Q	C7-C6-O1-C5
2	F	303	U8Q	C4-C5-O1-C6

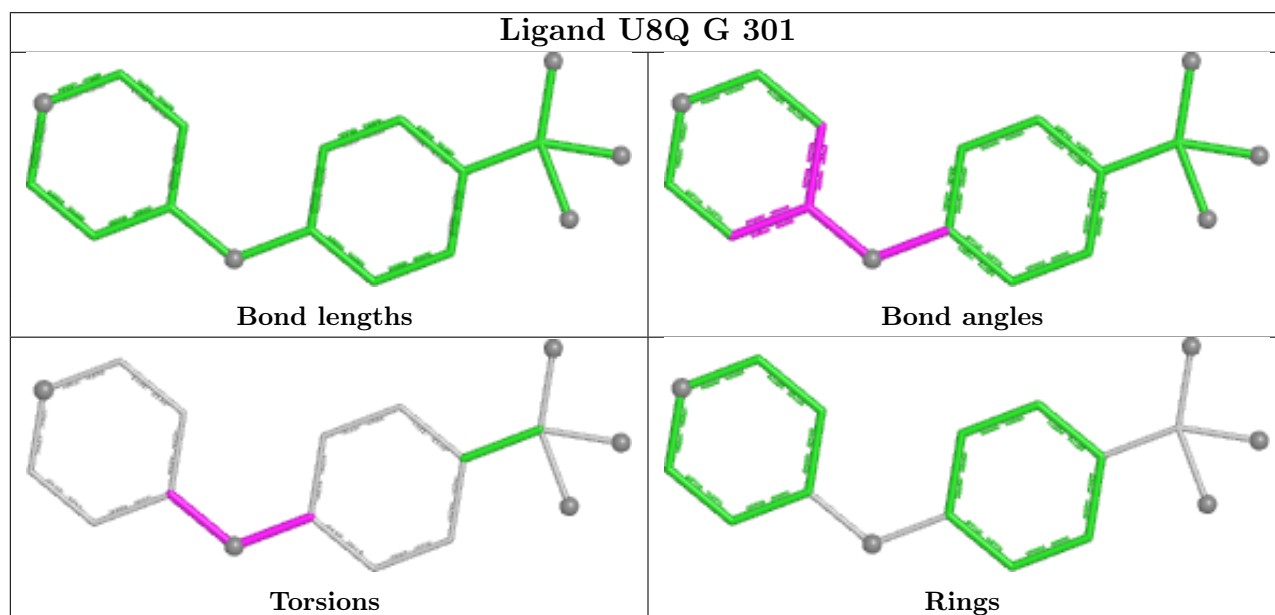
All (4) ring outliers are listed below:

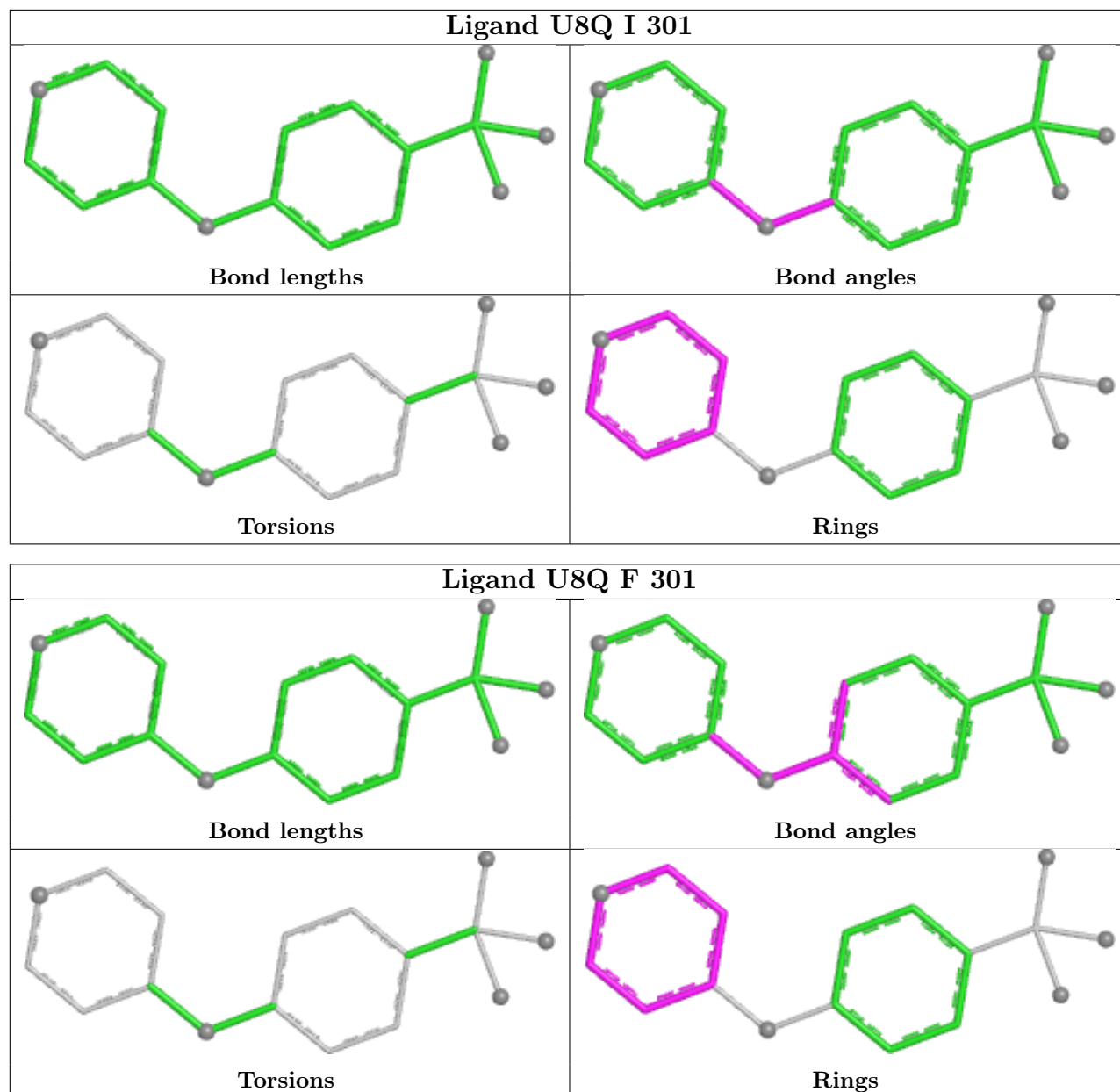
Mol	Chain	Res	Type	Atoms
2	D	301	U8Q	C10-C6-C7-C8-C9-N1
2	F	301	U8Q	C10-C6-C7-C8-C9-N1
2	H	301	U8Q	C10-C6-C7-C8-C9-N1
2	I	301	U8Q	C10-C6-C7-C8-C9-N1

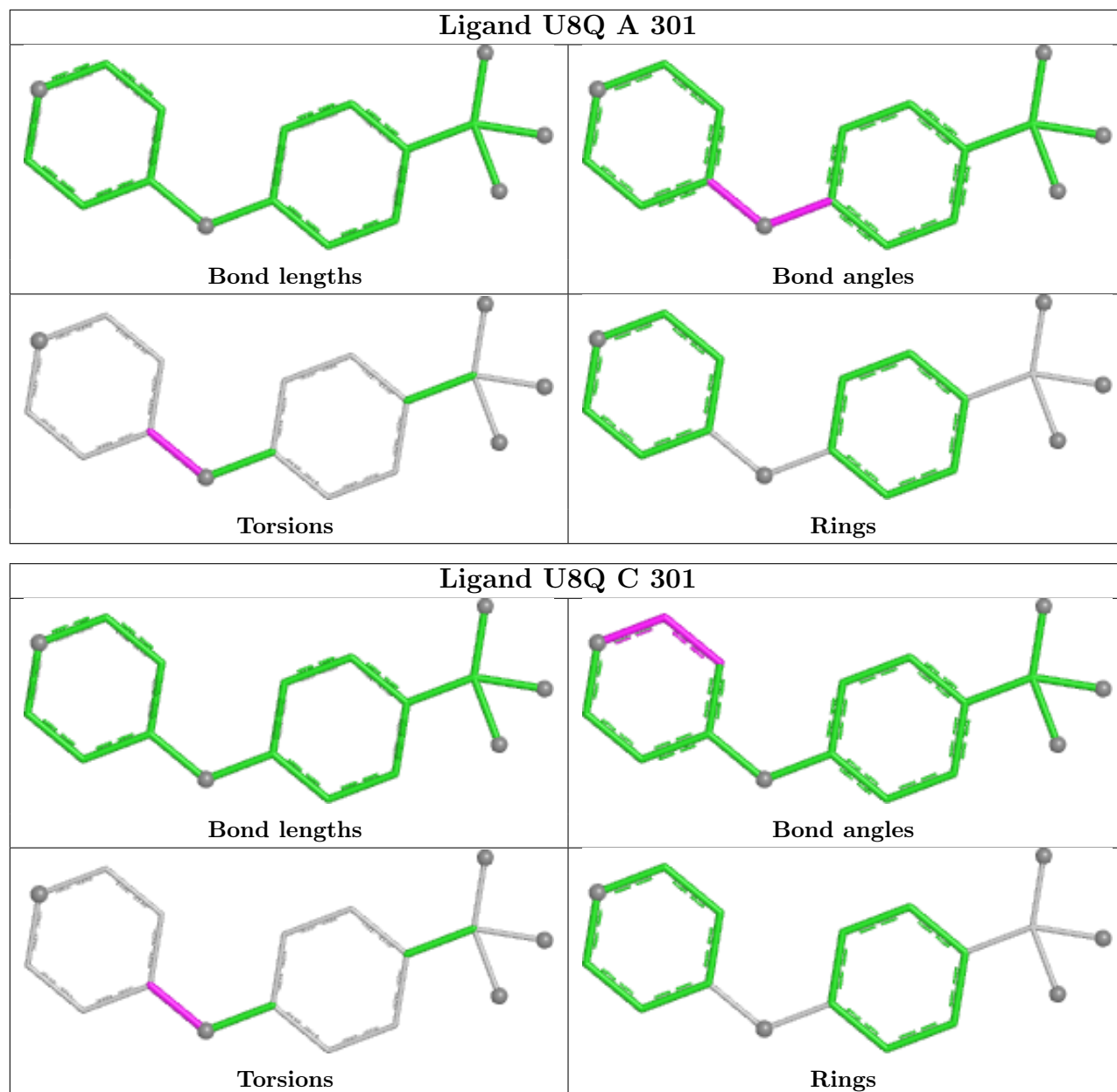
6 monomers are involved in 10 short contacts:

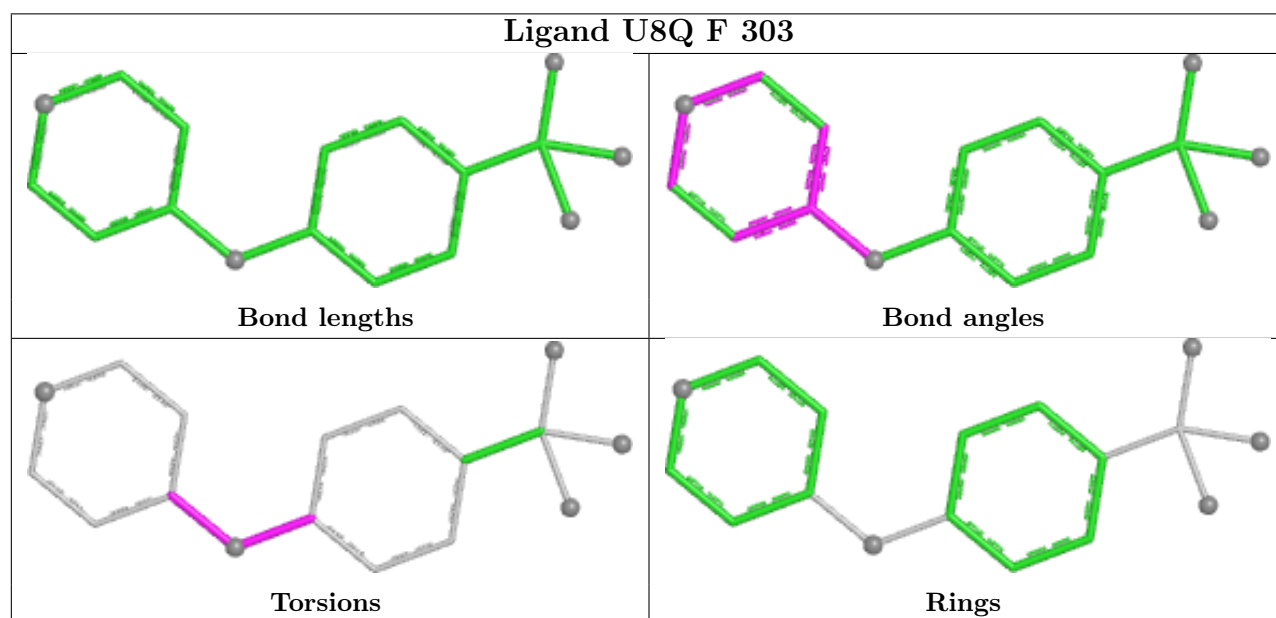
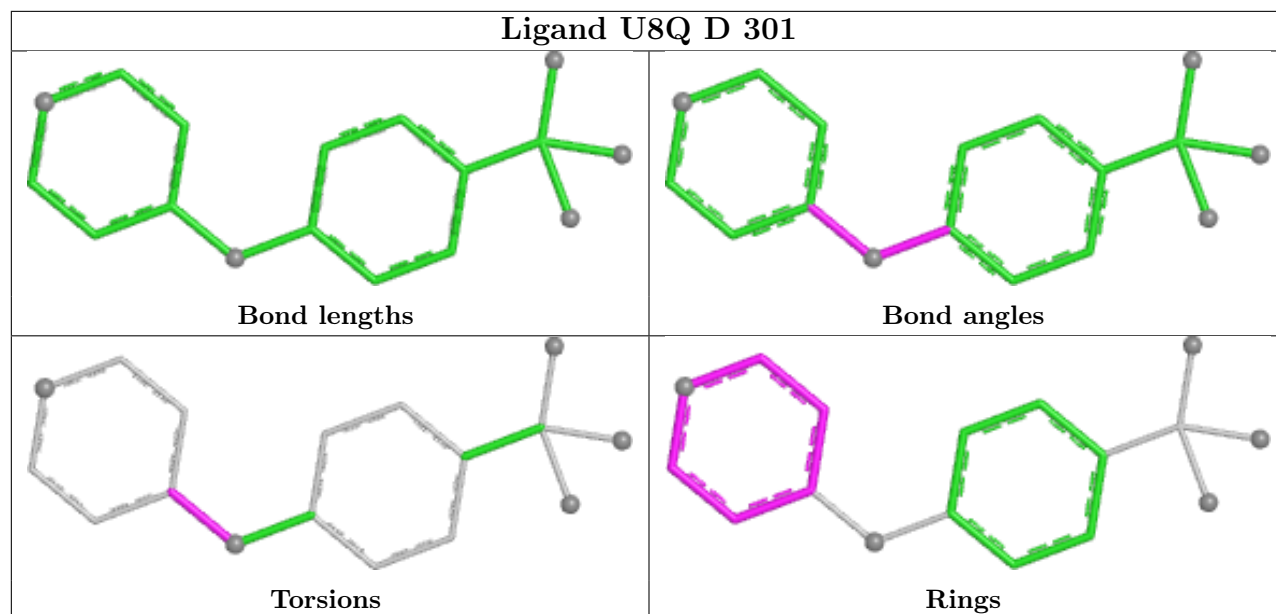
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	I	301	U8Q	4	0
4	G	302	SO4	1	0
2	C	301	U8Q	1	0
2	D	301	U8Q	1	0
3	C	302	NAG	1	0
3	H	302	NAG	1	1

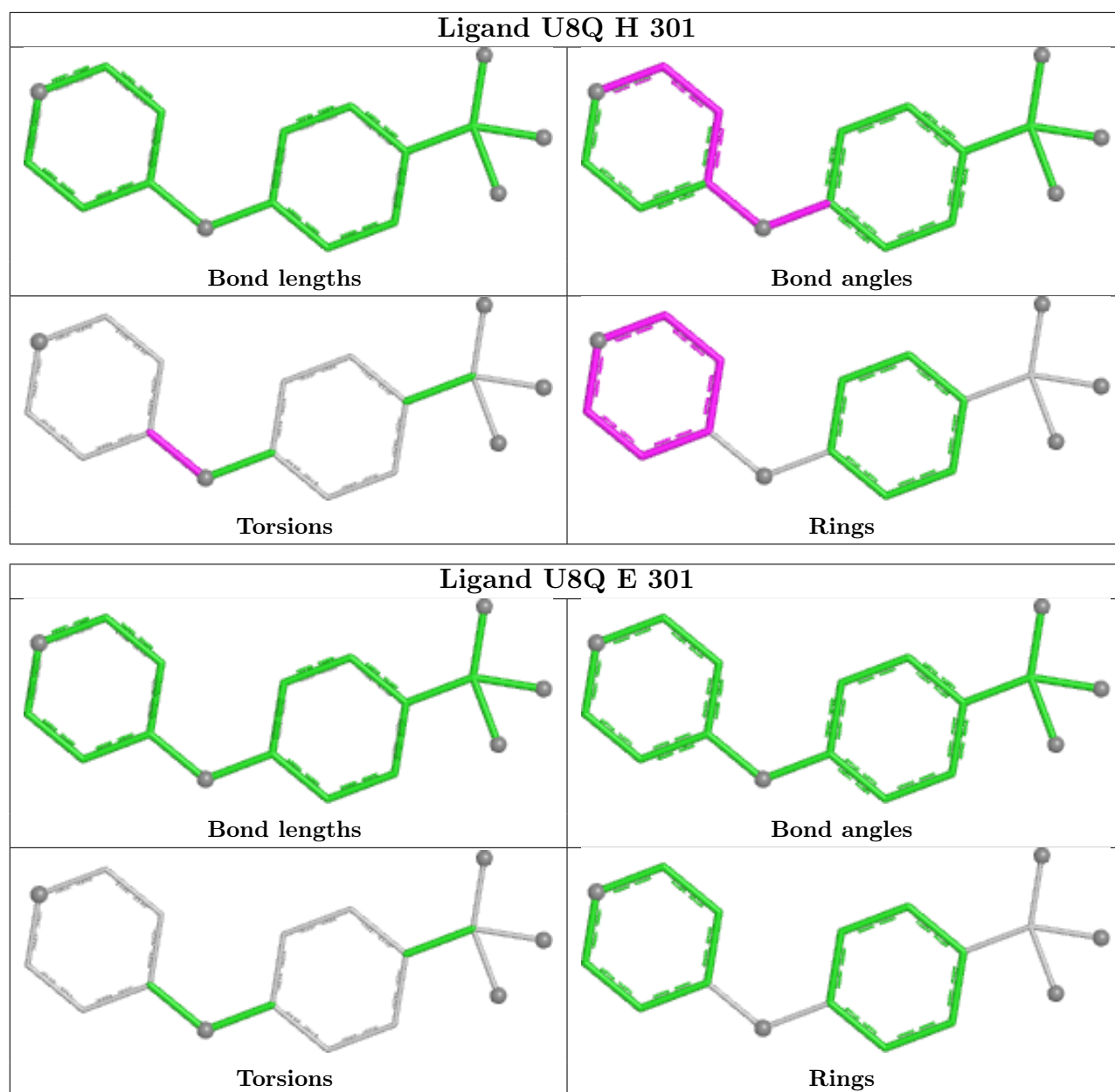
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.











## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	202/237 (85%)	0.77	11 (5%) 31 34	21, 41, 67, 85	4 (1%)
1	B	205/237 (86%)	1.15	37 (18%) 3 3	28, 46, 75, 99	1 (0%)
1	C	201/237 (84%)	1.00	22 (10%) 10 10	30, 42, 70, 117	0
1	D	203/237 (85%)	0.73	14 (6%) 23 25	22, 39, 67, 113	2 (0%)
1	E	200/237 (84%)	0.66	16 (8%) 18 19	20, 38, 65, 87	2 (1%)
1	F	204/237 (86%)	0.71	19 (9%) 14 15	16, 37, 64, 90	2 (0%)
1	G	210/237 (88%)	0.38	10 (4%) 35 39	16, 32, 59, 86	5 (2%)
1	H	212/237 (89%)	0.49	8 (3%) 44 48	17, 33, 62, 86	4 (1%)
1	I	203/237 (85%)	0.75	20 (9%) 13 13	21, 37, 69, 106	4 (1%)
1	J	201/237 (84%)	0.67	16 (7%) 18 19	20, 37, 68, 107	1 (0%)
All	All	2041/2370 (86%)	0.73	173 (8%) 16 17	16, 38, 69, 117	25 (1%)

The worst 5 of 173 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	174	THR	6.1
1	H	20	LEU	5.4
1	F	63	ILE	5.0
1	B	202	VAL	4.8
1	A	207	CYS	4.6

### 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 oligosaccharides in this entry.

### 6.4 Ligands [i](#)

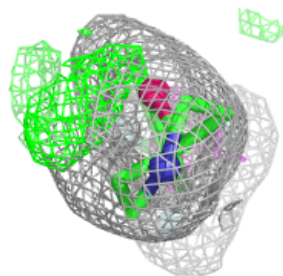
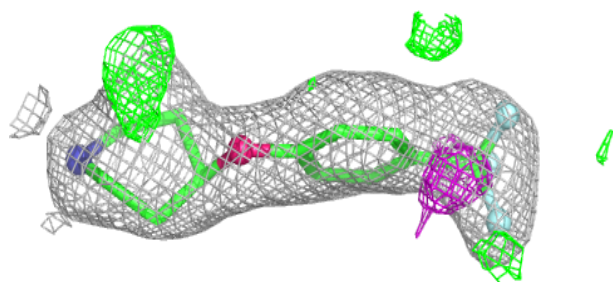
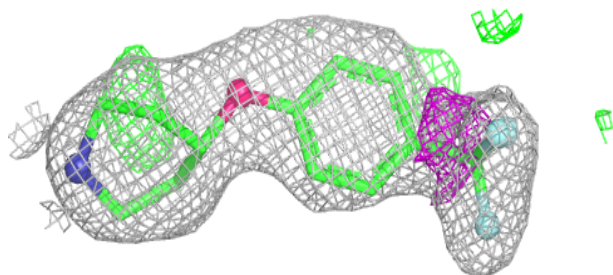
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	NAG	A	302	14/15	0.49	0.14	81,89,97,108	0
3	NAG	B	301	14/15	0.50	0.17	80,95,96,97	0
3	NAG	C	302	14/15	0.57	0.15	79,90,97,99	0
3	NAG	F	302	14/15	0.63	0.14	77,84,92,99	0
4	SO4	H	303	5/5	0.68	0.14	58,64,72,77	0
4	SO4	G	302	5/5	0.72	0.13	64,66,76,78	0
4	SO4	J	301	5/5	0.73	0.10	84,89,96,98	0
3	NAG	H	302	14/15	0.75	0.14	58,64,68,71	0
2	U8Q	D	301	17/17	0.81	0.14	45,55,63,66	0
2	U8Q	C	301	17/17	0.82	0.14	49,54,63,66	0
2	U8Q	I	301	17/17	0.84	0.14	48,61,85,86	0
2	U8Q	F	303	17/17	0.85	0.12	36,49,63,68	0
2	U8Q	A	301	17/17	0.87	0.12	36,53,64,65	0
2	U8Q	H	301	17/17	0.90	0.10	33,41,53,57	0
4	SO4	D	302	5/5	0.91	0.07	60,64,66,71	0
2	U8Q	G	301	17/17	0.93	0.08	28,32,45,45	0
2	U8Q	F	301	17/17	0.93	0.08	30,38,51,58	0
2	U8Q	E	301	17/17	0.93	0.08	35,45,69,71	0

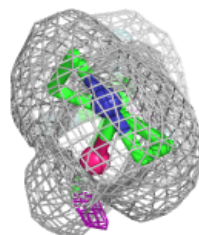
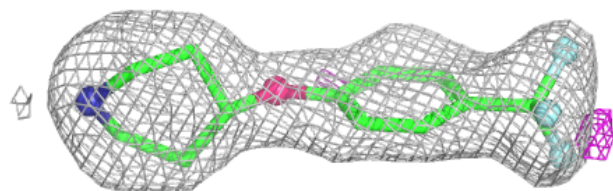
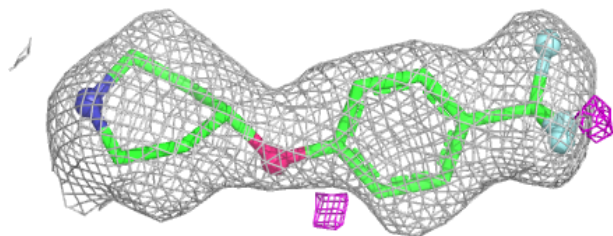
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around U8Q D 301:**

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

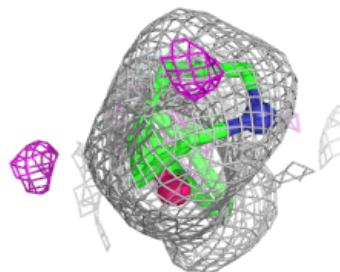
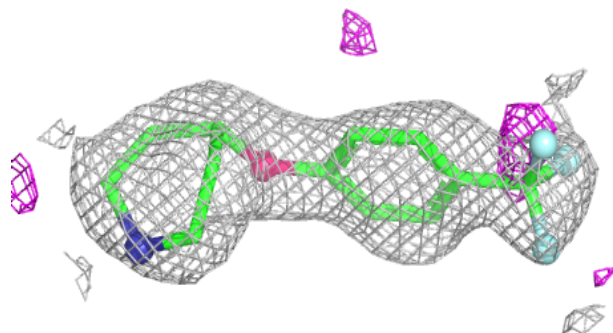
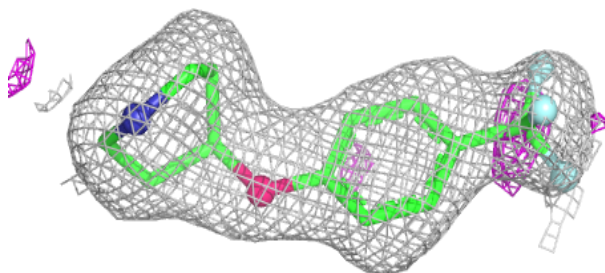
**Electron density around U8Q C 301:**

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

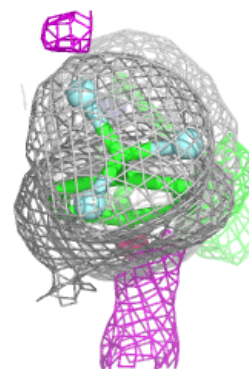
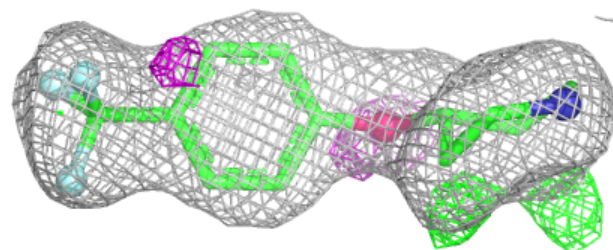
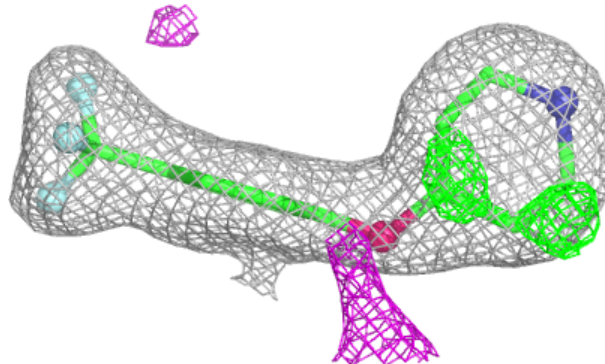


**Electron density around U8Q I 301:**

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

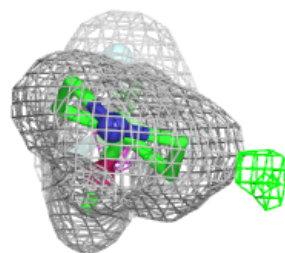
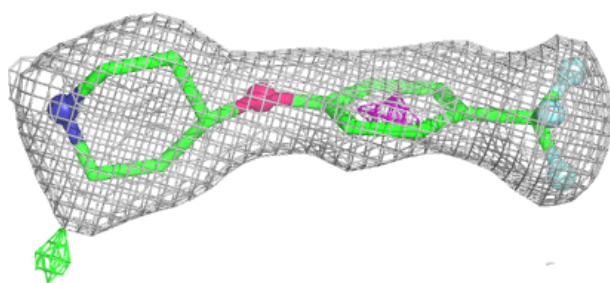
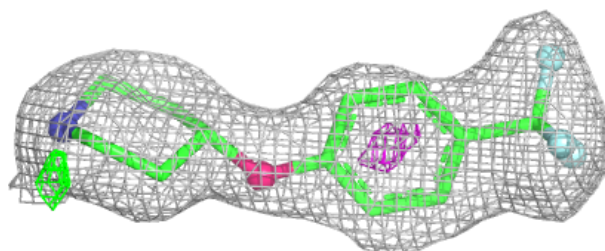
**Electron density around U8Q F 303:**

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

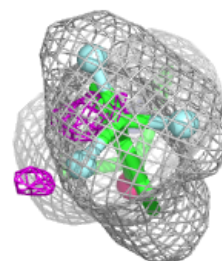
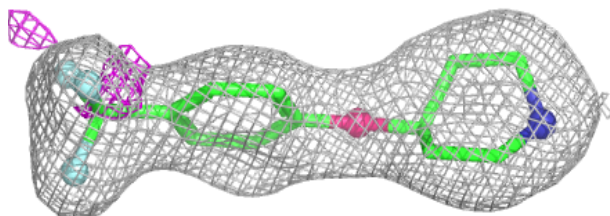
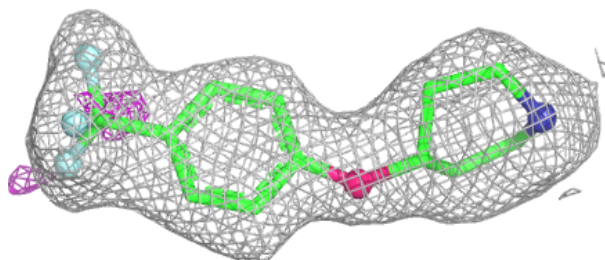


**Electron density around U8Q A 301:**

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

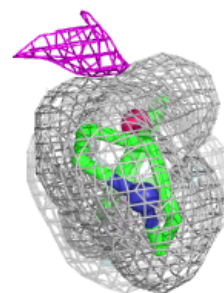
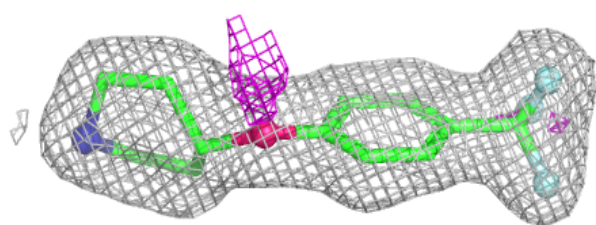
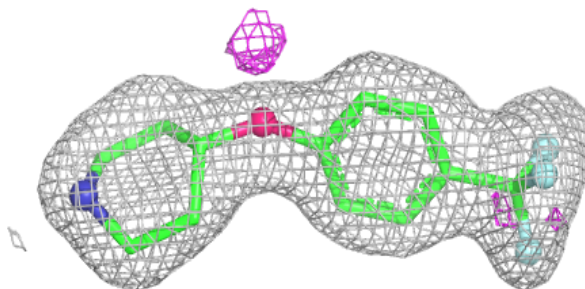
**Electron density around U8Q H 301:**

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

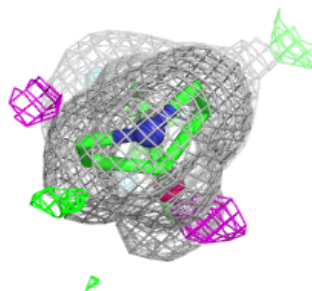
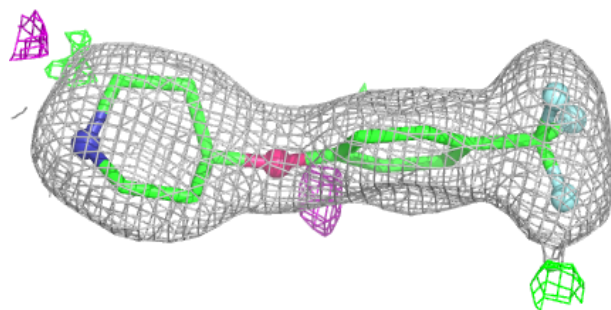
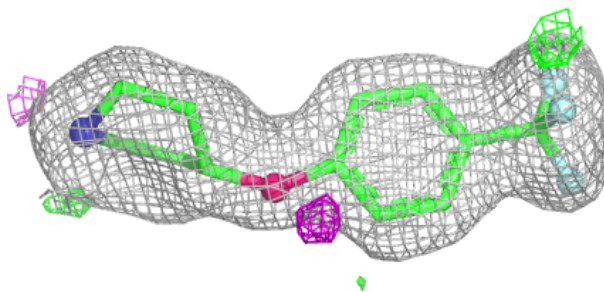


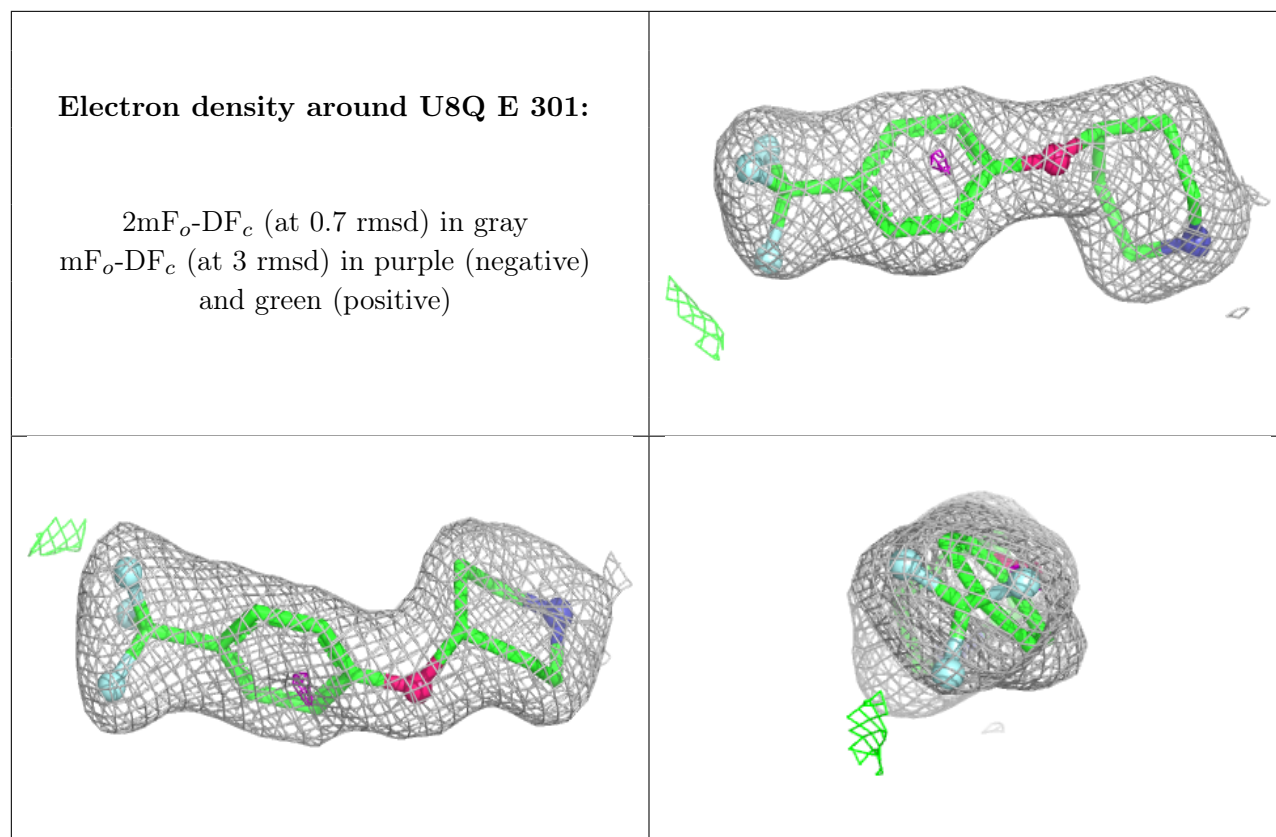
**Electron density around U8Q G 301:**

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

**Electron density around U8Q F 301:**

$2mF_o-DF_c$  (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.