



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 21, 2024 – 05:50 am BST

PDB ID : 4BQV
Title : MOUSE CATHEPSIN S WITH COVALENT LIGAND
Authors : Banner, D.W.; Benz, J.; Gsell, B.; Stihle, M.; Ruf, A.; Haap, W.
Deposited on : 2013-06-03
Resolution : 1.70 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36.2
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

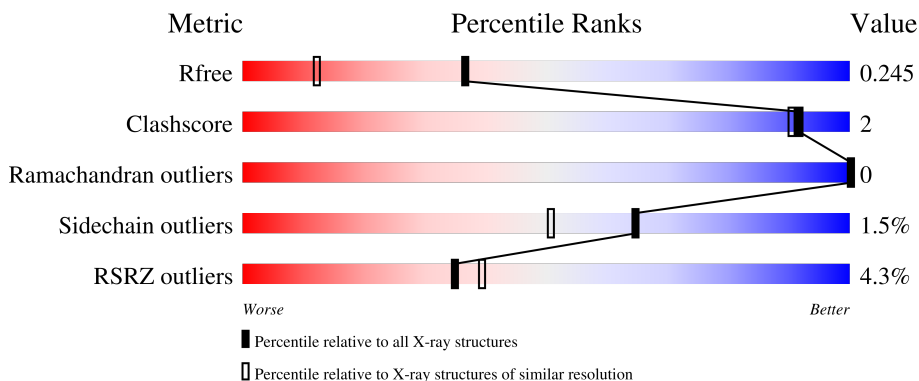
1 Overall quality at a glance

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.



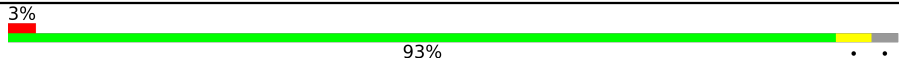
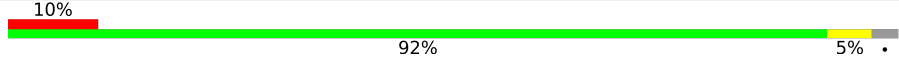
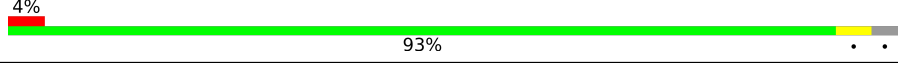
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 ≥ 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	225	 92% 5%
1	B	225	 94%
1	C	225	 95%
1	D	225	 92% 5%
1	E	225	 92% 5%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	225	 3% 93% . .
1	G	225	 10% 92% 5% . .
1	H	225	 4% 93% . .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 15034 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.

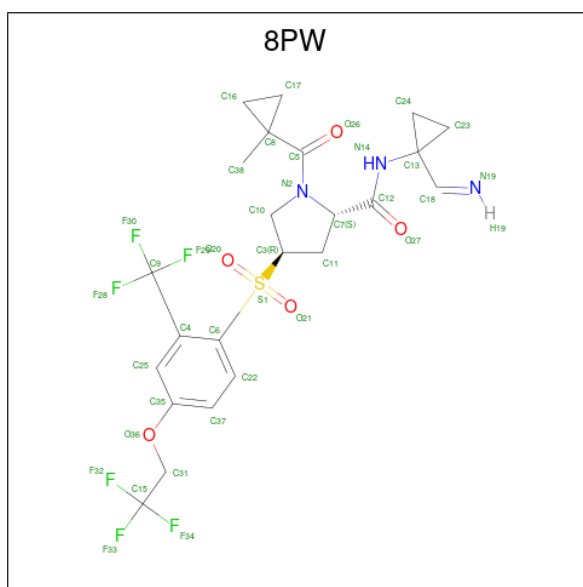
- Molecule 1 is a protein called CATHEPSIN S.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	219	1696	1063	284	334	15	0	3	0
1	B	219	1696	1063	284	334	15	0	3	0
1	C	219	1696	1063	284	334	15	0	3	0
1	D	219	1696	1063	284	334	15	0	3	0
1	E	219	1705	1068	286	336	15	0	4	0
1	F	219	1696	1063	284	334	15	0	3	0
1	G	219	1705	1068	286	336	15	0	4	0
1	H	219	1705	1069	286	335	15	0	4	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	218	MET	THR	variant	UNP O70370
B	218	MET	THR	variant	UNP O70370
C	218	MET	THR	variant	UNP O70370
D	218	MET	THR	variant	UNP O70370
E	218	MET	THR	variant	UNP O70370
F	218	MET	THR	variant	UNP O70370
G	218	MET	THR	variant	UNP O70370
H	218	MET	THR	variant	UNP O70370

- Molecule 2 is (2S,4R)-N-(1-cyanocyclopropyl)-1-(1-methylcyclopropanecarbonyl)-4-[4-(2,2,2-trifluoroethoxy)-2-(trifluoromethyl)phenyl]sulfonylpyrrolidine-2-carboxamide (three-letter code: 8PW) (formula: C₂₃H₂₅F₆N₃O₅S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	F	N	O			S
2	A	1	Total 38	C 23	F 6	N 3	O 5	S 1	0	0
2	B	1	Total 38	C 23	F 6	N 3	O 5	S 1	0	0
2	C	1	Total 38	C 23	F 6	N 3	O 5	S 1	0	0
2	D	1	Total 38	C 23	F 6	N 3	O 5	S 1	0	0
2	E	1	Total 38	C 23	F 6	N 3	O 5	S 1	0	0
2	F	1	Total 38	C 23	F 6	N 3	O 5	S 1	0	0
2	G	1	Total 38	C 23	F 6	N 3	O 5	S 1	0	0
2	H	1	Total 38	C 23	F 6	N 3	O 5	S 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	203	Total 203	O 203	0	0
3	B	142	Total 142	O 142	0	0
3	C	136	Total 136	O 136	0	0
3	D	193	Total 193	O 193	0	0

Continued on next page...

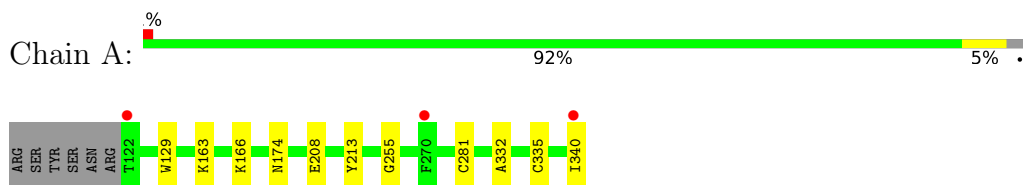
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	113	Total 113	O 113	0	0
3	F	129	Total 129	O 129	0	0
3	G	98	Total 98	O 98	0	0
3	H	121	Total 121	O 121	0	0

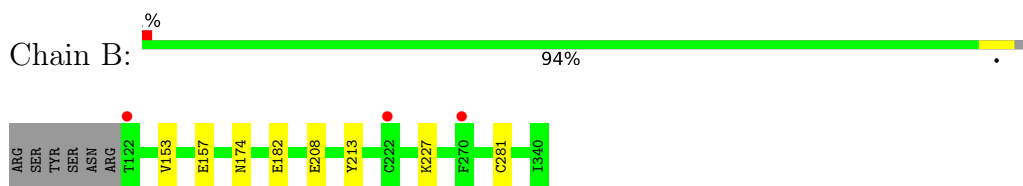
3 Residue-property plots [i](#)

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.

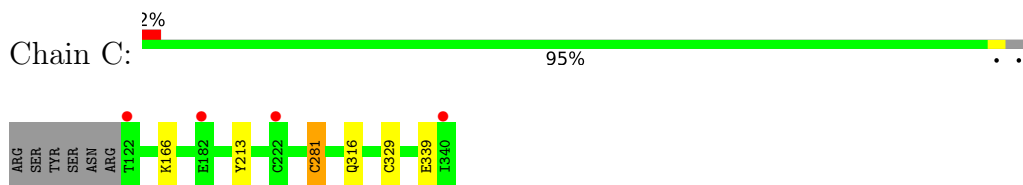
- Molecule 1: CATHEPSIN S



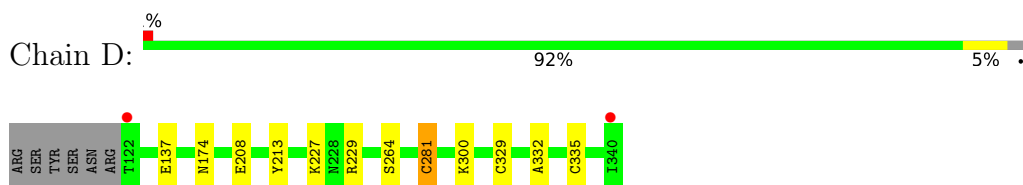
- Molecule 1: CATHEPSIN S



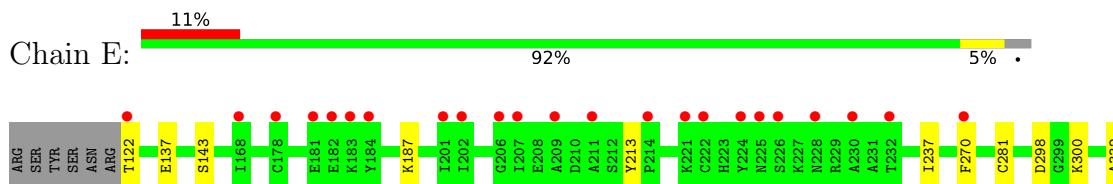
- Molecule 1: CATHEPSIN S



- Molecule 1: CATHEPSIN S

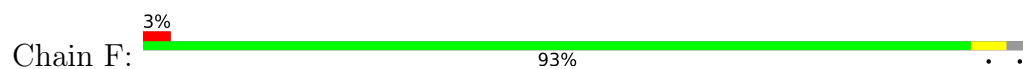


- Molecule 1: CATHEPSIN S

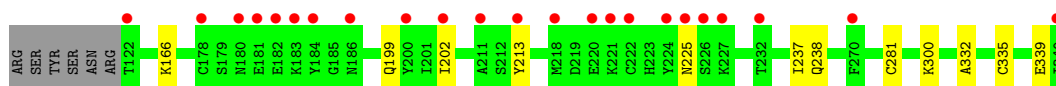
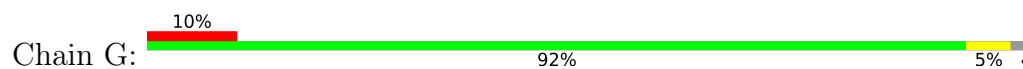




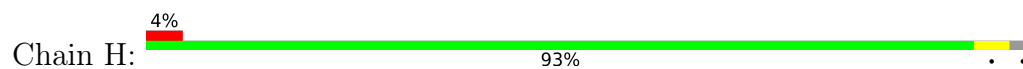
- Molecule 1: CATHEPSIN S



- Molecule 1: CATHEPSIN S



- Molecule 1: CATHEPSIN S



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	63.88Å 66.98Å 103.33Å 90.04° 96.68° 89.90°	Depositor
Resolution (Å)	43.49 – 1.70 43.46 – 1.70	Depositor EDS
% Data completeness (in resolution range)	87.5 (43.49-1.70) 87.1 (43.46-1.70)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.57 (at 1.70Å)	Xtrriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.202 , 0.240 0.211 , 0.245	Depositor DCC
R_{free} test set	8262 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	15.8	Xtrriage
Anisotropy	0.194	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 35.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.440 for -h,k,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	15034	wwPDB-VP
Average B, all atoms (Å ²)	23.0	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 61.87 % 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 1.2267e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 8PW

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	0.67	0/1735	0.74	0/2343
1	B	0.58	0/1735	0.68	0/2343
1	C	0.59	0/1735	0.69	0/2343
1	D	0.69	0/1735	0.73	2/2343 (0.1%)
1	E	0.49	0/1744	0.61	0/2355
1	F	0.58	0/1735	0.70	0/2343
1	G	0.49	0/1744	0.62	0/2355
1	H	0.60	0/1744	0.68	0/2354
All	All	0.59	0/13907	0.68	2/18779 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	229	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	D	229	ARG	NE-CZ-NH1	5.31	122.95	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1696	0	1593	7	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1696	0	1593	4	0
1	C	1696	0	1593	2	0
1	D	1696	0	1593	7	0
1	E	1705	0	1600	7	0
1	F	1696	0	1593	8	0
1	G	1705	0	1600	6	0
1	H	1705	0	1605	4	0
2	A	38	0	23	2	0
2	B	38	0	23	0	0
2	C	38	0	23	0	0
2	D	38	0	23	1	0
2	E	38	0	23	0	0
2	F	38	0	23	1	0
2	G	38	0	23	0	0
2	H	38	0	23	0	0
3	A	203	0	0	1	0
3	B	142	0	0	0	0
3	C	136	0	0	0	0
3	D	193	0	0	2	0
3	E	113	0	0	2	0
3	F	129	0	0	4	0
3	G	98	0	0	1	0
3	H	121	0	0	0	0
All	All	15034	0	12954	44	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 2.

All (44) 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:E:143[B]:SER:OG	3:E:2025:HOH:O	1.93	0.86
1:E:270:PHE:HB2	3:E:2074:HOH:O	1.86	0.74
1:D:137:GLU:OE1	3:D:2023:HOH:O	2.09	0.71
1:B:153:VAL:O	1:B:157:GLU:HG3	1.96	0.64
1:H:278:ASP:HB3	1:H:281[B]:CYS:SG	2.45	0.56
1:C:316:GLN:OE1	1:G:238:GLN:NE2	2.40	0.55
1:F:300:LYS:CE	3:F:2109:HOH:O	2.54	0.55
1:F:300:LYS:HD2	1:G:300:LYS:HD2	1.88	0.55
1:H:174:ASN:HD22	1:H:208:GLU:H	1.58	0.51
1:B:182:GLU:OE2	1:E:137:GLU:OE2	2.29	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:300:LYS:HE2	3:F:2109:HOH:O	2.11	0.49
1:F:174:ASN:HD22	1:F:208:GLU:H	1.60	0.49
1:F:300:LYS:HE3	3:F:2109:HOH:O	2.13	0.49
1:E:237:ILE:HD12	1:E:237:ILE:N	2.29	0.48
1:A:174:ASN:HD22	1:A:208:GLU:H	1.62	0.47
1:B:227:LYS:HG3	1:D:227:LYS:HG3	1.97	0.47
1:G:199:GLN:HA	1:G:202:ILE:HD12	1.97	0.45
2:A:1341:8PW:O26	2:A:1341:8PW:C12	2.64	0.45
2:F:1341:8PW:C12	2:F:1341:8PW:O26	2.65	0.45
1:A:174:ASN:ND2	1:A:208:GLU:H	2.15	0.44
1:B:174:ASN:ND2	1:B:208:GLU:H	2.16	0.44
1:A:129:TRP:CE2	1:A:255:GLY:HA2	2.53	0.44
2:D:1341:8PW:F30	2:D:1341:8PW:H3	2.08	0.43
1:A:163:LYS:HD2	1:A:340:ILE:HB	2.01	0.43
1:G:225:ASN:HA	3:G:2038:HOH:O	2.19	0.43
1:A:332:ALA:HA	1:A:335:CYS:SG	2.59	0.42
1:G:332:ALA:HA	1:G:335:CYS:SG	2.59	0.42
1:D:300:LYS:HB3	3:D:2104:HOH:O	2.19	0.42
1:A:166:LYS:HE2	1:D:264:SER:O	2.19	0.41
1:F:187:LYS:HD3	3:F:2047:HOH:O	2.19	0.41
1:H:215:TYR:CE2	1:H:217:ALA:HB2	2.55	0.41
1:D:332:ALA:HA	1:D:335:CYS:SG	2.61	0.41
1:F:278:ASP:HB3	1:F:281[B]:CYS:SG	2.60	0.41
1:F:215:TYR:CE2	1:F:217:ALA:HB2	2.55	0.41
1:H:281[B]:CYS:HB3	1:H:329:CYS:SG	2.61	0.41
1:E:187:LYS:HE3	1:E:187:LYS:HB2	1.92	0.41
1:E:298:ASP:O	1:E:300:LYS:HE3	2.21	0.41
2:A:1341:8PW:H3	2:A:1341:8PW:F30	2.11	0.40
1:C:281[B]:CYS:HB3	1:C:329:CYS:SG	2.61	0.40
1:D:174:ASN:HD22	1:D:208:GLU:H	1.69	0.40
1:G:237:ILE:HD12	1:G:237:ILE:N	2.36	0.40
1:D:281[B]:CYS:HB3	1:D:329:CYS:SG	2.62	0.40
1:E:332:ALA:HA	1:E:335:CYS:SG	2.62	0.40
1:A:163:LYS:NZ	3:A:2046:HOH:O	2.54	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	220/225 (98%)	215 (98%)	5 (2%)	0	100	100
1	B	220/225 (98%)	211 (96%)	9 (4%)	0	100	100
1	C	220/225 (98%)	213 (97%)	7 (3%)	0	100	100
1	D	220/225 (98%)	215 (98%)	5 (2%)	0	100	100
1	E	221/225 (98%)	215 (97%)	6 (3%)	0	100	100
1	F	220/225 (98%)	215 (98%)	5 (2%)	0	100	100
1	G	221/225 (98%)	217 (98%)	4 (2%)	0	100	100
1	H	221/225 (98%)	213 (96%)	8 (4%)	0	100	100
All	All	1763/1800 (98%)	1714 (97%)	49 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	179/182 (98%)	176 (98%)	3 (2%)	60	46
1	B	179/182 (98%)	176 (98%)	3 (2%)	60	46
1	C	179/182 (98%)	174 (97%)	5 (3%)	43	25
1	D	179/182 (98%)	176 (98%)	3 (2%)	60	46
1	E	180/182 (99%)	176 (98%)	4 (2%)	52	34
1	F	179/182 (98%)	178 (99%)	1 (1%)	86	80

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	180/182 (99%)	175 (97%)	5 (3%)	43	25
1	H	180/182 (99%)	176 (98%)	4 (2%)	52	34
All	All	1435/1456 (99%)	1407 (98%)	28 (2%)	65	38

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	213	TYR
1	A	281[A]	CYS
1	A	281[B]	CYS
1	B	213	TYR
1	B	281[A]	CYS
1	B	281[B]	CYS
1	C	166	LYS
1	C	213	TYR
1	C	281[A]	CYS
1	C	281[B]	CYS
1	C	339	GLU
1	D	213	TYR
1	D	281[A]	CYS
1	D	281[B]	CYS
1	E	122	THR
1	E	213	TYR
1	E	281[A]	CYS
1	E	281[B]	CYS
1	F	213	TYR
1	G	166	LYS
1	G	213	TYR
1	G	281[A]	CYS
1	G	281[B]	CYS
1	G	339	GLU
1	H	122	THR
1	H	213	TYR
1	H	281[A]	CYS
1	H	281[B]	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	174	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	223	HIS
1	A	312	ASN
1	B	174	ASN
1	B	312	ASN
1	B	316	GLN
1	C	174	ASN
1	C	223	HIS
1	C	316	GLN
1	D	174	ASN
1	D	223	HIS
1	D	312	ASN
1	E	174	ASN
1	E	228	ASN
1	E	312	ASN
1	F	174	ASN
1	F	328	HIS
1	G	228	ASN
1	G	238	GLN
1	G	312	ASN
1	H	174	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

8 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	8PW	G	1341	1	35,41,41	1.76	3 (8%)	51,67,67	2.18	12 (23%)
2	8PW	D	1341	1	35,41,41	2.32	6 (17%)	51,67,67	2.26	14 (27%)
2	8PW	F	1341	1	35,41,41	2.04	6 (17%)	51,67,67	2.15	10 (19%)
2	8PW	B	1341	1	35,41,41	2.01	7 (20%)	51,67,67	1.94	9 (17%)
2	8PW	H	1341	1	35,41,41	2.13	6 (17%)	51,67,67	2.00	12 (23%)
2	8PW	C	1341	1	35,41,41	1.96	6 (17%)	51,67,67	1.77	9 (17%)
2	8PW	E	1341	1	35,41,41	1.81	6 (17%)	51,67,67	1.89	9 (17%)
2	8PW	A	1341	1	35,41,41	2.24	7 (20%)	51,67,67	2.70	11 (21%)

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	8PW	G	1341	1	-	3/41/66/66	0/4/4/4
2	8PW	D	1341	1	-	3/41/66/66	0/4/4/4
2	8PW	F	1341	1	-	0/41/66/66	0/4/4/4
2	8PW	B	1341	1	-	2/41/66/66	0/4/4/4
2	8PW	H	1341	1	-	0/41/66/66	0/4/4/4
2	8PW	C	1341	1	-	2/41/66/66	0/4/4/4
2	8PW	E	1341	1	-	0/41/66/66	0/4/4/4
2	8PW	A	1341	1	-	3/41/66/66	0/4/4/4

All (47) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	1341	8PW	C4-C6	8.58	1.51	1.40
2	H	1341	8PW	C4-C6	8.36	1.51	1.40
2	D	1341	8PW	C4-C6	8.21	1.51	1.40
2	B	1341	8PW	C4-C6	7.61	1.50	1.40
2	E	1341	8PW	C4-C6	7.60	1.50	1.40
2	C	1341	8PW	C4-C6	7.55	1.50	1.40
2	G	1341	8PW	C4-C6	7.55	1.50	1.40
2	A	1341	8PW	C4-C6	7.46	1.50	1.40
2	D	1341	8PW	O20-S1	-6.74	1.38	1.44

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1341	8PW	C5-N2	-5.73	1.25	1.34
2	D	1341	8PW	C5-N2	-5.01	1.26	1.34
2	A	1341	8PW	O21-S1	-4.95	1.39	1.44
2	H	1341	8PW	C5-N2	-4.86	1.26	1.34
2	C	1341	8PW	C5-N2	-4.54	1.27	1.34
2	B	1341	8PW	C5-N2	-4.49	1.27	1.34
2	F	1341	8PW	C5-N2	-4.44	1.27	1.34
2	A	1341	8PW	C24-C13	4.20	1.54	1.51
2	E	1341	8PW	C3-S1	-4.19	1.68	1.78
2	A	1341	8PW	C3-S1	-4.13	1.68	1.78
2	G	1341	8PW	C5-N2	-4.10	1.28	1.34
2	D	1341	8PW	C3-S1	-3.95	1.69	1.78
2	B	1341	8PW	O21-S1	-3.89	1.40	1.44
2	H	1341	8PW	O20-S1	-3.83	1.40	1.44
2	G	1341	8PW	C3-S1	-3.82	1.69	1.78
2	H	1341	8PW	C3-S1	-3.69	1.69	1.78
2	C	1341	8PW	C3-S1	-3.67	1.69	1.78
2	E	1341	8PW	C5-N2	-3.58	1.28	1.34
2	C	1341	8PW	O21-S1	-3.57	1.41	1.44
2	B	1341	8PW	C3-S1	-3.42	1.70	1.78
2	F	1341	8PW	C3-S1	-3.29	1.70	1.78
2	F	1341	8PW	C23-C13	3.14	1.54	1.51
2	B	1341	8PW	C11-C3	-2.87	1.51	1.54
2	C	1341	8PW	C11-C3	-2.87	1.51	1.54
2	B	1341	8PW	C23-C13	2.83	1.53	1.51
2	H	1341	8PW	C24-C13	2.44	1.53	1.51
2	H	1341	8PW	C25-C4	2.43	1.43	1.39
2	E	1341	8PW	C23-C13	2.42	1.53	1.51
2	F	1341	8PW	O21-S1	-2.39	1.42	1.44
2	E	1341	8PW	C11-C3	-2.34	1.52	1.54
2	B	1341	8PW	C24-C13	2.30	1.53	1.51
2	D	1341	8PW	C37-C22	2.28	1.42	1.38
2	C	1341	8PW	C24-C13	2.24	1.53	1.51
2	A	1341	8PW	C37-C22	2.24	1.42	1.38
2	F	1341	8PW	C24-C13	2.20	1.53	1.51
2	E	1341	8PW	C24-C13	2.14	1.53	1.51
2	D	1341	8PW	O21-S1	-2.14	1.42	1.44
2	A	1341	8PW	O20-S1	-2.04	1.42	1.44

All (86) bond angle outliers are listed below:

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1341	8PW	C24-C13-N14	-11.35	106.25	117.30
2	F	1341	8PW	C8-C5-N2	-8.44	114.15	121.65
2	G	1341	8PW	C24-C13-N14	-8.19	109.33	117.30
2	D	1341	8PW	C24-C13-N14	-7.92	109.59	117.30
2	A	1341	8PW	C8-C5-N2	-7.58	114.92	121.65
2	B	1341	8PW	C24-C13-N14	-7.54	109.97	117.30
2	D	1341	8PW	C8-C5-N2	-7.14	115.31	121.65
2	A	1341	8PW	C17-C8-C5	-6.57	108.58	115.23
2	H	1341	8PW	C8-C5-N2	-6.26	116.09	121.65
2	H	1341	8PW	O21-S1-O20	-6.02	113.19	118.71
2	F	1341	8PW	O21-S1-O20	-5.79	113.40	118.71
2	G	1341	8PW	O21-S1-O20	-5.48	113.68	118.71
2	F	1341	8PW	C16-C8-C5	5.20	120.50	115.23
2	E	1341	8PW	C24-C13-N14	-5.12	112.31	117.30
2	E	1341	8PW	O21-S1-O20	-5.09	114.04	118.71
2	G	1341	8PW	C8-C5-N2	-4.84	117.35	121.65
2	H	1341	8PW	C17-C8-C5	-4.82	110.35	115.23
2	C	1341	8PW	C8-C5-N2	-4.72	117.46	121.65
2	A	1341	8PW	C16-C8-C5	4.63	119.93	115.23
2	B	1341	8PW	C17-C8-C5	-4.52	110.65	115.23
2	E	1341	8PW	C8-C5-N2	-4.43	117.72	121.65
2	G	1341	8PW	C16-C8-C5	4.33	119.62	115.23
2	A	1341	8PW	C11-C3-C10	-4.31	100.92	105.44
2	B	1341	8PW	C16-C8-C5	4.19	119.48	115.23
2	C	1341	8PW	C24-C13-N14	-4.16	113.25	117.30
2	E	1341	8PW	C16-C8-C5	4.12	119.41	115.23
2	E	1341	8PW	C22-C6-C4	-4.05	116.32	121.63
2	A	1341	8PW	C22-C6-C4	-4.02	116.37	121.63
2	C	1341	8PW	C17-C8-C5	-4.01	111.17	115.23
2	C	1341	8PW	C16-C8-C5	3.89	119.17	115.23
2	A	1341	8PW	F30-C9-C4	-3.80	106.09	112.70
2	B	1341	8PW	C22-C6-C4	-3.80	116.66	121.63
2	C	1341	8PW	C22-C6-C4	-3.79	116.67	121.63
2	G	1341	8PW	C22-C6-C4	-3.69	116.80	121.63
2	C	1341	8PW	F30-C9-C4	-3.64	106.36	112.70
2	H	1341	8PW	F28-C9-C4	-3.62	106.40	112.70
2	B	1341	8PW	C6-S1-C3	3.61	110.21	104.62
2	H	1341	8PW	C16-C8-C5	3.61	118.89	115.23
2	D	1341	8PW	C17-C8-C5	-3.56	111.63	115.23
2	D	1341	8PW	C22-C6-C4	-3.55	116.98	121.63
2	D	1341	8PW	C16-C8-C5	3.54	118.82	115.23

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	1341	8PW	C6-S1-C3	3.53	110.09	104.62
2	F	1341	8PW	C23-C13-N14	-3.44	113.96	117.30
2	D	1341	8PW	C11-C3-C10	-3.39	101.88	105.44
2	F	1341	8PW	C22-C6-C4	-3.37	117.21	121.63
2	H	1341	8PW	C22-C6-C4	-3.30	117.31	121.63
2	D	1341	8PW	F30-C9-C4	-3.26	107.02	112.70
2	F	1341	8PW	O20-S1-C3	3.10	111.78	108.35
2	F	1341	8PW	C17-C8-C5	-3.04	112.15	115.23
2	E	1341	8PW	O21-S1-C3	2.99	111.65	108.35
2	D	1341	8PW	O26-C5-N2	2.99	127.27	120.22
2	H	1341	8PW	C24-C13-N14	-2.93	114.45	117.30
2	F	1341	8PW	C11-C3-C10	-2.92	102.38	105.44
2	D	1341	8PW	C10-N2-C7	-2.86	107.57	111.70
2	G	1341	8PW	O21-S1-C3	2.83	111.47	108.35
2	G	1341	8PW	O20-S1-C3	-2.76	105.30	108.35
2	D	1341	8PW	O21-S1-C3	2.76	111.40	108.35
2	A	1341	8PW	O26-C5-N2	2.67	126.52	120.22
2	F	1341	8PW	F28-C9-C4	-2.65	108.08	112.70
2	B	1341	8PW	C11-C3-C10	-2.61	102.70	105.44
2	E	1341	8PW	F29-C9-C4	-2.61	108.15	112.70
2	H	1341	8PW	C23-C13-N14	-2.56	114.81	117.30
2	C	1341	8PW	C6-S1-C3	2.51	108.51	104.62
2	D	1341	8PW	O21-S1-C6	-2.49	102.90	107.76
2	B	1341	8PW	F30-C9-C4	-2.48	108.38	112.70
2	A	1341	8PW	C10-N2-C5	2.47	133.00	129.85
2	B	1341	8PW	C8-C5-N2	-2.47	119.46	121.65
2	E	1341	8PW	O20-S1-C3	-2.37	105.74	108.35
2	G	1341	8PW	F28-C9-C4	-2.35	108.61	112.70
2	A	1341	8PW	C25-C4-C6	2.34	120.93	117.14
2	D	1341	8PW	F28-C9-C4	-2.33	108.65	112.70
2	H	1341	8PW	C6-S1-C3	2.28	108.14	104.62
2	G	1341	8PW	F29-C9-C4	-2.23	108.81	112.70
2	D	1341	8PW	C11-C7-N2	2.22	106.03	103.10
2	D	1341	8PW	F33-C15-C31	-2.19	103.69	111.89
2	B	1341	8PW	F30-C9-F28	2.14	113.56	105.72
2	H	1341	8PW	O21-S1-C3	2.14	110.71	108.35
2	C	1341	8PW	C11-C3-C10	-2.13	103.21	105.44
2	A	1341	8PW	F33-C15-C31	-2.13	103.94	111.89
2	G	1341	8PW	C31-O36-C35	2.11	124.42	117.81
2	C	1341	8PW	F30-C9-F28	2.07	113.31	105.72
2	F	1341	8PW	C22-C37-C35	2.07	122.26	119.73
2	E	1341	8PW	C6-S1-C3	2.03	107.77	104.62

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	1341	8PW	C7-N2-C5	2.03	121.11	118.09
2	H	1341	8PW	O20-S1-C3	2.03	110.59	108.35
2	H	1341	8PW	O36-C31-C15	2.00	112.70	108.15

There are no chirality outliers.

All (13) torsion outliers are listed below:

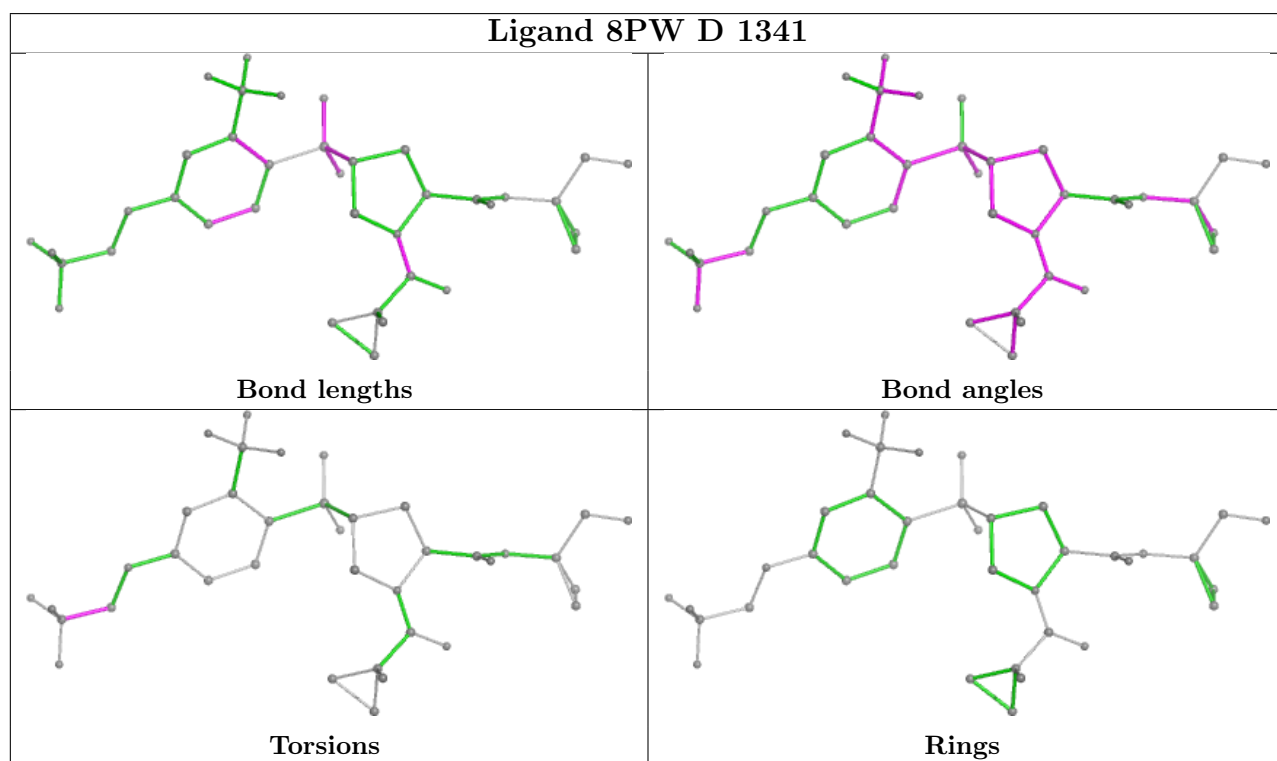
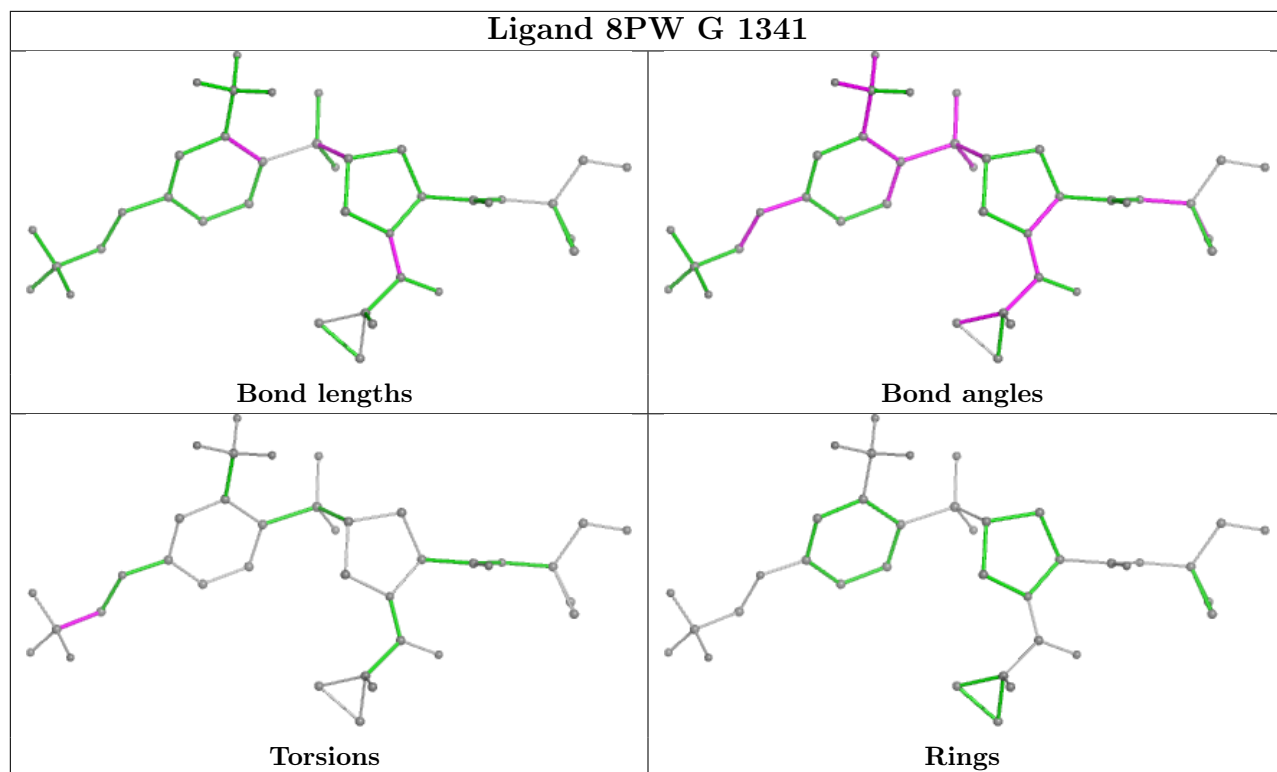
Mol	Chain	Res	Type	Atoms
2	A	1341	8PW	F33-C15-C31-O36
2	D	1341	8PW	F32-C15-C31-O36
2	D	1341	8PW	F33-C15-C31-O36
2	D	1341	8PW	F34-C15-C31-O36
2	A	1341	8PW	F32-C15-C31-O36
2	A	1341	8PW	F34-C15-C31-O36
2	C	1341	8PW	C37-C35-O36-C31
2	C	1341	8PW	C25-C35-O36-C31
2	G	1341	8PW	F32-C15-C31-O36
2	B	1341	8PW	C37-C35-O36-C31
2	G	1341	8PW	F33-C15-C31-O36
2	B	1341	8PW	C25-C35-O36-C31
2	G	1341	8PW	F34-C15-C31-O36

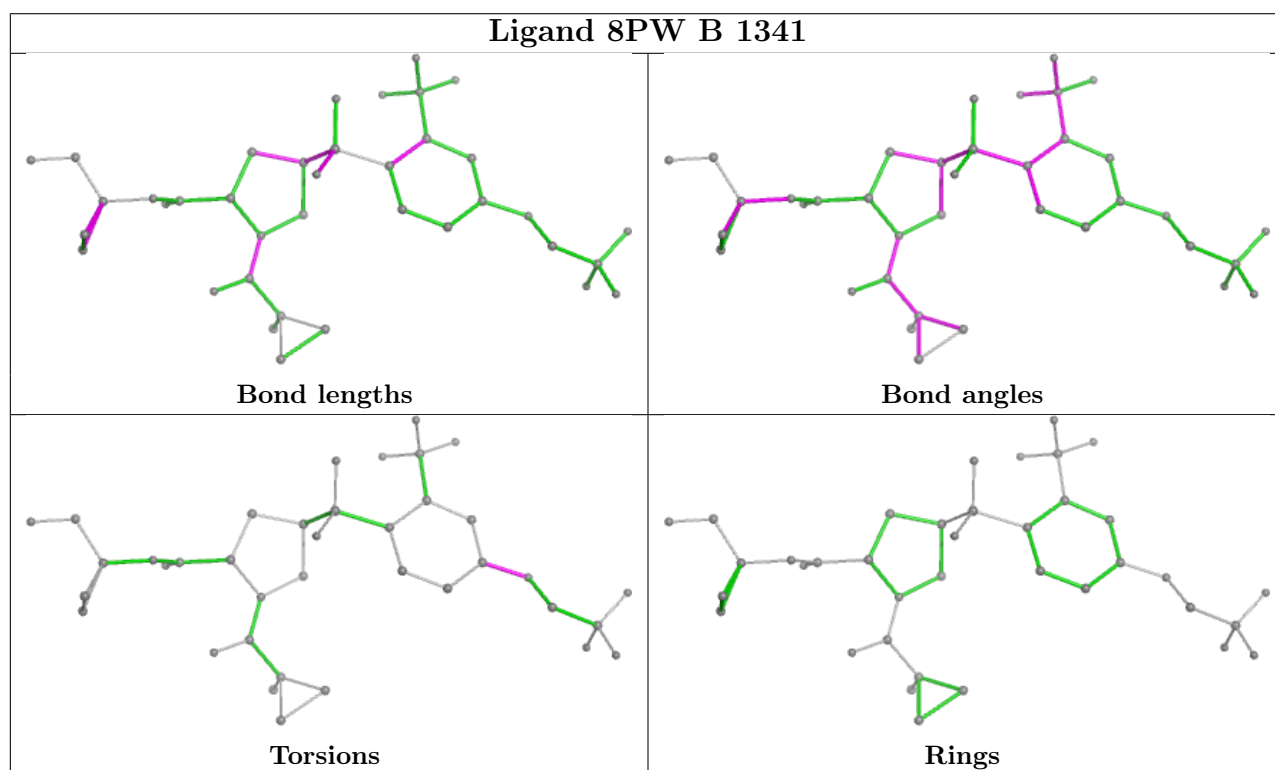
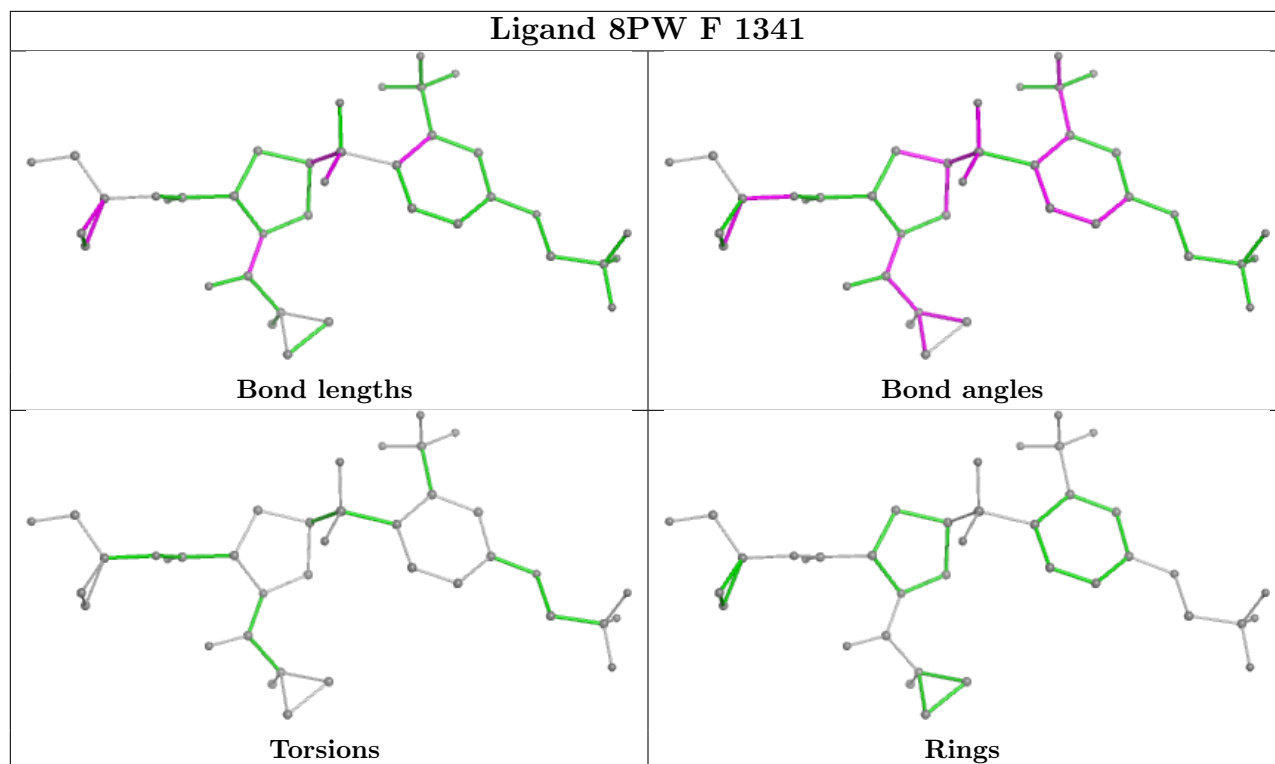
There are no ring outliers.

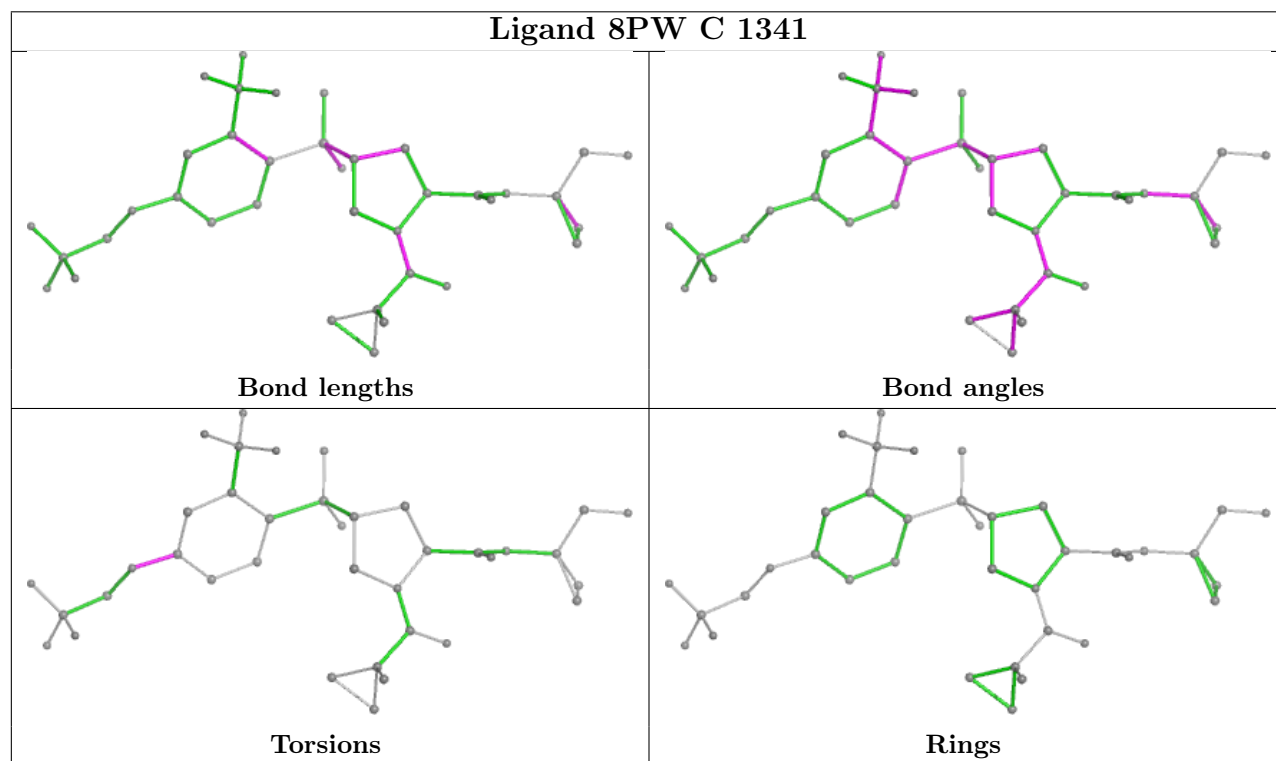
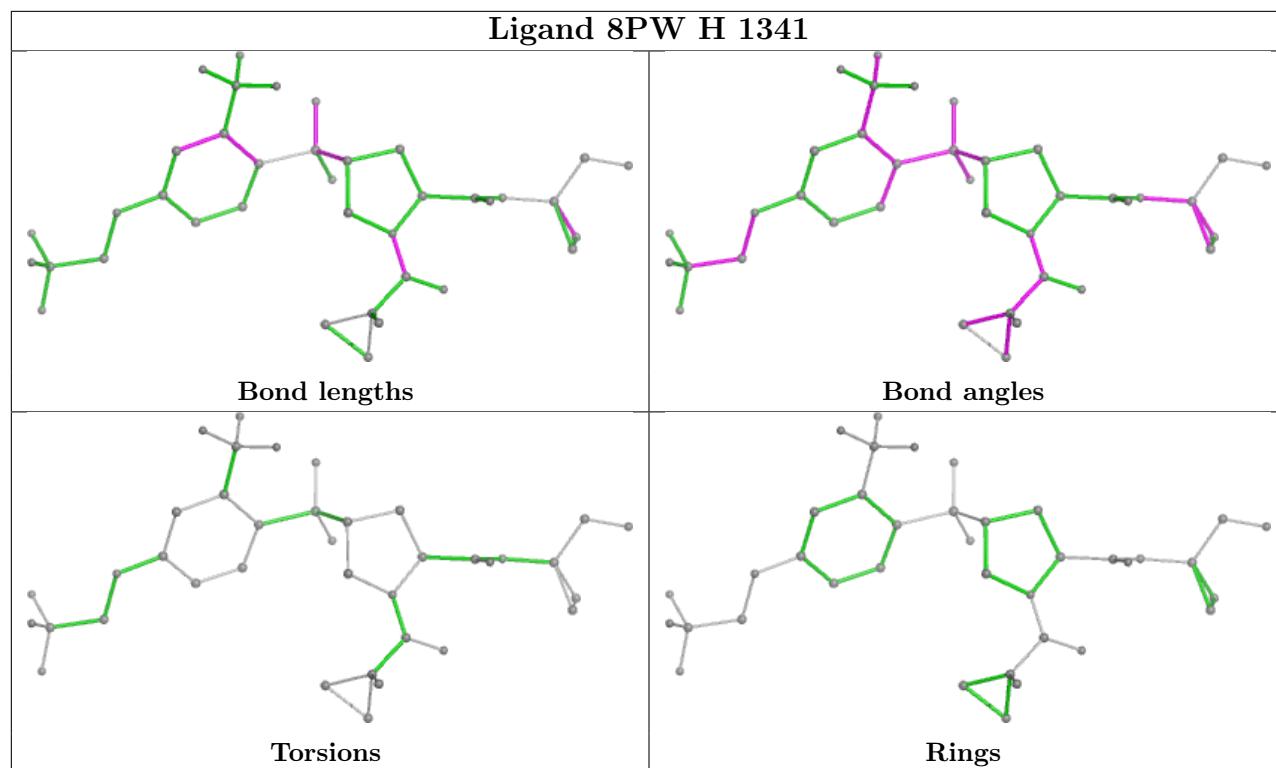
3 monomers are involved in 4 short contacts:

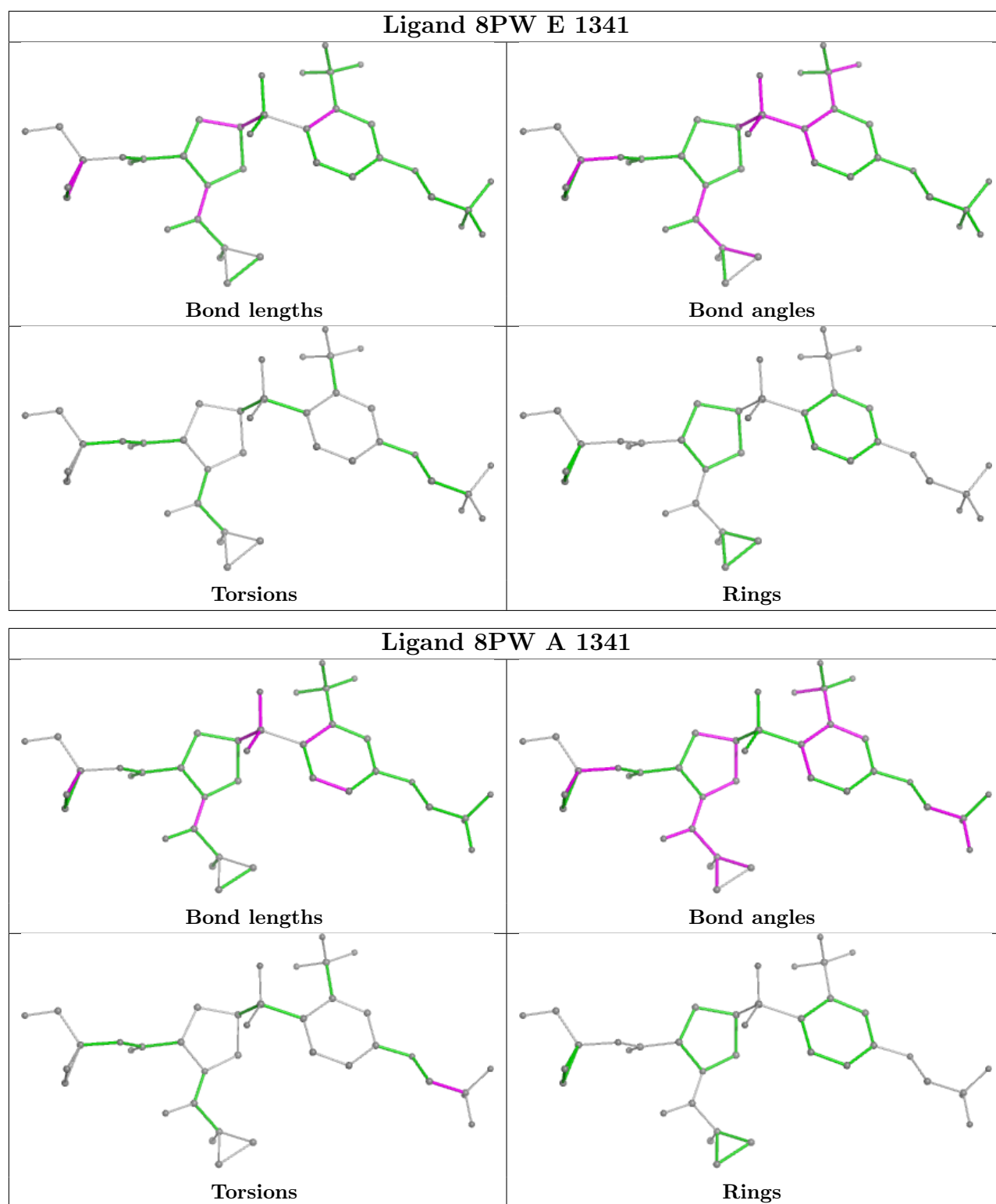
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1341	8PW	1	0
2	F	1341	8PW	1	0
2	A	1341	8PW	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	219/225 (97%)	-0.08	3 (1%) 75 79	8, 14, 27, 48	12 (5%)
1	B	219/225 (97%)	0.08	3 (1%) 75 79	10, 19, 39, 55	12 (5%)
1	C	219/225 (97%)	0.13	4 (1%) 68 72	11, 19, 40, 50	12 (5%)
1	D	219/225 (97%)	-0.07	2 (0%) 84 87	8, 14, 27, 45	11 (5%)
1	E	219/225 (97%)	0.63	24 (10%) 5 6	16, 25, 54, 71	12 (5%)
1	F	219/225 (97%)	0.39	6 (2%) 54 58	13, 21, 37, 45	11 (5%)
1	G	219/225 (97%)	0.68	23 (10%) 6 7	15, 26, 53, 71	12 (5%)
1	H	219/225 (97%)	0.48	10 (4%) 32 36	14, 21, 37, 47	12 (5%)
All	All	1752/1800 (97%)	0.28	75 (4%) 35 39	8, 20, 42, 71	94 (5%)

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	183	LYS	5.6
1	G	122	THR	5.5
1	E	122	THR	5.1
1	E	224	TYR	4.5
1	C	122	THR	4.4
1	F	122	THR	4.2
1	G	222	CYS	4.1
1	G	221	LYS	4.1
1	G	224	TYR	3.9
1	H	122	THR	3.9
1	A	122	THR	3.9
1	G	270	PHE	3.7
1	H	270	PHE	3.6
1	F	270	PHE	3.5
1	F	222	CYS	3.5
1	E	222	CYS	3.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	E	270	PHE	3.4
1	D	122	THR	3.4
1	E	340	ILE	3.3
1	B	122	THR	3.3
1	G	183	LYS	3.2
1	G	180	ASN	3.1
1	G	226	SER	3.1
1	E	221	LYS	3.1
1	G	200	TYR	3.0
1	E	181	GLU	3.0
1	E	202	ILE	3.0
1	G	218[A]	MET	3.0
1	A	270	PHE	2.9
1	B	222	CYS	2.9
1	C	182	GLU	2.9
1	G	184	TYR	2.9
1	H	334	TYR	2.9
1	G	211	ALA	2.9
1	H	281[A]	CYS	2.8
1	E	182	GLU	2.8
1	E	184	TYR	2.7
1	E	230	ALA	2.7
1	G	182	GLU	2.7
1	E	228	ASN	2.6
1	G	202	ILE	2.6
1	G	213	TYR	2.6
1	F	221	LYS	2.5
1	E	168	ILE	2.5
1	G	181	GLU	2.5
1	E	214	PRO	2.4
1	E	178	CYS	2.4
1	H	222	CYS	2.4
1	E	201	ILE	2.4
1	E	207	ILE	2.4
1	H	277	ASP	2.4
1	E	209	ALA	2.4
1	F	227	LYS	2.4
1	G	186	ASN	2.4
1	G	340	ILE	2.4
1	F	218[A]	MET	2.4
1	H	168	ILE	2.3
1	C	340	ILE	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	G	232	THR	2.3
1	G	178	CYS	2.2
1	E	206	GLY	2.2
1	H	266	SER	2.2
1	H	309	TRP	2.2
1	H	180	ASN	2.1
1	E	232	THR	2.1
1	B	270	PHE	2.1
1	G	220	GLU	2.1
1	C	222	CYS	2.1
1	E	226	SER	2.1
1	G	227	LYS	2.1
1	A	340	ILE	2.1
1	E	225	ASN	2.1
1	E	211	ALA	2.1
1	D	340	ILE	2.1
1	G	225	ASN	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.

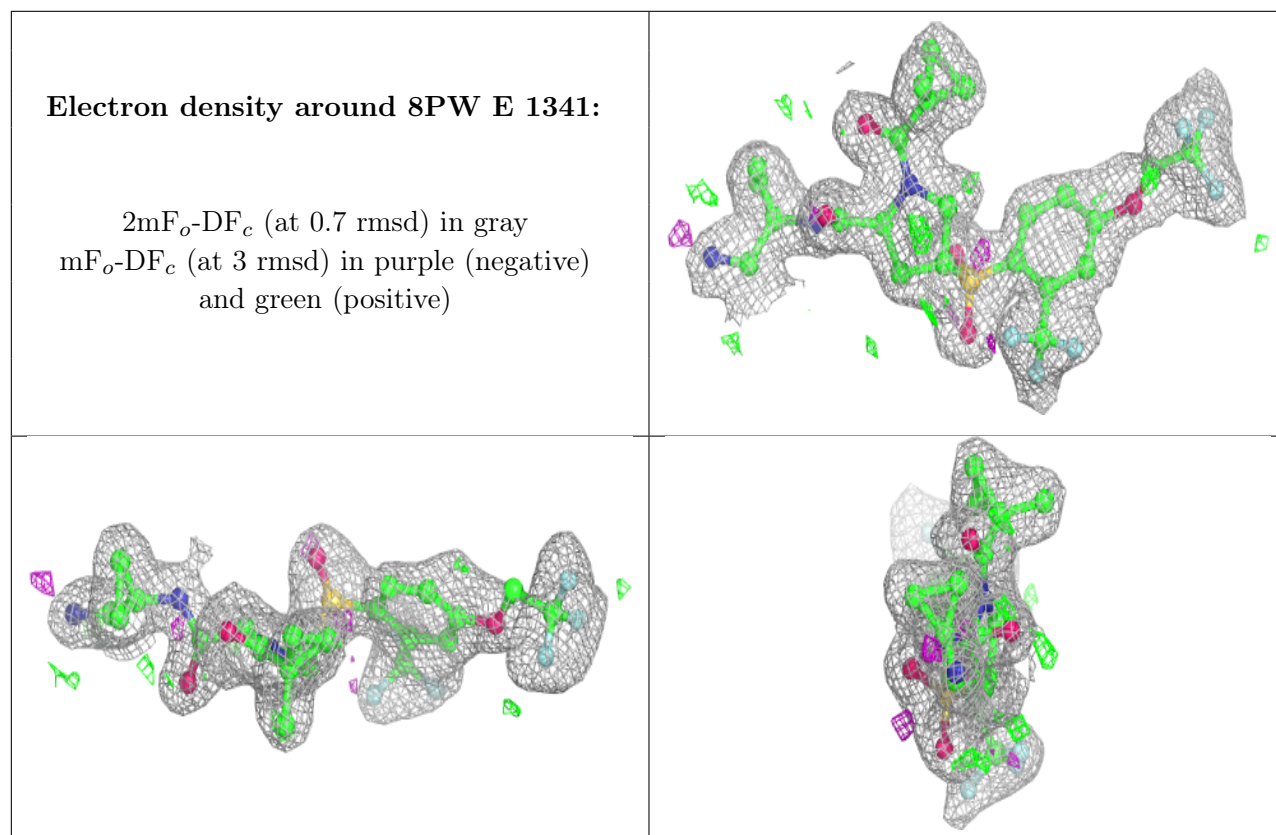
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	8PW	E	1341	38/38	0.90	0.13	22,30,46,47	0
2	8PW	H	1341	38/38	0.90	0.16	17,20,37,41	0
2	8PW	G	1341	38/38	0.91	0.13	22,31,50,51	0
2	8PW	B	1341	38/38	0.93	0.11	15,19,31,35	0
2	8PW	F	1341	38/38	0.93	0.12	16,20,36,39	0
2	8PW	A	1341	38/38	0.95	0.10	8,13,31,36	0

Continued on next page...

Continued from previous page...

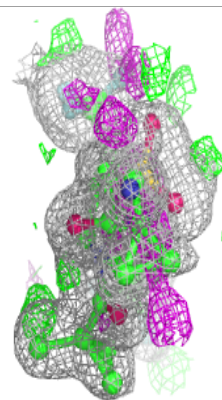
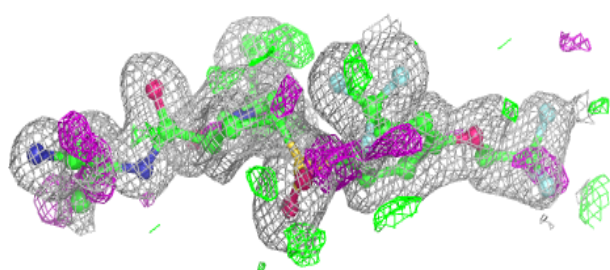
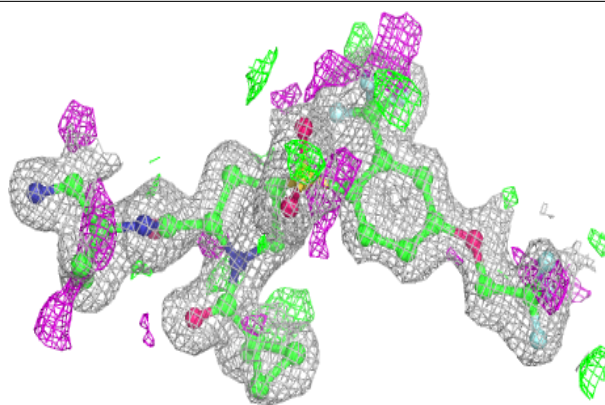
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	8PW	C	1341	38/38	0.95	0.09	16,20,32,37	0
2	8PW	D	1341	38/38	0.96	0.10	9,14,30,35	0

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.

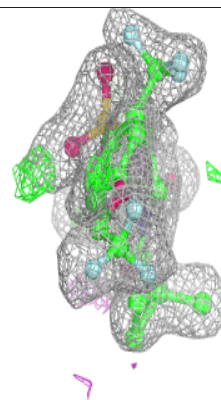
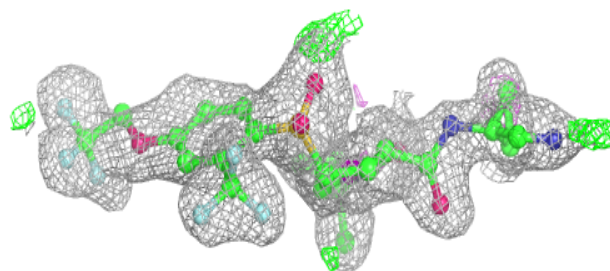
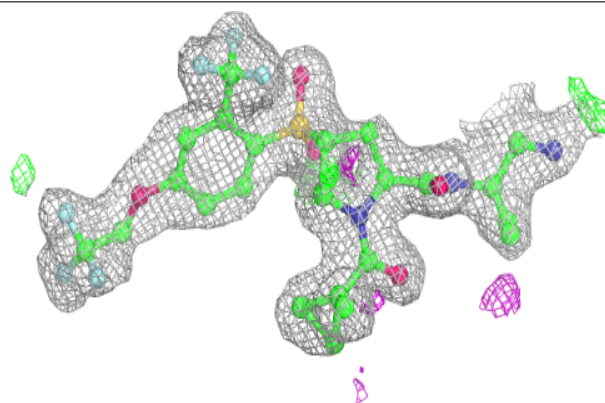


Electron density around 8PW H 1341:

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

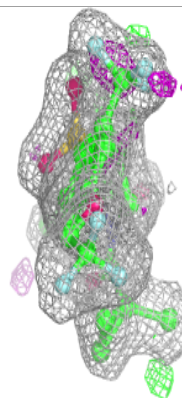
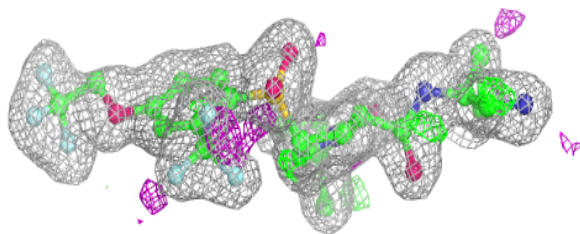
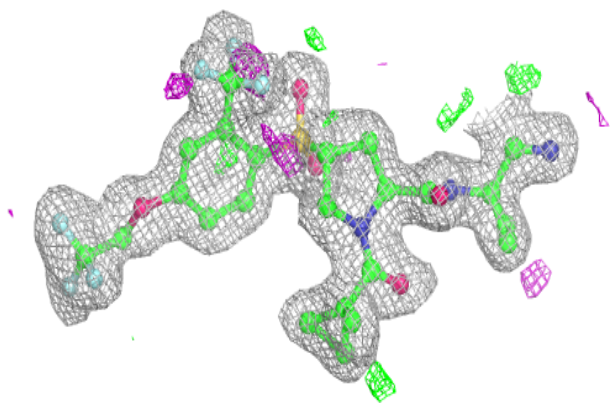
**Electron density around 8PW G 1341:**

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

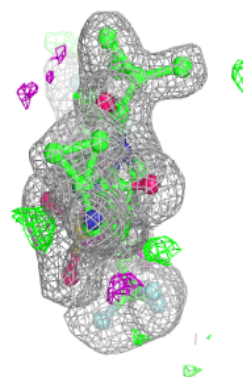
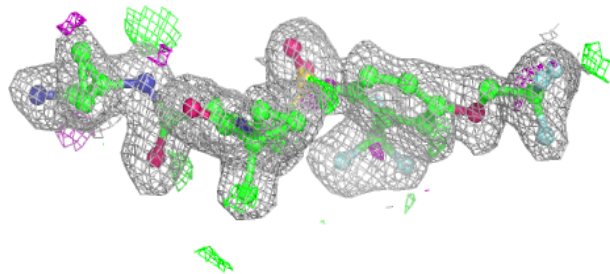
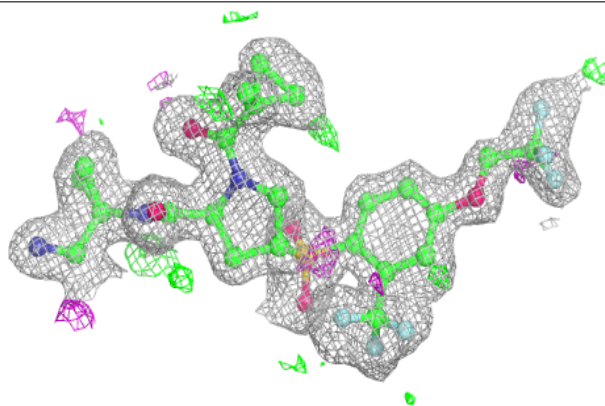


Electron density around 8PW B 1341:

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

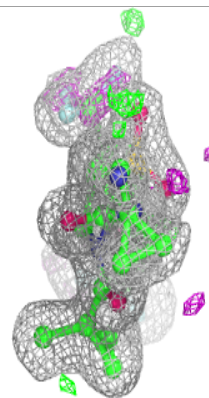
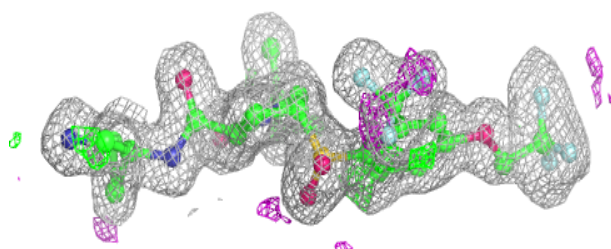
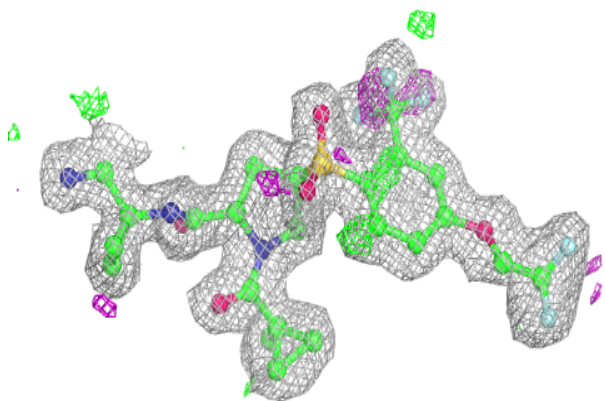
**Electron density around 8PW F 1341:**

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

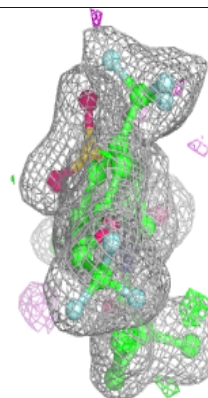
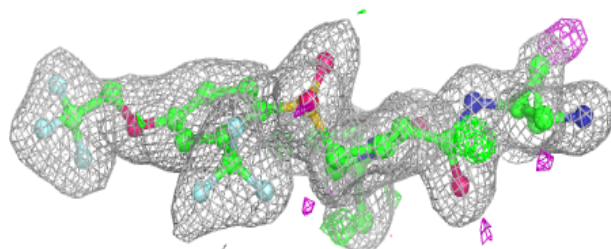
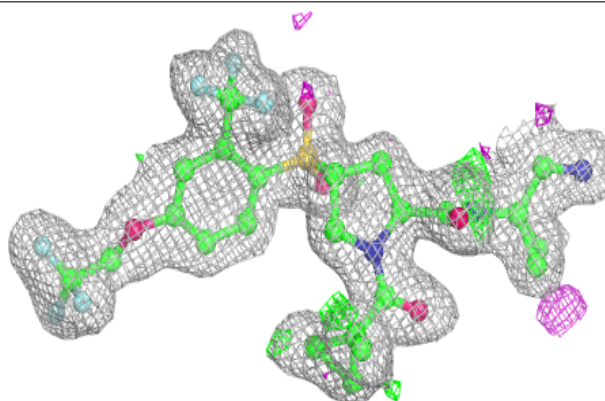


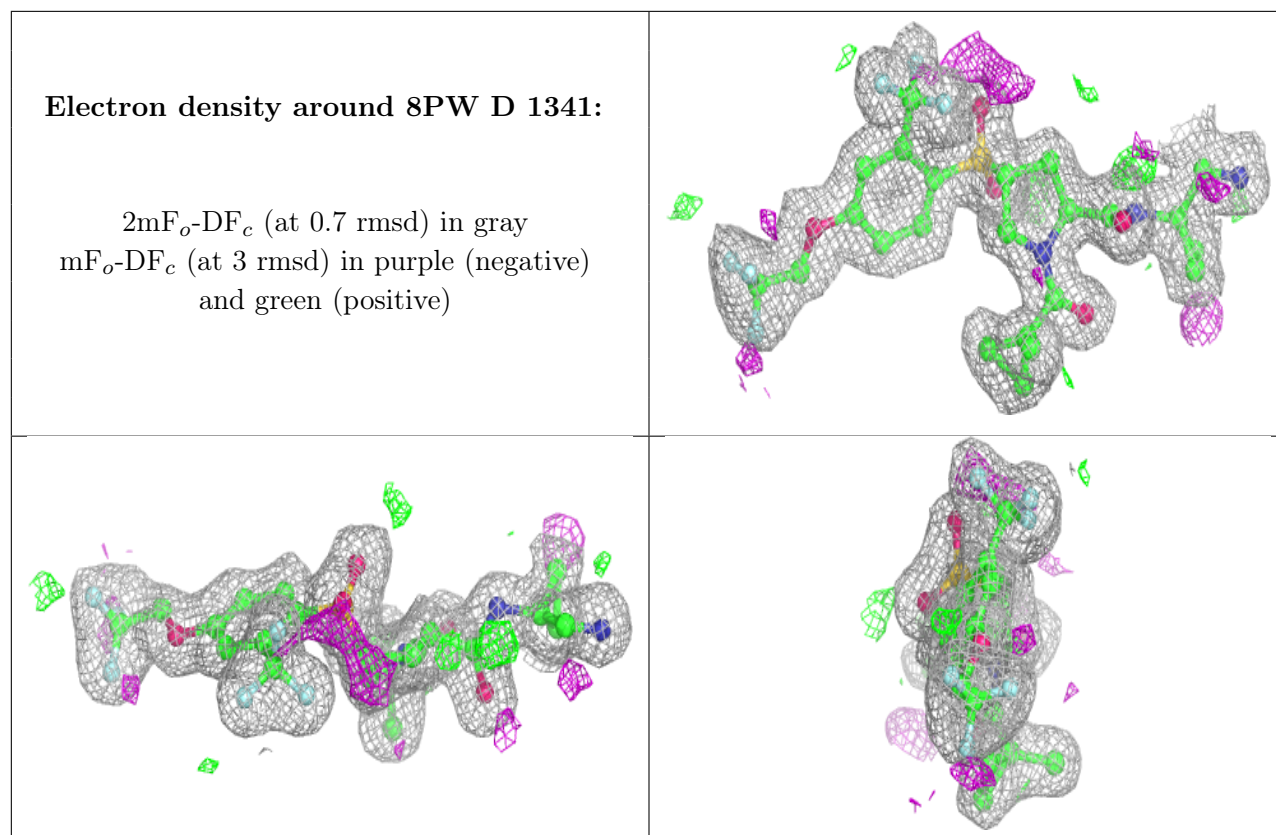
Electron density around 8PW A 1341:

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

**Electron density around 8PW C 1341:**

$2mF_o-DF_c$ (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.