



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 21, 2020 – 06:32 PM EST

PDB ID : 5QCY
Title : Crystal structure of BACE complex with BMC008
Authors : Rondeau, J.M.; Shao, C.; Yang, H.; Burley, S.K.
Deposited on : 2017-12-01
Resolution : 2.15 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 : 2.16
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) : 2.16

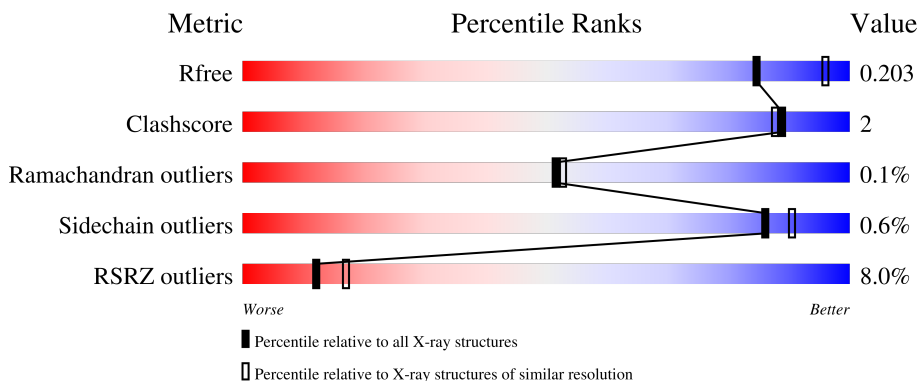
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


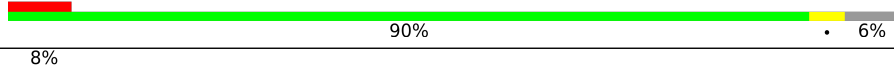
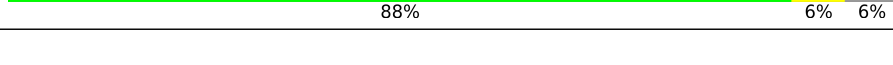
The reported resolution of this entry is 2.15 Å.

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	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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	402	
1	B	402	
1	C	402	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9510 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.

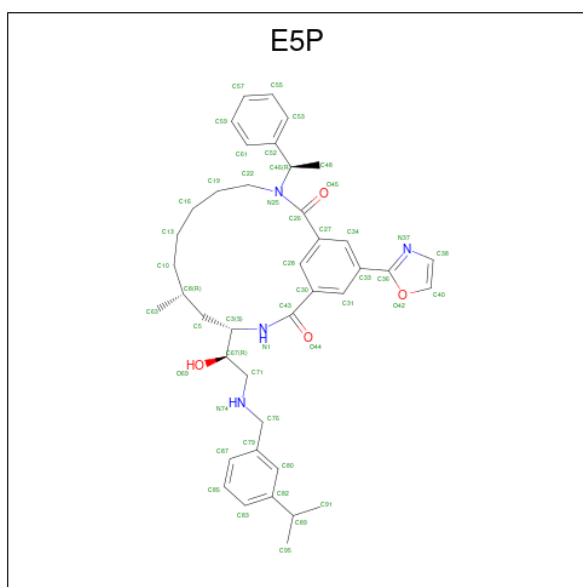
- Molecule 1 is a protein called Beta-secretase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	377	2966	1898	493	561	14	0	0	0
1	B	377	2966	1898	493	561	14	0	0	0
1	C	378	2971	1901	494	562	14	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	GLY	-	expression tag	UNP P56817
A	-14	PRO	-	expression tag	UNP P56817
B	-15	GLY	-	expression tag	UNP P56817
B	-14	PRO	-	expression tag	UNP P56817
C	-15	GLY	-	expression tag	UNP P56817
C	-14	PRO	-	expression tag	UNP P56817

- Molecule 2 is (9R,11S)-11-[(1R)-1-hydroxy-2-({[3-(propan-2-yl)phenyl]methyl}amino)ethyl]-9-methyl-16-(1,3-oxazol-2-yl)-3-[(1R)-1-phenylethyl]-3,12-diazabicyclo[12.3.1]octadeca-1(18),14,16-triene-2,13-dione (three-letter code: E5P) (formula: C₄₀H₅₀N₄O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			48	40	4	4		
2	B	1	Total	C	N	O	0	0
			48	40	4	4		
2	C	1	Total	C	N	O	0	0
			48	40	4	4		

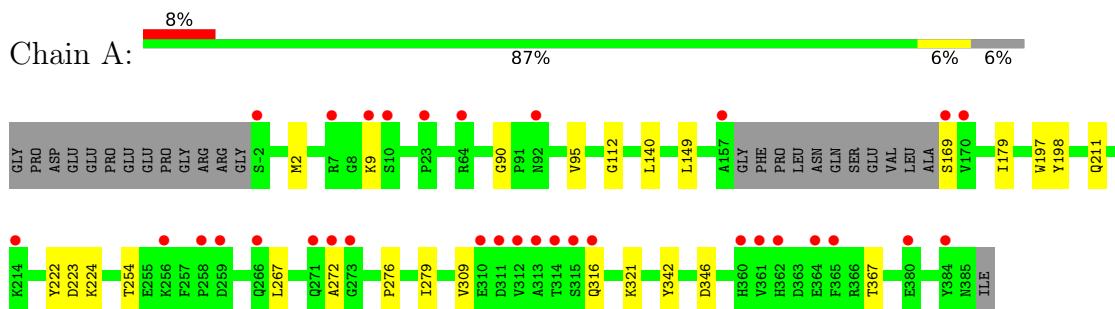
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	153	Total	O	0	0
			153	153		
3	B	151	Total	O	0	0
			151	151		
3	C	159	Total	O	0	0
			159	159		

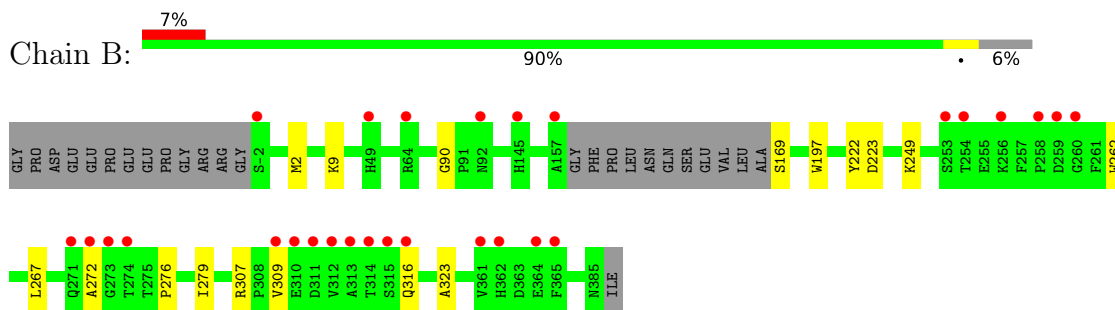
3 Residue-property plots [i](#)

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.

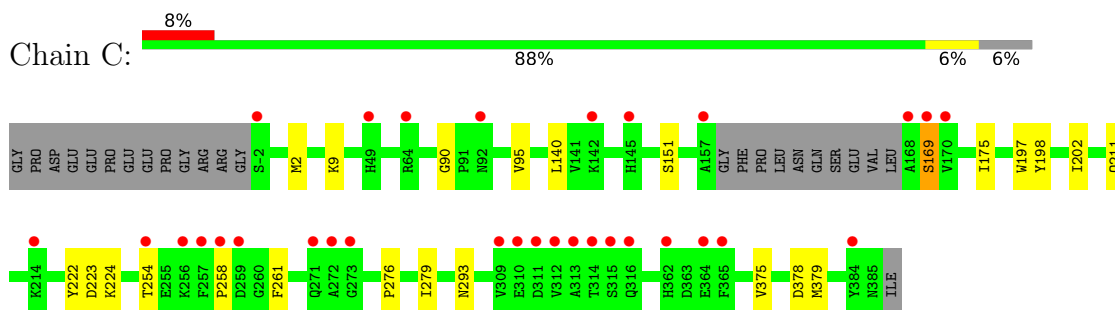
- Molecule 1: Beta-secretase 1



- Molecule 1: Beta-secretase 1



- Molecule 1: Beta-secretase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.09Å 102.87Å 101.06Å 90.00° 103.90° 90.00°	Depositor
Resolution (Å)	17.42 – 2.15 17.42 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.9 (17.42-2.15) 100.0 (17.42-2.15)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.52 (at 2.15Å)	Xtrriage
Refinement program	PHENIX 1.12_2829, CNX	Depositor
R, R_{free}	0.169 , 0.203 0.169 , 0.203	Depositor DCC
R_{free} test set	4451 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	38.4	Xtrriage
Anisotropy	0.061	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 45.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9510	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: E5P

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	0.41	0/3041	0.58	0/4133
1	B	0.40	0/3041	0.57	0/4133
1	C	0.40	0/3046	0.59	0/4140
All	All	0.40	0/9128	0.58	0/12406

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2966	0	2878	14	0
1	B	2966	0	2878	9	0
1	C	2971	0	2883	12	0
2	A	48	0	0	0	0
2	B	48	0	0	0	0
2	C	48	0	0	0	0
3	A	153	0	0	0	0
3	B	151	0	0	0	1
3	C	159	0	0	1	1
All	All	9510	0	8639	34	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 2.

All (34) 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:A:254:THR:HG21	1:C:254:THR:HG21	1.82	0.60
1:C:202:ILE:CD1	1:C:379:MET:HG3	2.41	0.51
1:B:276:PRO:O	1:B:279:ILE:HG12	2.09	0.51
1:A:267:LEU:HD22	1:A:309:VAL:HG21	1.93	0.49
1:C:9:LYS:HA	1:C:169:SER:HB3	1.95	0.48
1:B:272:ALA:HB2	1:B:316:GLN:O	2.13	0.48
1:C:2:MET:HG2	1:C:90:GLY:HA2	1.96	0.48
1:A:9:LYS:HA	1:A:169:SER:HB3	1.96	0.47
1:C:222:TYR:HA	1:C:223:ASP:HA	1.73	0.47
1:C:198:TYR:CE2	1:C:224:LYS:HE3	2.49	0.47
1:B:222:TYR:HA	1:B:223:ASP:HA	1.72	0.47
1:A:2:MET:HG2	1:A:90:GLY:HA2	1.97	0.46
1:A:198:TYR:CE2	1:A:224:LYS:HE3	2.51	0.46
1:A:222:TYR:HA	1:A:223:ASP:HA	1.67	0.46
1:B:267:LEU:HD22	1:B:309:VAL:HG21	1.97	0.45
1:A:9:LYS:HD3	1:A:112:GLY:O	2.16	0.45
1:C:293:ASN:HA	1:C:375:VAL:HA	1.97	0.45
1:A:272:ALA:HB2	1:A:316:GLN:O	2.17	0.44
1:B:267:LEU:HD13	1:B:309:VAL:HG21	2.00	0.44
1:B:307:ARG:HG2	1:B:323:ALA:HB2	2.00	0.43
1:A:95:VAL:HG11	1:A:140:LEU:HA	2.01	0.43
1:A:179:ILE:HG23	1:A:342:TYR:HE2	1.84	0.42
1:C:378:ASP:HB2	3:C:618:HOH:O	2.19	0.42
1:A:321:LYS:HE3	1:A:321:LYS:HB2	1.88	0.42
1:A:149:LEU:HB2	1:A:346:ASP:HA	2.02	0.42
1:C:151:SER:OG	1:C:175:ILE:HB	2.20	0.41
1:B:9:LYS:HA	1:B:169:SER:HB3	2.02	0.41
1:A:267:LEU:HD13	1:A:309:VAL:HG21	2.03	0.41
1:B:249:LYS:HE2	1:B:262:TRP:CD1	2.56	0.41
1:B:2:MET:HG2	1:B:90:GLY:HA2	2.02	0.41
1:C:276:PRO:O	1:C:279:ILE:HG12	2.21	0.41
1:C:95:VAL:HG11	1:C:140:LEU:HA	2.03	0.40
1:A:276:PRO:O	1:A:279:ILE:HG12	2.21	0.40
1:C:258:PRO:O	1:C:261:PHE:HB3	2.21	0.40

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)
3:B:509:HOH:O	3:C:647:HOH:O[2_655]	1.99	0.21

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	373/402 (93%)	365 (98%)	8 (2%)	0	100	100
1	B	373/402 (93%)	366 (98%)	7 (2%)	0	100	100
1	C	374/402 (93%)	365 (98%)	8 (2%)	1 (0%)	41	37
All	All	1120/1206 (93%)	1096 (98%)	23 (2%)	1 (0%)	51	53

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	169	SER

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	322/342 (94%)	319 (99%)	3 (1%)	78	83
1	B	322/342 (94%)	321 (100%)	1 (0%)	92	95
1	C	322/342 (94%)	320 (99%)	2 (1%)	86	90
All	All	966/1026 (94%)	960 (99%)	6 (1%)	86	90

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	197	TRP
1	A	211	GLN
1	A	367	THR
1	B	197	TRP
1	C	197	TRP
1	C	211	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

3 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	E5P	B	401	-	49,52,52	0.62	1 (2%)	62,71,71	1.03	5 (8%)
2	E5P	A	401	-	49,52,52	0.74	1 (2%)	62,71,71	1.07	4 (6%)
2	E5P	C	401	-	49,52,52	0.76	1 (2%)	62,71,71	0.95	3 (4%)

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	E5P	B	401	-	-	8/52/54/54	0/4/5/5
2	E5P	A	401	-	-	9/52/54/54	0/4/5/5
2	E5P	C	401	-	-	7/52/54/54	0/4/5/5

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	401	E5P	C22-N25	2.93	1.51	1.46
2	A	401	E5P	C22-N25	2.68	1.51	1.46
2	B	401	E5P	C22-N25	2.34	1.50	1.46

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	E5P	C67-C71-N74	-4.24	106.15	111.97
2	A	401	E5P	C33-C36-N37	3.77	128.97	123.42
2	B	401	E5P	C33-C36-N37	3.75	128.95	123.42
2	C	401	E5P	C33-C36-N37	3.69	128.85	123.42
2	B	401	E5P	C67-C71-N74	-3.44	107.25	111.97
2	B	401	E5P	C8-C5-C3	-2.78	110.47	115.83
2	A	401	E5P	C8-C5-C3	-2.75	110.52	115.83
2	C	401	E5P	C67-C71-N74	-2.72	108.24	111.97
2	A	401	E5P	C27-C26-N25	2.39	123.52	118.77
2	B	401	E5P	C27-C26-N25	2.36	123.46	118.77
2	C	401	E5P	C27-C26-N25	2.34	123.41	118.77
2	B	401	E5P	C34-C27-C26	-2.15	115.35	120.14

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	401	E5P	C52-C46-N25-C22
2	A	401	E5P	C52-C46-N25-C22
2	C	401	E5P	C52-C46-N25-C22
2	A	401	E5P	C48-C46-N25-C22
2	C	401	E5P	C48-C46-N25-C22
2	A	401	E5P	C10-C13-C16-C19

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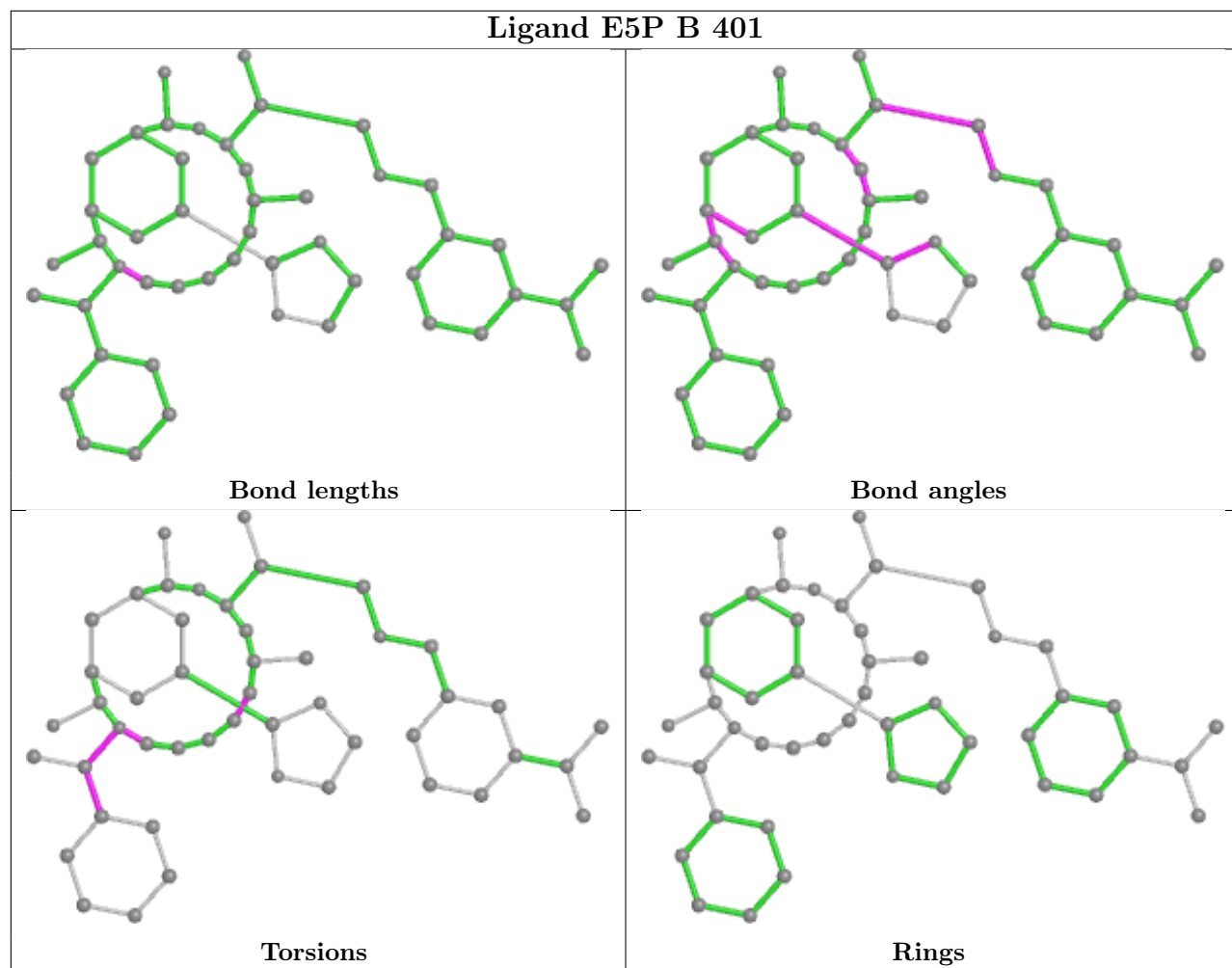
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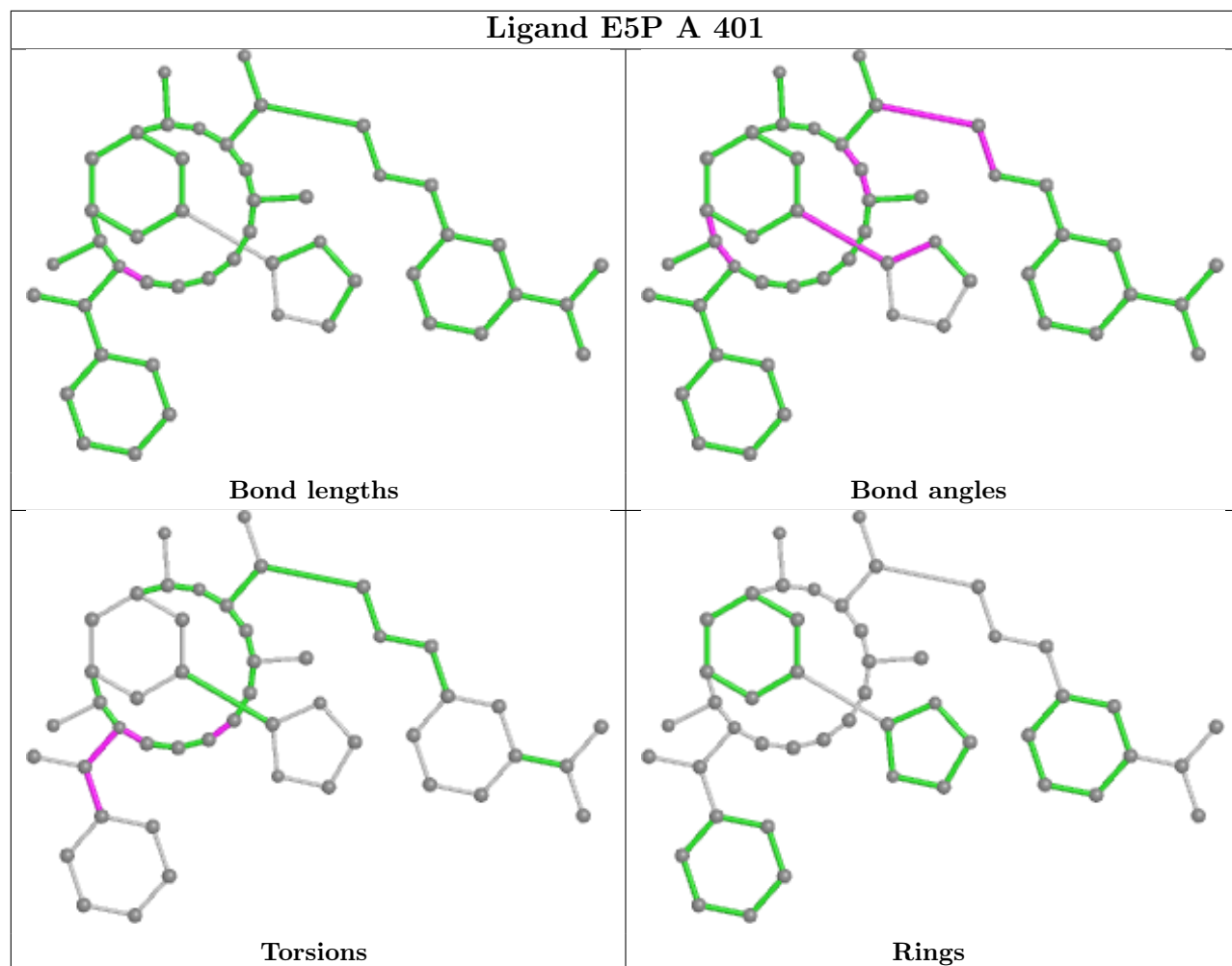
Mol	Chain	Res	Type	Atoms
2	A	401	E5P	C19-C22-N25-C26
2	C	401	E5P	C8-C10-C13-C16
2	B	401	E5P	C48-C46-N25-C22
2	A	401	E5P	C48-C46-N25-C26
2	A	401	E5P	N25-C46-C52-C61
2	C	401	E5P	N25-C46-C52-C61
2	B	401	E5P	N25-C46-C52-C61
2	C	401	E5P	C31-C33-C36-N37
2	B	401	E5P	C8-C10-C13-C16
2	A	401	E5P	N25-C46-C52-C53
2	B	401	E5P	C48-C46-N25-C26
2	A	401	E5P	C52-C46-N25-C26
2	C	401	E5P	C48-C46-N25-C26
2	B	401	E5P	N25-C46-C52-C53
2	C	401	E5P	N25-C46-C52-C53
2	B	401	E5P	C19-C22-N25-C26
2	B	401	E5P	C19-C22-N25-C46
2	A	401	E5P	C19-C22-N25-C46

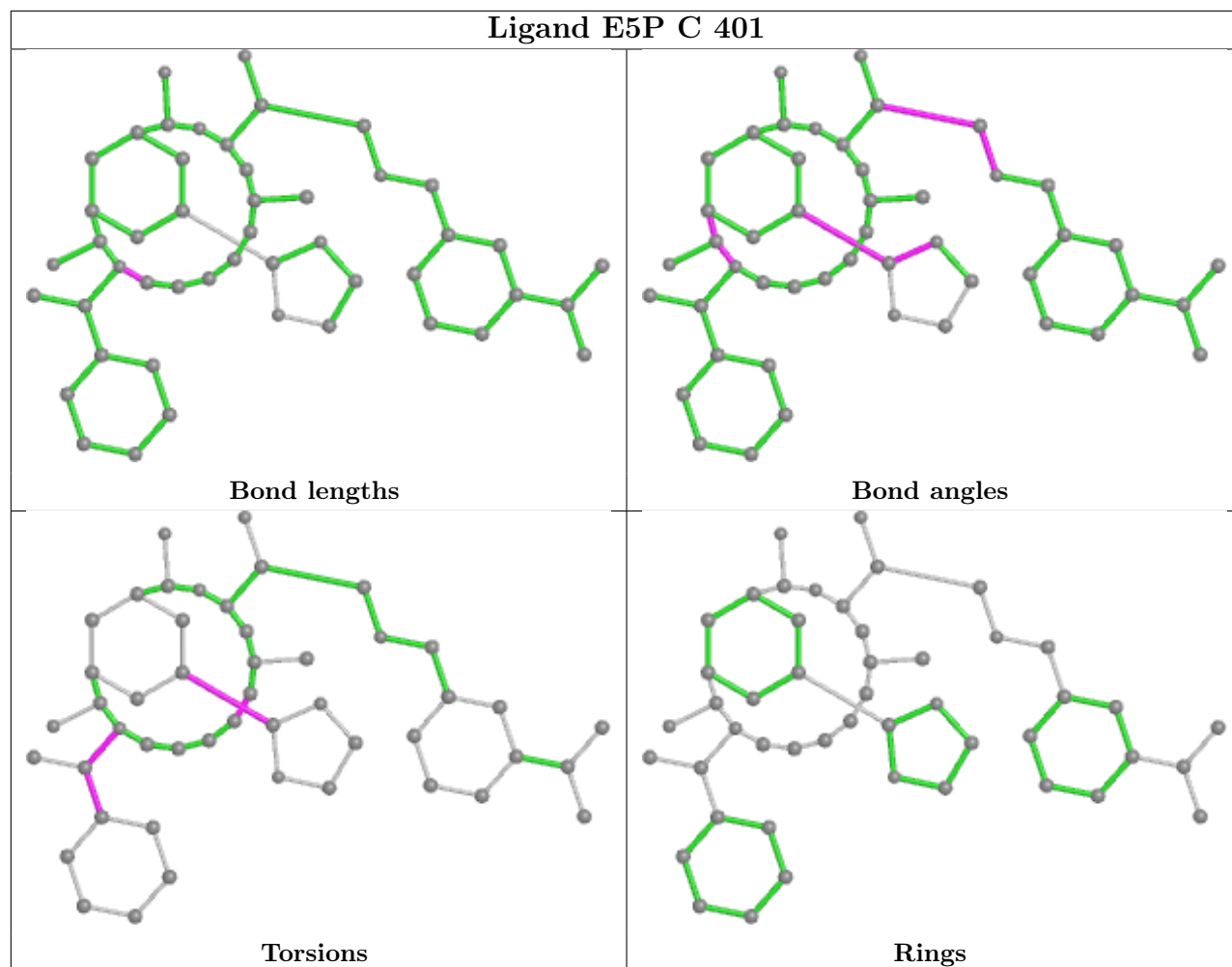
There are no ring outliers.

No monomer is involved in short contacts.

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

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	377/402 (93%)	0.29	32 (8%) 10 15	27, 41, 83, 178	0
1	B	377/402 (93%)	0.29	28 (7%) 14 20	26, 43, 87, 186	0
1	C	378/402 (94%)	0.22	31 (8%) 11 16	29, 43, 80, 159	0
All	All	1132/1206 (93%)	0.27	91 (8%) 12 17	26, 42, 85, 186	0

All (91) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	314	THR	14.2
1	A	312	VAL	11.0
1	A	314	THR	10.2
1	A	316	GLN	9.5
1	B	312	VAL	9.0
1	C	312	VAL	8.8
1	C	168	ALA	8.1
1	B	157	ALA	8.1
1	B	313	ALA	7.2
1	C	316	GLN	7.0
1	C	314	THR	6.8
1	C	-2	SER	6.6
1	A	313	ALA	6.5
1	C	310	GLU	6.2
1	A	157	ALA	5.7
1	B	316	GLN	5.7
1	A	311	ASP	5.4
1	C	272	ALA	5.4
1	A	310	GLU	5.4
1	A	364	GLU	5.3
1	C	365	PHE	5.3
1	A	365	PHE	5.2
1	C	169	SER	5.2

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Mol	Chain	Res	Type	RSRZ
1	C	362	HIS	5.0
1	C	256	LYS	4.9
1	B	64	ARG	4.7
1	C	64	ARG	4.4
1	B	256	LYS	4.4
1	B	362	HIS	4.4
1	C	364	GLU	4.2
1	B	310	GLU	4.1
1	B	364	GLU	4.0
1	B	361	VAL	3.9
1	C	313	ALA	3.9
1	B	-2	SER	3.8
1	A	170	VAL	3.8
1	C	273	GLY	3.7
1	B	259	ASP	3.7
1	A	64	ARG	3.7
1	B	315	SER	3.7
1	B	254	THR	3.6
1	C	259	ASP	3.6
1	A	256	LYS	3.5
1	B	271	GLN	3.5
1	C	311	ASP	3.4
1	A	362	HIS	3.4
1	A	258	PRO	3.4
1	B	311	ASP	3.3
1	A	360	HIS	3.2
1	A	7	ARG	3.2
1	C	157	ALA	3.1
1	C	145	HIS	3.1
1	B	274	THR	3.1
1	A	315	SER	3.0
1	B	253	SER	3.0
1	A	361	VAL	3.0
1	A	272	ALA	3.0
1	B	49	HIS	2.9
1	B	365	PHE	2.9
1	A	169	SER	2.9
1	C	254	THR	2.9
1	A	-2	SER	2.9
1	A	259	ASP	2.8
1	B	273	GLY	2.8
1	A	273	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	145	HIS	2.6
1	A	10	SER	2.6
1	C	258	PRO	2.6
1	B	272	ALA	2.5
1	B	258	PRO	2.5
1	A	9	LYS	2.5
1	C	257	PHE	2.5
1	A	92	ASN	2.5
1	A	271	GLN	2.4
1	C	49	HIS	2.4
1	A	266	GLN	2.3
1	A	214	LYS	2.3
1	C	271	GLN	2.3
1	C	214	LYS	2.3
1	A	384	TYR	2.3
1	B	260	GLY	2.3
1	C	170	VAL	2.2
1	B	92	ASN	2.2
1	A	23	PRO	2.2
1	C	384	TYR	2.2
1	C	315	SER	2.2
1	A	380	GLU	2.1
1	C	92	ASN	2.1
1	B	309	VAL	2.1
1	C	309	VAL	2.1
1	C	142	LYS	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 [\(i\)](#)

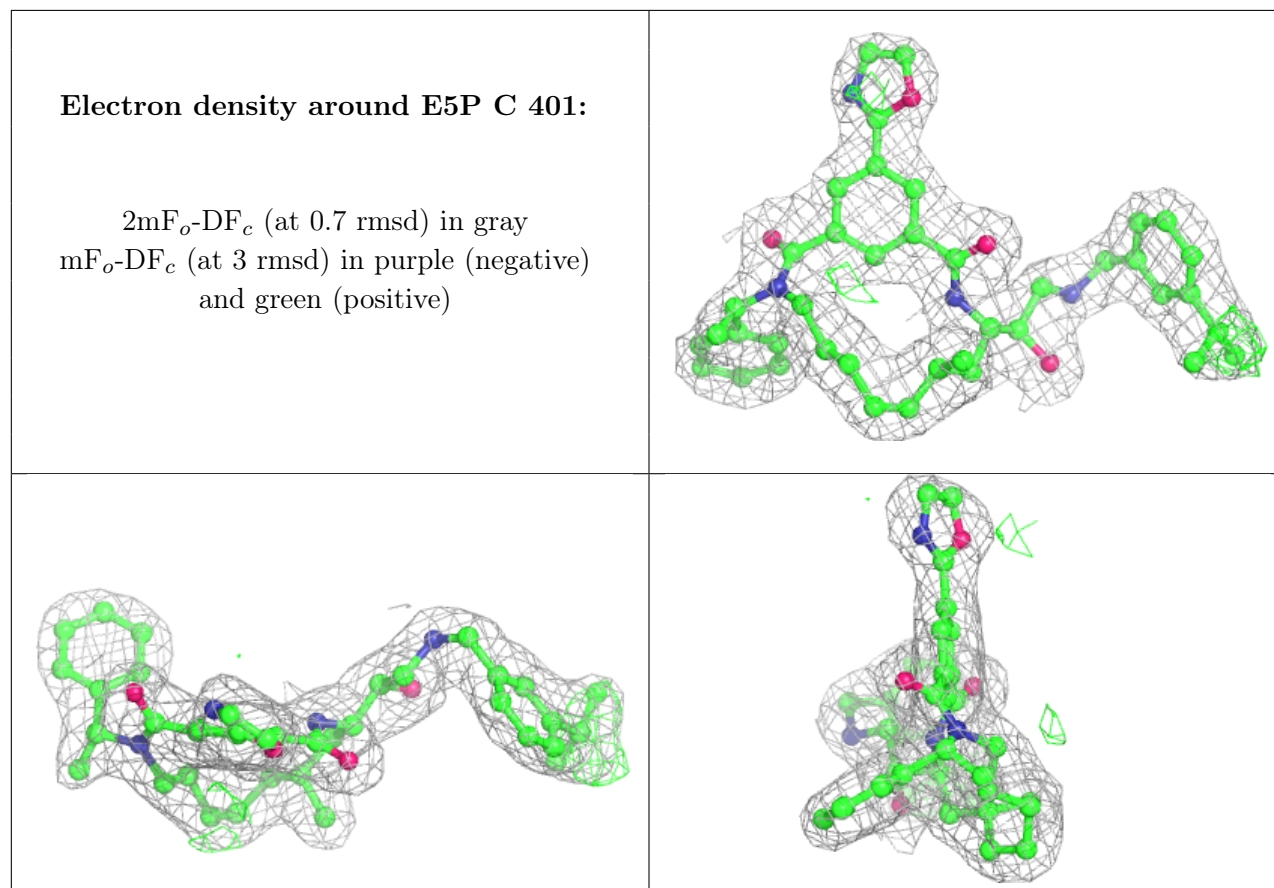
There are no monosaccharides in this entry.

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.

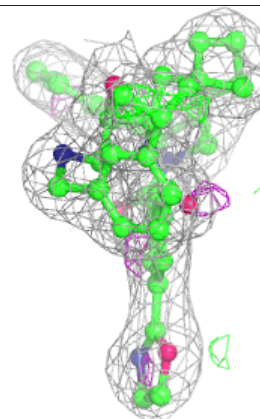
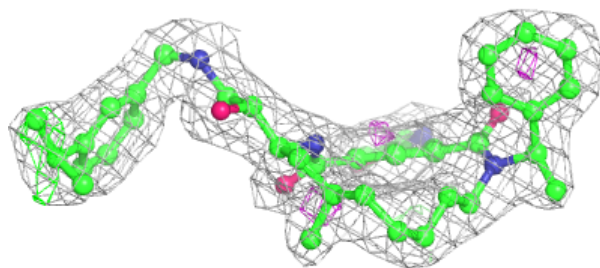
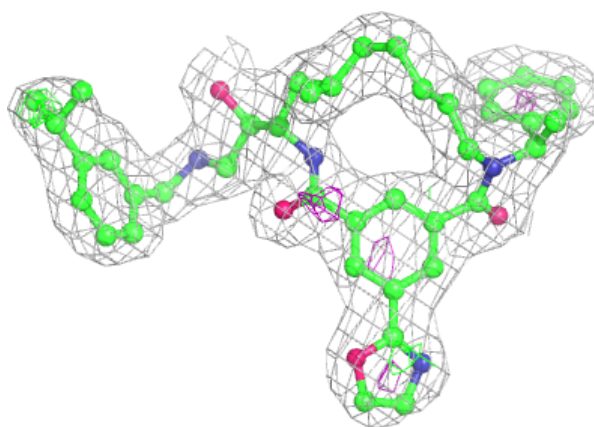
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	E5P	C	401	48/48	0.88	0.16	29,35,53,53	2
2	E5P	B	401	48/48	0.89	0.17	29,35,47,52	2
2	E5P	A	401	48/48	0.91	0.14	29,35,49,51	2

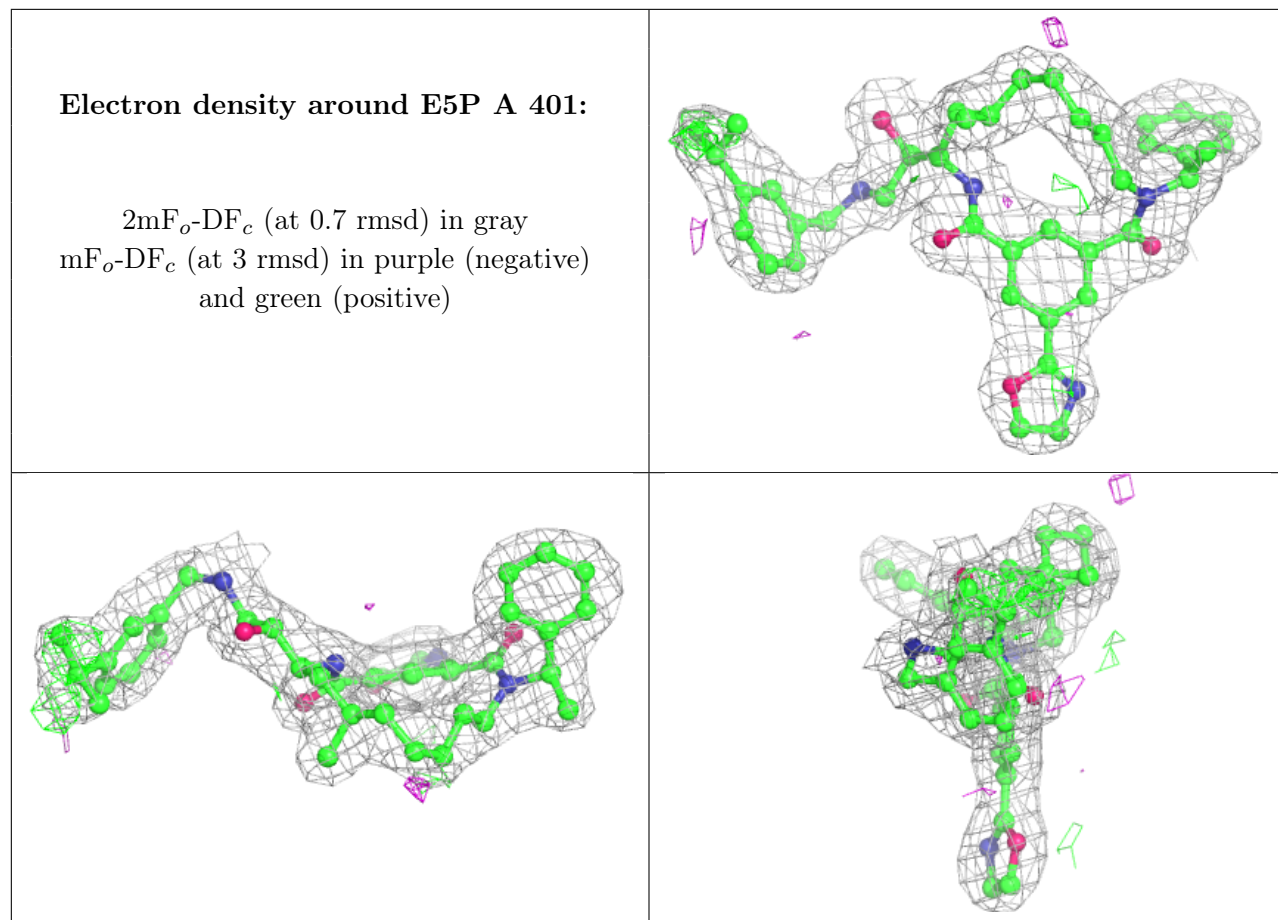
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



Electron density around E5P B 401:

$2mF_o-DF_c$ (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.