Full wwPDB X-ray Structure Validation Report (i)

Jun 25, 2024 – 02:26 AM EDT

PDB ID	:	5QD5
Title	:	Crystal structure of BACE complex with BMC009
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Deposited on	:	2017-12-01
Resolution	:	2.30 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 (i) 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 (i)) were used in the production of this report:

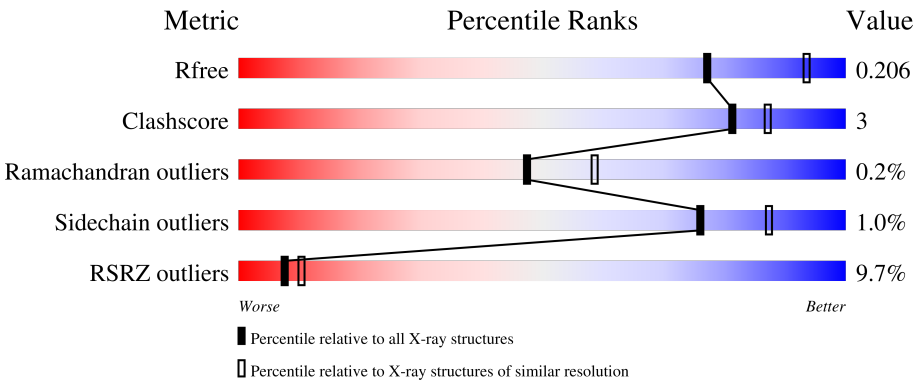
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 <=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	9% 86% 7% 6%
1	B	402	9% 87% 6% 6%
1	C	402	9% 89% 5% 6%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 9380 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.

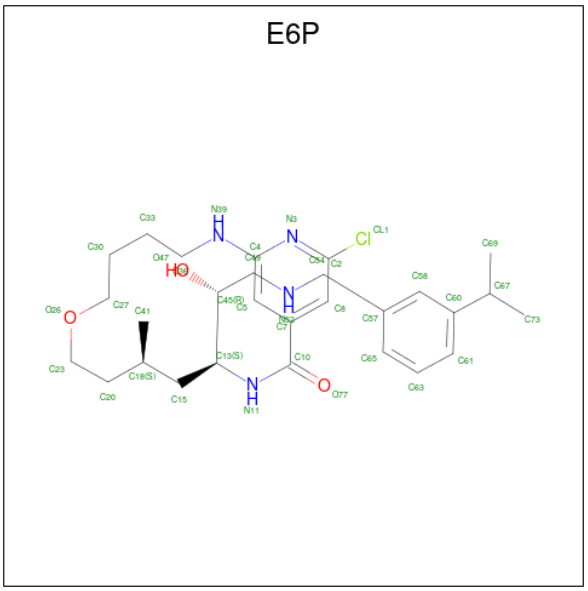
- Molecule 1 is a protein called Beta-secretase 1.

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 (10S,12S)-17-chloro-12-[(1R)-1-hydroxy-2-({[3-(propan-2-yl)phenyl]methyl}amino)ethyl]-10-methyl-7-oxa-2,13,18-triazabicyclo[13.3.1]nonadeca-1(19),15,17-trien-14-one (three-letter code: E6P) (formula: $C_{28}H_{41}ClN_4O_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	0	0
			36	28	1	4	3		
2	B	1	Total	C	Cl	N	O	0	0
			36	28	1	4	3		
2	C	1	Total	C	Cl	N	O	0	0
			36	28	1	4	3		

- Molecule 3 is water.

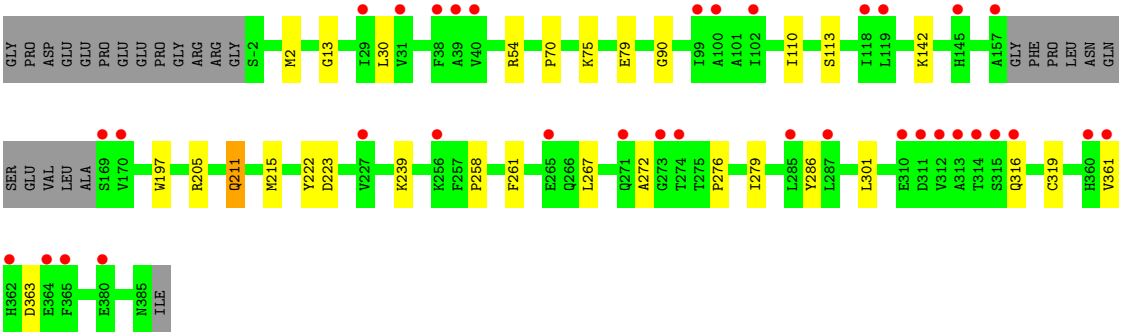
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	119	Total	O	0	0
			119	119		
3	B	115	Total	O	0	0
			115	115		
3	C	135	Total	O	0	0
			135	135		

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.

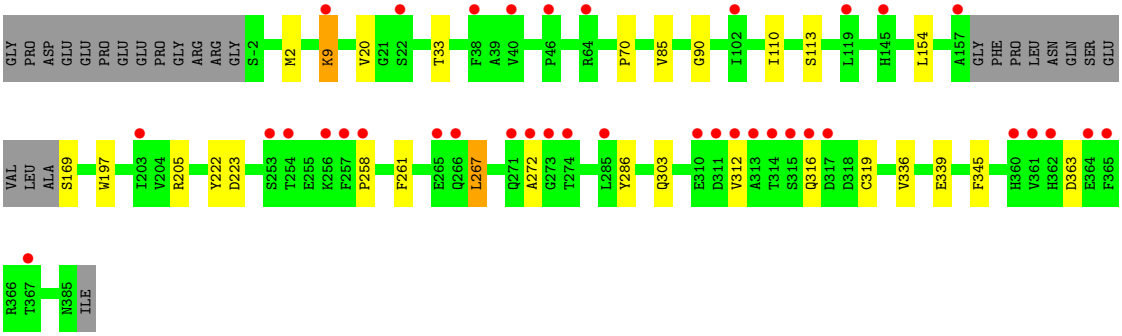
• Molecule 1: Beta-secretase 1

Chain A: 9% 86% 7% 6%



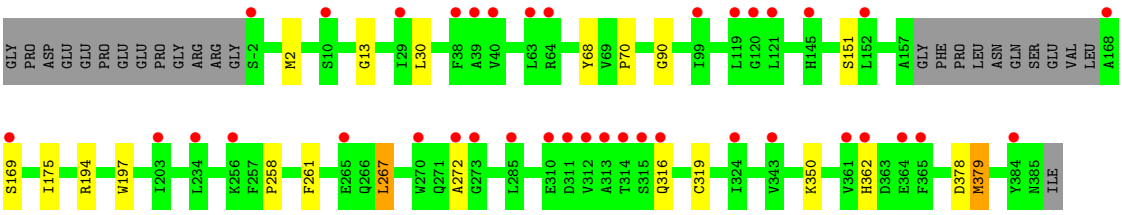
• Molecule 1: Beta-secretase 1

Chain B: 9% 87% 6% 6%



• Molecule 1: Beta-secretase 1

Chain C: 9% 89% 5% 6%



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	82.01Å 103.31Å 99.80Å 90.00° 104.18° 90.00°	Depositor
Resolution (Å)	24.25 – 2.30 24.25 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.4 (24.25-2.30) 98.5 (24.25-2.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.59 (at 2.31Å)	Xtriage
Refinement program	PHENIX 1.12_2829, CNX	Depositor
R, R_{free}	0.177 , 0.207 0.177 , 0.206	Depositor DCC
R_{free} test set	3599 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	39.6	Xtriage
Anisotropy	0.115	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 47.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	9380	wwPDB-VP
Average B, all atoms (Å^2)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.37% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: E6P

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	0.41	0/3041	0.58	0/4133
1	C	0.40	0/3046	0.58	0/4140
All	All	0.41	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	18	0
1	B	2966	0	2878	15	0
1	C	2971	0	2883	12	0
2	A	36	0	0	0	0
2	B	36	0	0	0	0
2	C	36	0	0	0	0
3	A	119	0	0	1	0
3	B	115	0	0	1	0
3	C	135	0	0	1	0
All	All	9380	0	8639	45	0

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

All (45) 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:B:205:ARG:NH1	3:B:501:HOH:O	2.06	0.88
1:A:301:LEU:HD12	1:A:361:VAL:HG23	1.82	0.61
1:A:267:LEU:H	1:A:267:LEU:HD23	1.64	0.61
1:B:267:LEU:H	1:B:267:LEU:HD23	1.67	0.60
1:C:267:LEU:HD23	1:C:267:LEU:H	1.67	0.59
1:C:68:TYR:OH	1:C:70:PRO:HB3	2.03	0.57
1:B:9:LYS:HE2	1:B:169:SER:HB2	1.87	0.55
1:A:215:MET:HE3	1:A:239:LYS:HE3	1.89	0.53
1:A:267:LEU:HD12	1:A:319:CYS:HB3	1.89	0.53
1:A:272:ALA:HB2	1:A:316:GLN:O	2.09	0.53
1:B:303:GLN:NE2	1:B:363:ASP:HB3	2.26	0.51
1:C:272:ALA:HB2	1:C:316:GLN:O	2.12	0.50
1:A:110:ILE:HB	1:A:113:SER:HB3	1.94	0.49
1:B:110:ILE:HB	1:B:113:SER:HB3	1.94	0.49
1:B:205:ARG:HB3	1:B:286:TYR:HB2	1.95	0.49
1:B:267:LEU:HD11	1:B:312:VAL:HG13	1.94	0.49
1:B:272:ALA:HB2	1:B:316:GLN:O	2.11	0.49
1:A:2:MET:HG2	1:A:90:GLY:HA2	1.95	0.48
1:B:2:MET:HG2	1:B:90:GLY:HA2	1.96	0.47
1:A:301:LEU:HD13	1:A:363:ASP:HB2	1.96	0.47
1:C:258:PRO:O	1:C:261:PHE:HB3	2.14	0.47
1:B:222:TYR:HA	1:B:223:ASP:HA	1.63	0.47
1:A:211:GLN:HB2	3:A:552:HOH:O	2.14	0.47
1:A:276:PRO:O	1:A:279:ILE:HG12	2.17	0.45
1:A:258:PRO:O	1:A:261:PHE:HB3	2.18	0.44
1:C:13:GLY:HA3	1:C:30:LEU:HD11	2.01	0.43
1:A:142:LYS:HE2	1:A:142:LYS:HB2	1.85	0.42
1:C:379:MET:HE2	1:C:379:MET:HB2	1.86	0.42
1:A:13:GLY:HA3	1:A:30:LEU:HD11	2.00	0.42
1:C:194:ARG:HG3	1:C:379:MET:SD	2.59	0.42
1:B:20:VAL:HG12	1:B:85:VAL:HG22	2.02	0.42
1:C:350:LYS:HE2	1:C:350:LYS:HB3	1.92	0.42
1:C:378:ASP:HB2	3:C:602:HOH:O	2.19	0.41
1:A:215:MET:HE1	1:A:239:LYS:HG2	2.01	0.41
1:B:154:LEU:O	1:B:339:GLU:HA	2.21	0.41
1:B:33:THR:HG21	1:B:345:PHE:CZ	2.55	0.41
1:B:258:PRO:O	1:B:261:PHE:HB3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:267:LEU:HD12	1:B:319:CYS:HB3	2.02	0.41
1:A:70:PRO:HA	1:A:75:LYS:HB3	2.02	0.41
1:A:54:ARG:NH1	1:A:79:GLU:OE1	2.32	0.41
1:C:151:SER:OG	1:C:175:ILE:HB	2.21	0.41
1:C:2:MET:HG2	1:C:90:GLY:HA2	2.03	0.40
1:C:267:LEU:HD12	1:C:319:CYS:HB3	2.01	0.40
1:A:205:ARG:HB3	1:A:286:TYR:HB2	2.03	0.40
1:A:222:TYR:HA	1:A:223:ASP:HA	1.70	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	373/402 (93%)	362 (97%)	11 (3%)	0	100	100
1	B	373/402 (93%)	363 (97%)	9 (2%)	1 (0%)	41	50
1	C	374/402 (93%)	364 (97%)	9 (2%)	1 (0%)	41	50
All	All	1120/1206 (93%)	1089 (97%)	29 (3%)	2 (0%)	47	58

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	169	SER
1	B	70	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	322/342 (94%)	320 (99%)	2 (1%)	86 94
1	B	322/342 (94%)	318 (99%)	4 (1%)	71 84
1	C	322/342 (94%)	318 (99%)	4 (1%)	71 84
All	All	966/1026 (94%)	956 (99%)	10 (1%)	76 87

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	197	TRP
1	A	211	GLN
1	B	9	LYS
1	B	197	TRP
1	B	267	LEU
1	B	336	VAL
1	C	197	TRP
1	C	267	LEU
1	C	362	HIS
1	C	379	MET

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	E6P	B	401	-	38,38,38	0.49	0	47,50,50	0.59	2 (4%)
2	E6P	C	401	-	38,38,38	0.46	0	47,50,50	0.53	1 (2%)
2	E6P	A	401	-	38,38,38	0.40	0	47,50,50	0.59	1 (2%)

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	E6P	B	401	-	-	0/37/37/37	0/2/3/3
2	E6P	C	401	-	-	2/37/37/37	0/2/3/3
2	E6P	A	401	-	-	0/37/37/37	0/2/3/3

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	401	E6P	C18-C15-C13	-2.61	110.78	115.83
2	B	401	E6P	C45-C49-N52	-2.52	108.50	111.97
2	B	401	E6P	C18-C15-C13	-2.27	111.45	115.83
2	A	401	E6P	C18-C15-C13	-2.01	111.95	115.83

There are no chirality outliers.

All (2) torsion outliers are listed below:

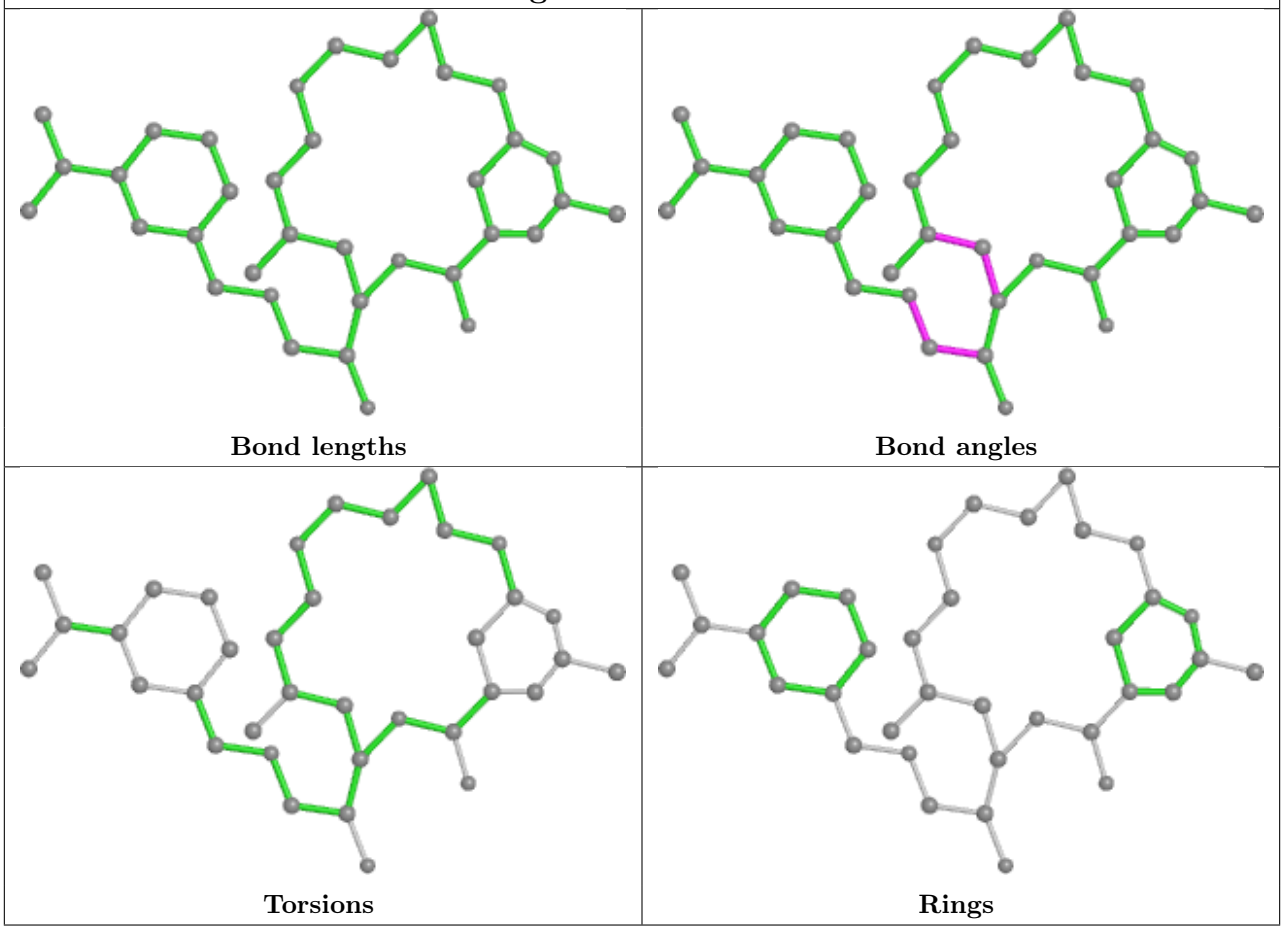
Mol	Chain	Res	Type	Atoms
2	C	401	E6P	O26-C27-C30-C33
2	C	401	E6P	C20-C23-O26-C27

There are no ring outliers.

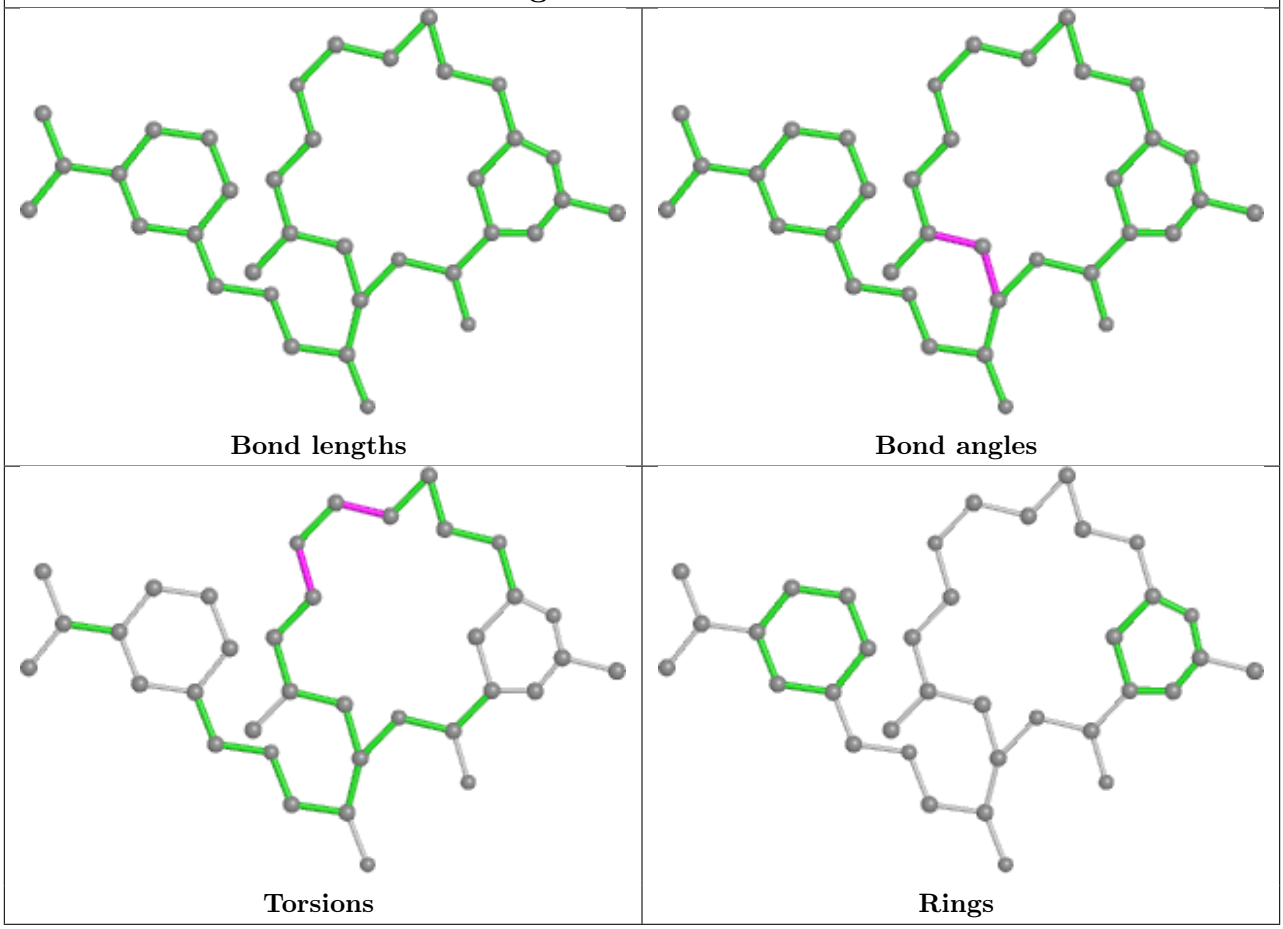
No monomer is involved in short contacts.

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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

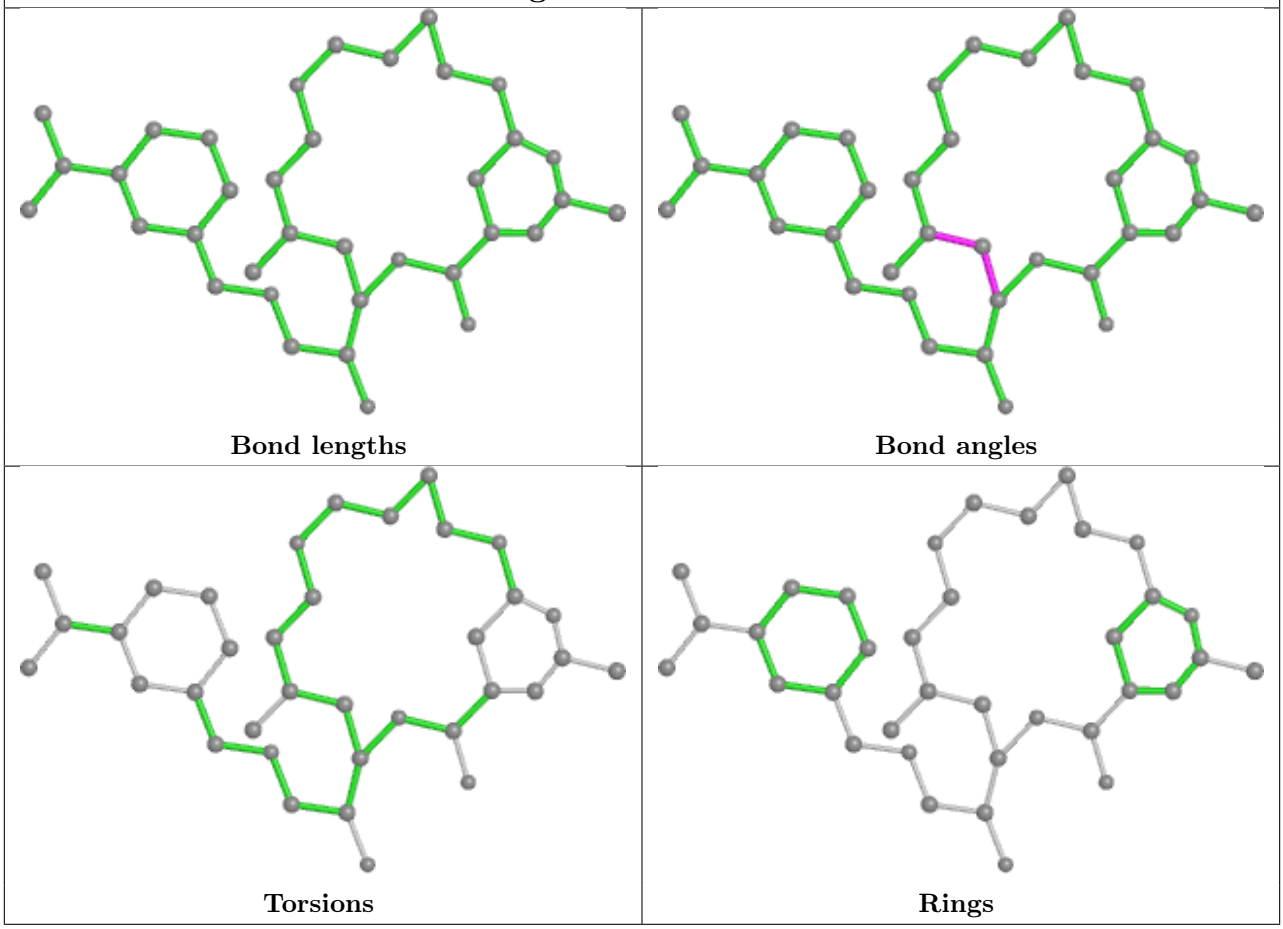
Ligand E6P B 401



Ligand E6P C 401



Ligand E6P A 401



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, 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%)	0.34	35 (9%)	8	11	28, 42, 82, 166	0
1	B	377/402 (93%)	0.45	37 (9%)	7	10	26, 43, 97, 171	0
1	C	378/402 (94%)	0.36	38 (10%)	7	9	28, 42, 90, 140	0
All	All	1132/1206 (93%)	0.38	110 (9%)	7	10	26, 43, 90, 171	0

All (110) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	314	THR	14.5
1	A	313	ALA	9.7
1	A	314	THR	9.3
1	B	313	ALA	8.8
1	B	312	VAL	8.3
1	C	312	VAL	8.0
1	C	168	ALA	7.5
1	C	314	THR	7.0
1	A	312	VAL	6.9
1	B	361	VAL	6.7
1	B	316	GLN	6.5
1	A	316	GLN	6.1
1	B	157	ALA	5.8
1	B	310	GLU	5.7
1	C	313	ALA	5.6
1	A	157	ALA	5.2
1	C	310	GLU	5.1
1	B	364	GLU	5.0
1	B	315	SER	4.9
1	C	272	ALA	4.8
1	A	311	ASP	4.6
1	B	256	LYS	4.6
1	A	315	SER	4.5

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Mol	Chain	Res	Type	RSRZ
1	C	273	GLY	4.5
1	C	316	GLN	4.3
1	A	364	GLU	4.2
1	B	311	ASP	4.2
1	A	39	ALA	4.2
1	A	169	SER	4.2
1	C	169	SER	4.1
1	B	254	THR	4.0
1	A	361	VAL	4.0
1	B	365	PHE	3.9
1	B	253	SER	3.9
1	C	362	HIS	3.8
1	C	39	ALA	3.8
1	C	365	PHE	3.7
1	A	256	LYS	3.7
1	C	361	VAL	3.6
1	A	40	VAL	3.6
1	A	38	PHE	3.5
1	B	271	GLN	3.5
1	A	170	VAL	3.5
1	C	64	ARG	3.4
1	C	256	LYS	3.4
1	A	273	GLY	3.3
1	C	-2	SER	3.3
1	C	38	PHE	3.3
1	B	257	PHE	3.2
1	A	119	LEU	3.2
1	B	272	ALA	3.2
1	C	145	HIS	3.1
1	C	40	VAL	3.1
1	B	119	LEU	3.1
1	C	364	GLU	3.1
1	A	310	GLU	3.0
1	C	119	LEU	3.0
1	B	317	ASP	2.9
1	B	40	VAL	2.9
1	B	145	HIS	2.9
1	C	121	LEU	2.8
1	B	362	HIS	2.7
1	A	118	ILE	2.7
1	A	380	GLU	2.7
1	B	9	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	367	THR	2.6
1	A	360	HIS	2.6
1	A	285	LEU	2.6
1	B	64	ARG	2.5
1	B	46	PRO	2.5
1	C	29	ILE	2.5
1	A	271	GLN	2.5
1	B	266	GLN	2.5
1	A	265	GLU	2.5
1	A	365	PHE	2.4
1	C	265	GLU	2.4
1	A	287	LEU	2.4
1	C	311	ASP	2.4
1	B	38	PHE	2.4
1	B	265	GLU	2.4
1	B	203	ILE	2.4
1	A	29	ILE	2.3
1	C	152	LEU	2.3
1	A	145	HIS	2.3
1	A	99	ILE	2.3
1	C	10	SER	2.3
1	C	203	ILE	2.3
1	C	324	ILE	2.3
1	C	285	LEU	2.2
1	C	120	GLY	2.2
1	B	258	PRO	2.2
1	C	384	TYR	2.2
1	A	102	ILE	2.2
1	A	274	THR	2.2
1	B	102	ILE	2.1
1	C	99	ILE	2.1
1	C	234	LEU	2.1
1	C	270	TRP	2.1
1	A	362	HIS	2.1
1	A	31	VAL	2.1
1	A	100	ALA	2.1
1	B	274	THR	2.1
1	C	315	SER	2.1
1	C	63	LEU	2.1
1	B	273	GLY	2.1
1	B	285	LEU	2.0
1	C	343	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	360	HIS	2.0
1	B	22	SER	2.0
1	A	227	VAL	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

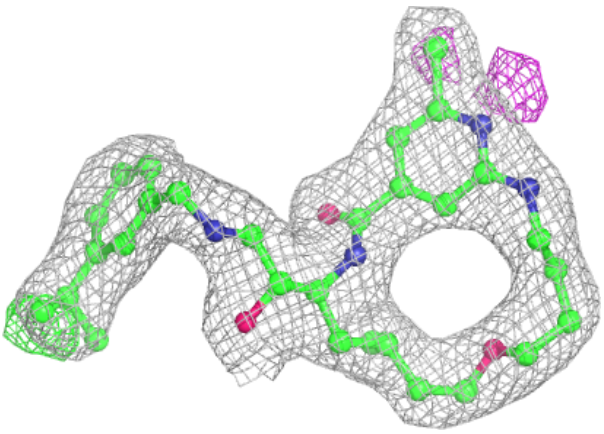
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

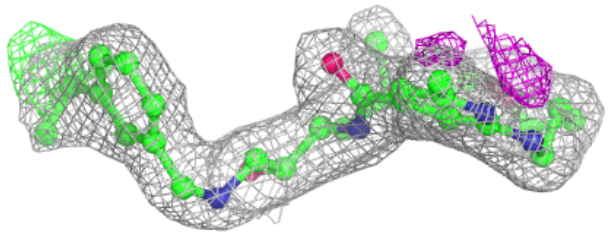
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	E6P	B	401	36/36	0.92	0.13	27,36,45,55	2
2	E6P	A	401	36/36	0.93	0.13	30,37,45,53	2
2	E6P	C	401	36/36	0.95	0.11	27,36,45,53	0

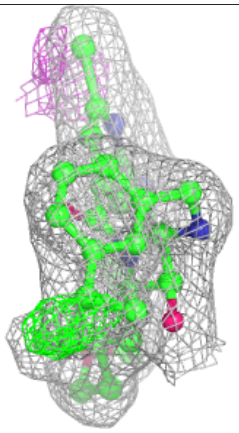
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around E6P 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)

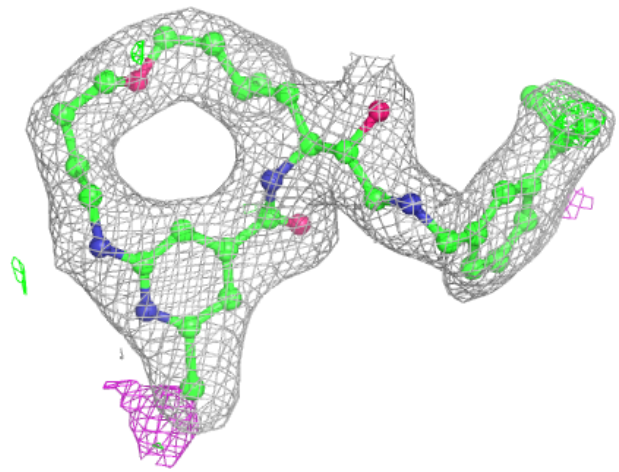


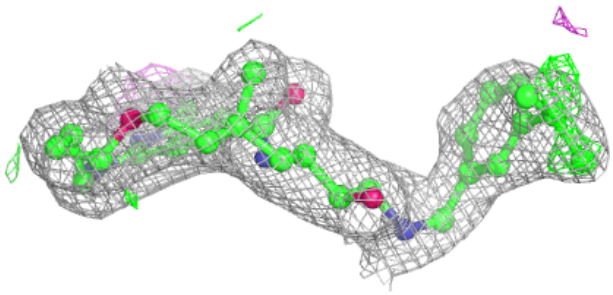


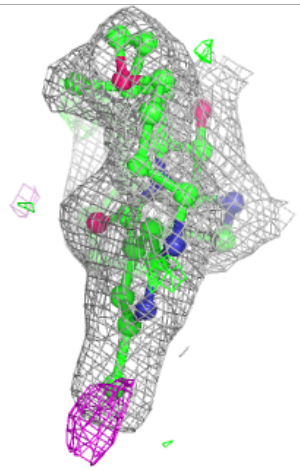


Electron density around E6P A 401:

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

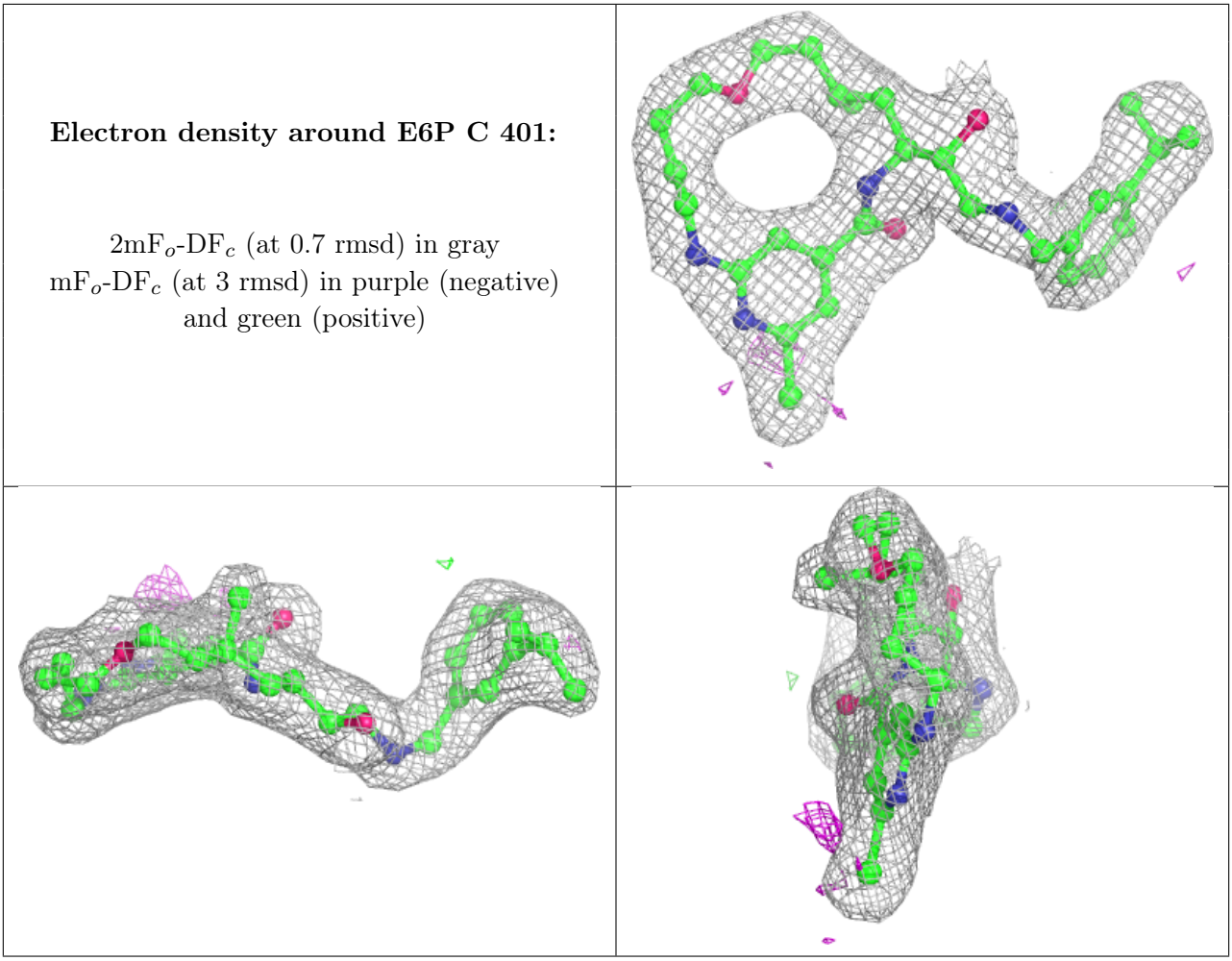






Electron density around E6P C 401:

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.