wwPDB X-ray Structure Validation Summary Report (i)

Sep 10, 2023 – 11:55 PM EDT

PDB ID	:	4KUX
Title	:	Crystal structure of Aspergillus terreus aristolochene synthase complexed with farnesyl thiolodiphosphate (FSPP)
Authors	:	Chen, M.; Faraldos, J.A.; Al-lami, N.; Janvier, M.; D'Antonio, E.L.; Cane, D.E.; Allemann, R.K.; Christianson, D.W.
Deposited on	:	2013-05-22
Resolution	:	1.90 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*
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:

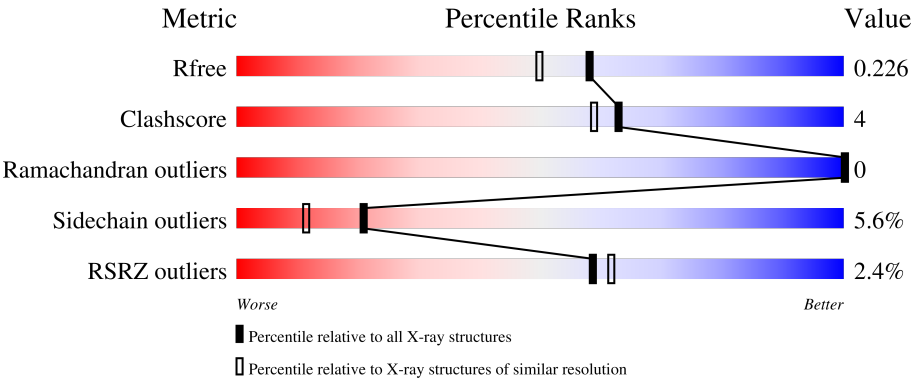
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	314	86% 9%
1	B	314	88% 8%
1	C	314	85% 10%
1	D	314	9% 82% 13%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 10929 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 Aristolochene synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	304	Total	C	N	O	S	0	1	0
			2459	1570	415	458	16			
1	B	304	Total	C	N	O	S	0	1	0
			2459	1570	415	458	16			
1	C	304	Total	C	N	O	S	0	0	0
			2454	1566	415	458	15			
1	D	304	Total	C	N	O	S	0	1	0
			2459	1570	415	458	16			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP Q9UR08
A	2	HIS	-	expression tag	UNP Q9UR08
A	3	HIS	-	expression tag	UNP Q9UR08
A	4	HIS	-	expression tag	UNP Q9UR08
A	5	HIS	-	expression tag	UNP Q9UR08
A	6	HIS	-	expression tag	UNP Q9UR08
A	7	HIS	-	expression tag	UNP Q9UR08
B	1	MET	-	expression tag	UNP Q9UR08
B	2	HIS	-	expression tag	UNP Q9UR08
B	3	HIS	-	expression tag	UNP Q9UR08
B	4	HIS	-	expression tag	UNP Q9UR08
B	5	HIS	-	expression tag	UNP Q9UR08
B	6	HIS	-	expression tag	UNP Q9UR08
B	7	HIS	-	expression tag	UNP Q9UR08
C	1	MET	-	expression tag	UNP Q9UR08
C	2	HIS	-	expression tag	UNP Q9UR08
C	3	HIS	-	expression tag	UNP Q9UR08
C	4	HIS	-	expression tag	UNP Q9UR08
C	5	HIS	-	expression tag	UNP Q9UR08
C	6	HIS	-	expression tag	UNP Q9UR08
C	7	HIS	-	expression tag	UNP Q9UR08

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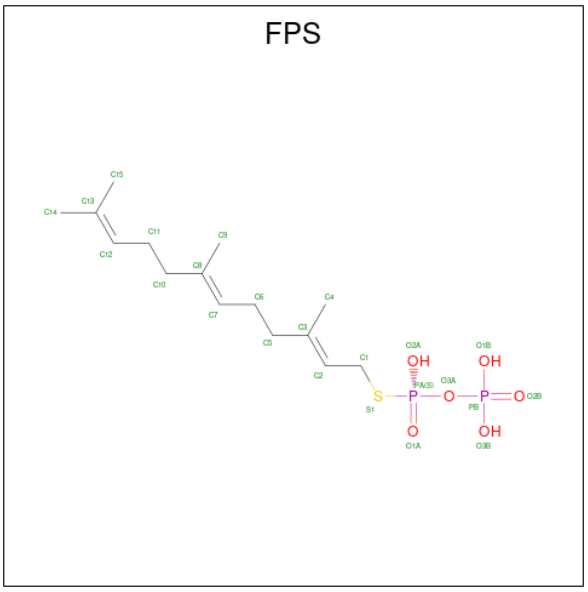
Chain	Residue	Modelled	Actual	Comment	Reference
D	1	MET	-	expression tag	UNP Q9UR08
D	2	HIS	-	expression tag	UNP Q9UR08
D	3	HIS	-	expression tag	UNP Q9UR08
D	4	HIS	-	expression tag	UNP Q9UR08
D	5	HIS	-	expression tag	UNP Q9UR08
D	6	HIS	-	expression tag	UNP Q9UR08
D	7	HIS	-	expression tag	UNP Q9UR08

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	3	Total Mg 3 3	0	0
2	B	3	Total Mg 3 3	0	0
2	C	3	Total Mg 3 3	0	0
2	D	3	Total Mg 3 3	0	0

- Molecule 3 is S-[(2E,6E)-3,7,11-TRIMETHYLDODECA-2,6,10-TRIENYL] TRIHYDROGEN THIODIPHOSPHATE (three-letter code: FPS) (formula: $C_{15}H_{28}O_6P_2S$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O P S 24 15 6 2 1	0	0

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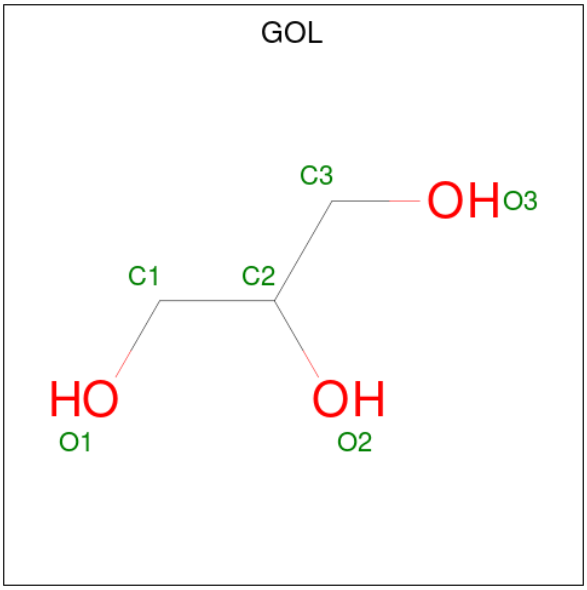
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	O	P	S	0	0
			24	15	6	2	1		
3	C	1	Total	C	O	P	S	0	0
			24	15	6	2	1		
3	D	1	Total	C	O	P	S	0	0
			24	15	6	2	1		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is water.

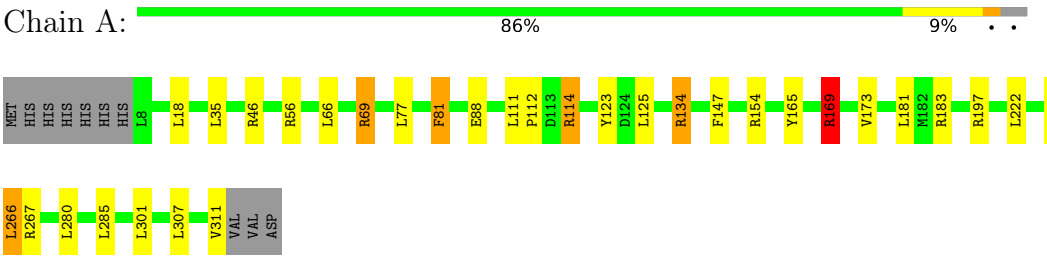
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	313	Total	O	0	0
			313	313		
5	B	337	Total	O	0	0
			337	337		
5	C	201	Total	O	0	0
			201	201		
5	D	127	Total	O	0	0
			127	127		

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.

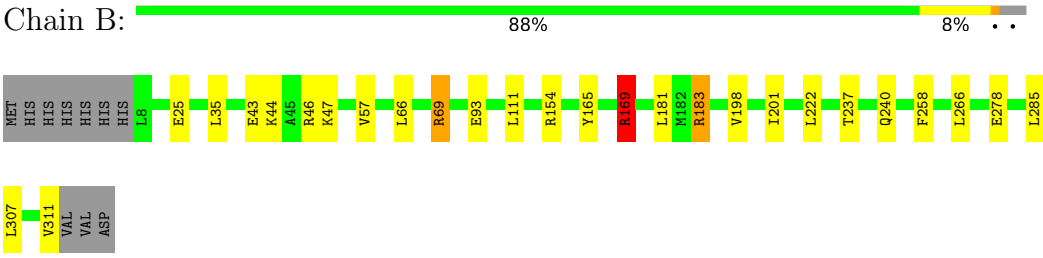
• Molecule 1: Aristolochene synthase

Chain A:



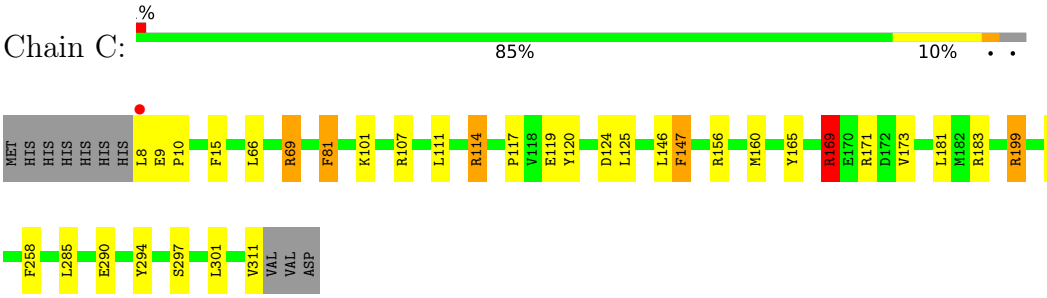
• Molecule 1: Aristolochene synthase

Chain B:



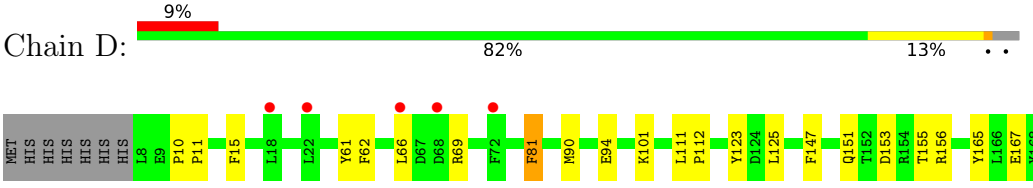
• Molecule 1: Aristolochene synthase

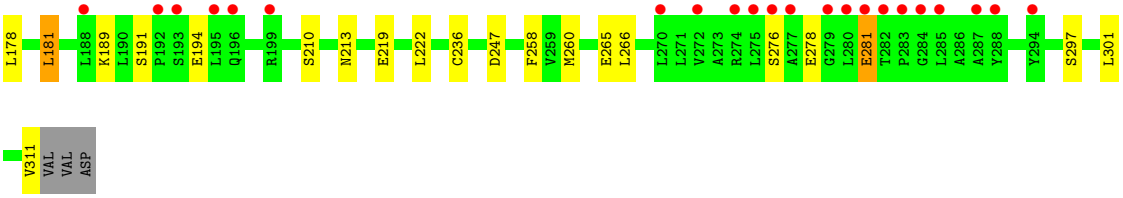
Chain C:



• Molecule 1: Aristolochene synthase

Chain D:




L178
L181
L188
K189
L190
S191
P192
S193
E194
L195
Q196
R199
S210
N213
E219
L222
C236
D247
F258
V259
M260
E265
L266
L270
L271
V272
A273
R274
L275
S276
A277
E278
G279
L280
E281
T282
P283
G284
L285
A286
A287
Y288
Y294
S297
L301
V311
VAL
VAL
ASP

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	123.95Å 123.95Å 203.54Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 1.90 47.48 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-1.90) 99.8 (47.48-1.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	1.65 (at 1.90Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1370)	Depositor
R, R_{free}	0.189 , 0.226 0.190 , 0.226	Depositor DCC
R_{free} test set	7147 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	30.7	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 42.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.015 for -h,-k,l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	10929	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.66% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FPS, MG, GOL

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	0.69	0/2517	0.85	6/3406 (0.2%)
1	B	0.70	0/2517	0.89	6/3406 (0.2%)
1	C	0.59	0/2509	0.78	8/3396 (0.2%)
1	D	0.48	0/2517	0.59	2/3406 (0.1%)
All	All	0.62	0/10060	0.79	22/13614 (0.2%)

There are no bond length outliers.

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	169	ARG	NE-CZ-NH2	-19.25	110.68	120.30
1	B	169	ARG	NE-CZ-NH1	16.83	128.72	120.30
1	A	169	ARG	NE-CZ-NH2	-13.97	113.31	120.30
1	C	114	ARG	NE-CZ-NH2	-13.48	113.56	120.30
1	A	69	ARG	NE-CZ-NH1	11.63	126.11	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2459	0	2434	19	0
1	B	2459	0	2434	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2454	0	2426	20	0
1	D	2459	0	2434	26	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0
2	D	3	0	0	0	0
3	A	24	0	25	4	0
3	B	24	0	25	1	0
3	C	24	0	25	3	0
3	D	24	0	25	3	0
4	B	6	0	8	0	0
4	C	6	0	8	0	0
5	A	313	0	0	11	0
5	B	337	0	0	7	0
5	C	201	0	0	7	0
5	D	127	0	0	5	0
All	All	10929	0	9844	85	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 4.

The worst 5 of 85 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:C:183:ARG:NE	5:C:998:HOH:O	2.01	0.92
1:C:165:TYR:CZ	1:C:169:ARG:HG3	2.13	0.84
1:B:43:GLU:HG3	1:B:47:LYS:HE2	1.61	0.82
1:B:35:LEU:O	1:B:46:ARG:NH2	2.14	0.81
1:D:169:ARG:NH2	3:D:704:FPS:S1	2.54	0.81

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	303/314 (96%)	299 (99%)	4 (1%)	0	100	100
1	B	303/314 (96%)	300 (99%)	3 (1%)	0	100	100
1	C	302/314 (96%)	299 (99%)	3 (1%)	0	100	100
1	D	303/314 (96%)	296 (98%)	7 (2%)	0	100	100
All	All	1211/1256 (96%)	1194 (99%)	17 (1%)	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	267/276 (97%)	250 (94%)	17 (6%)	17	8
1	B	267/276 (97%)	254 (95%)	13 (5%)	25	15
1	C	266/276 (96%)	252 (95%)	14 (5%)	22	13
1	D	267/276 (97%)	251 (94%)	16 (6%)	19	9
All	All	1067/1104 (97%)	1007 (94%)	60 (6%)	21	11

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	307	LEU
1	D	258	PHE
1	C	169	ARG
1	D	247	ASP
1	D	311	VAL

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)

Of 18 ligands modelled in this entry, 12 are monoatomic - leaving 6 for Mogul analysis.

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	$\#\|Z\| > 2$
3	FPS	D	704	2	19,23,23	1.23	2 (10%)	23,31,31	2.11	8 (34%)
3	FPS	B	405	2	19,23,23	1.25	2 (10%)	23,31,31	2.78	9 (39%)
4	GOL	B	402	-	5,5,5	0.32	0	5,5,5	0.42	0
3	FPS	C	705	2	19,23,23	1.21	2 (10%)	23,31,31	2.29	7 (30%)
4	GOL	C	704	-	5,5,5	0.46	0	5,5,5	0.84	0
3	FPS	A	704	2	19,23,23	1.39	2 (10%)	23,31,31	3.03	12 (52%)

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
3	FPS	D	704	2	-	3/19/25/25	-
3	FPS	B	405	2	-	3/19/25/25	-
4	GOL	B	402	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FPS	C	705	2	-	3/19/25/25	-
4	GOL	C	704	-	-	0/4/4/4	-
3	FPS	A	704	2	-	3/19/25/25	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	704	FPS	C1-S1	-4.91	1.78	1.84
3	D	704	FPS	C1-S1	-4.13	1.79	1.84
3	C	705	FPS	C1-S1	-3.93	1.79	1.84
3	B	405	FPS	C1-S1	-3.34	1.80	1.84
3	B	405	FPS	PA-O2A	-3.31	1.48	1.56

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	704	FPS	C15-C13-C12	-6.42	104.08	122.65
3	B	405	FPS	C15-C13-C12	-5.81	105.85	122.65
3	B	405	FPS	C9-C8-C10	5.71	124.87	115.27
3	A	704	FPS	C9-C8-C10	5.67	124.81	115.27
3	B	405	FPS	C10-C11-C12	-5.55	93.64	111.88

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	704	FPS	C8-C10-C11-C12
3	C	705	FPS	C8-C10-C11-C12
3	B	405	FPS	C8-C10-C11-C12
3	A	704	FPS	C11-C10-C8-C9
3	B	405	FPS	C11-C10-C8-C9

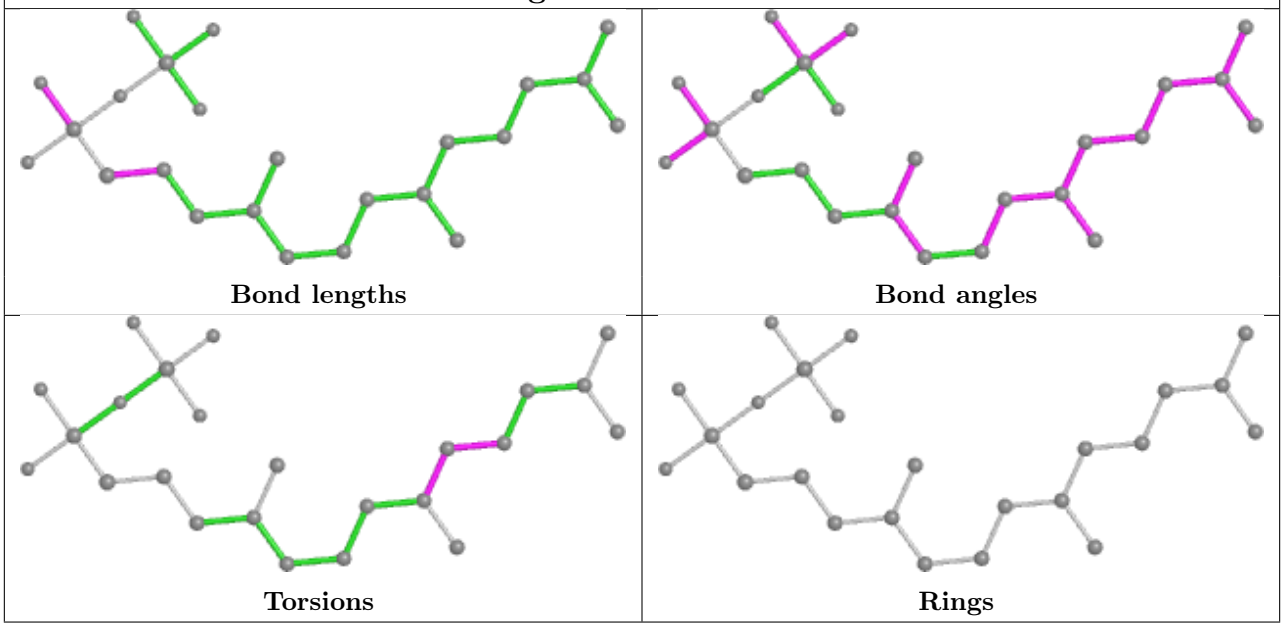
There are no ring outliers.

4 monomers are involved in 11 short contacts:

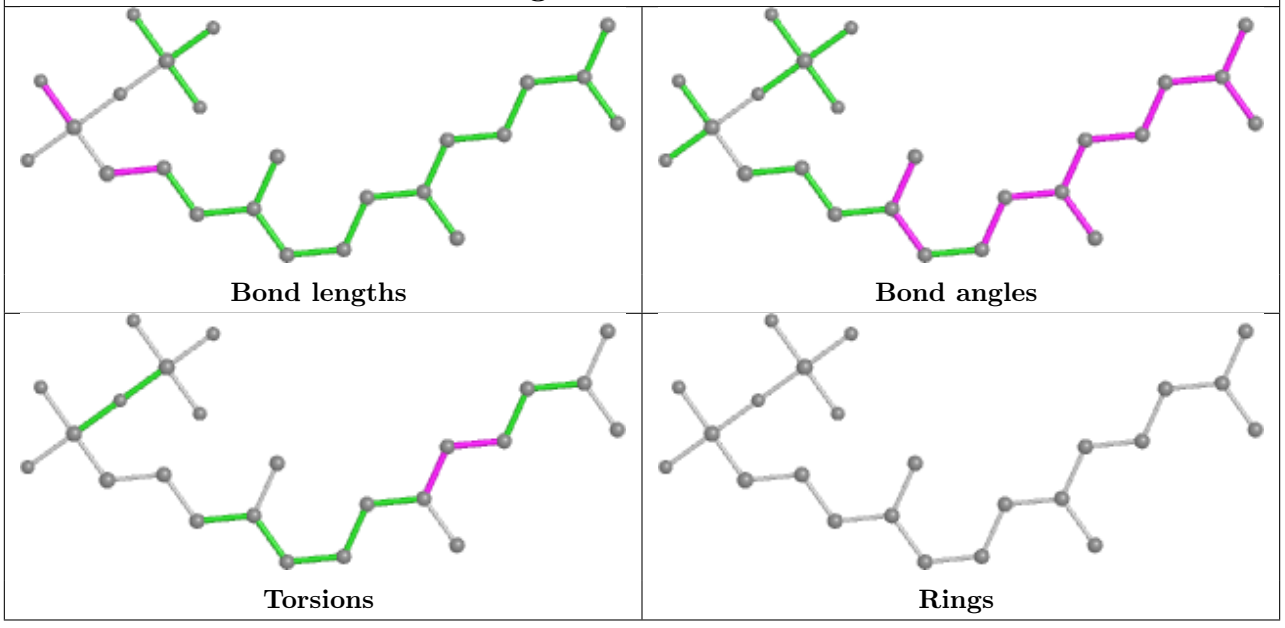
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	704	FPS	3	0
3	B	405	FPS	1	0
3	C	705	FPS	3	0
3	A	704	FPS	4	0

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 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.

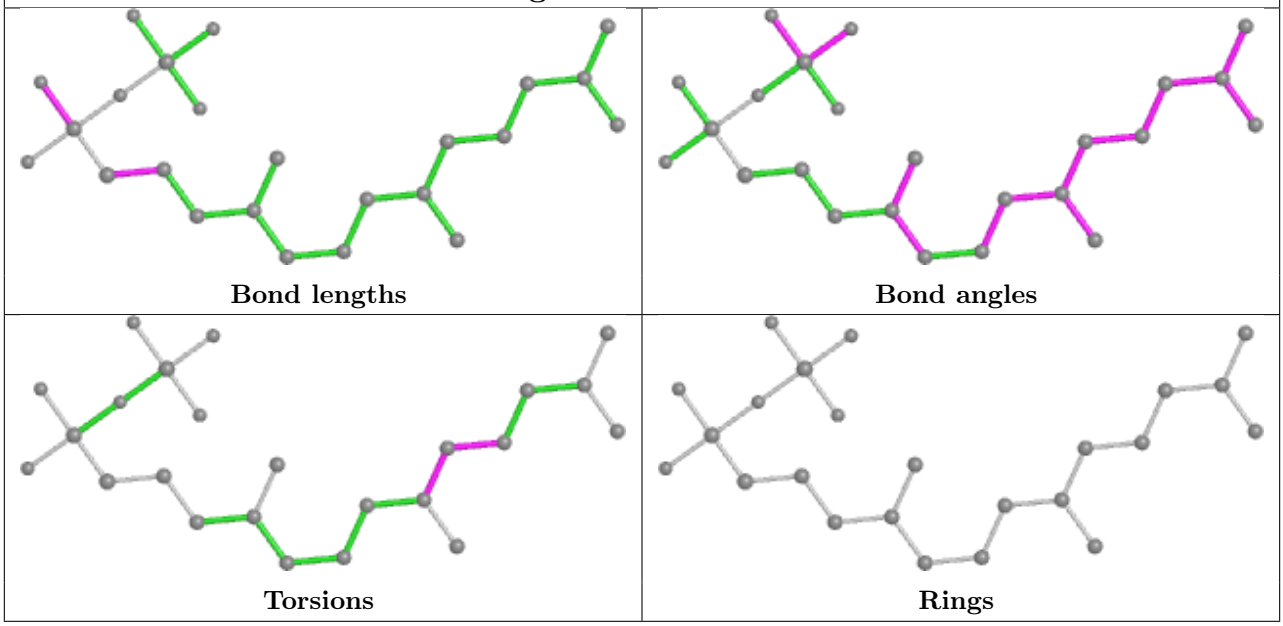
Ligand FPS D 704



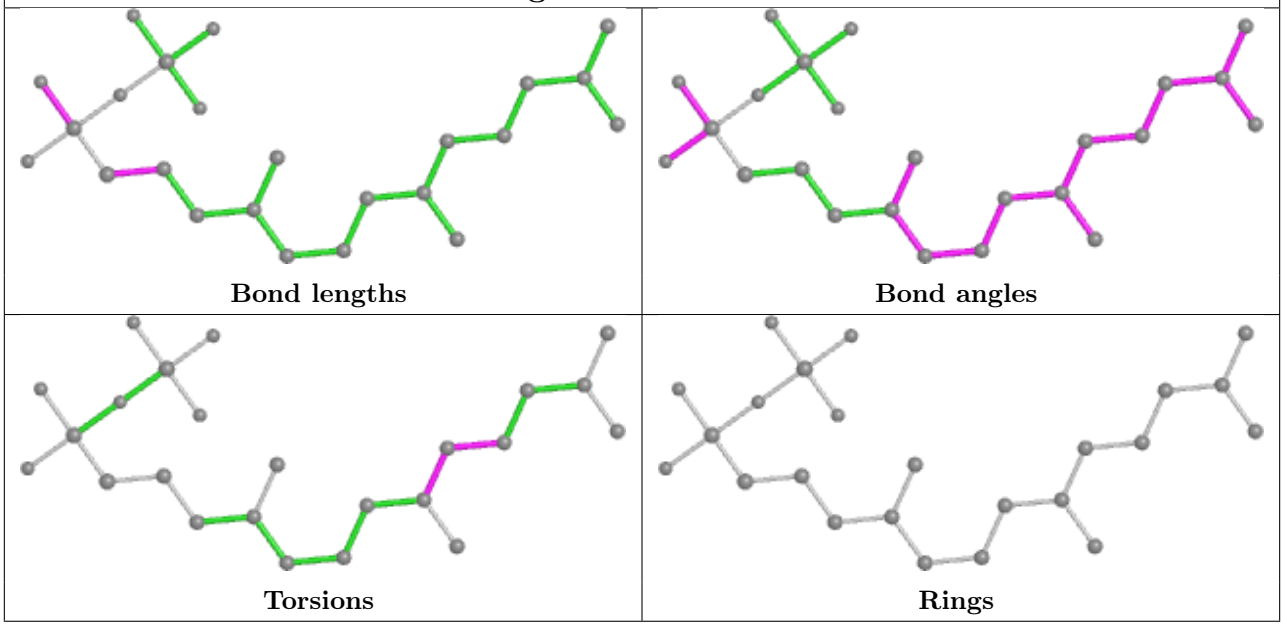
Ligand FPS B 405



Ligand FPS C 705



Ligand FPS A 704



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, 95^{th} 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	304/314 (96%)	-0.55	0 100 100	18, 25, 42, 55	0
1	B	304/314 (96%)	-0.54	0 100 100	17, 23, 37, 55	0
1	C	304/314 (96%)	-0.43	2 (0%) 87 88	21, 33, 51, 72	0
1	D	304/314 (96%)	0.47	27 (8%) 9 11	28, 47, 78, 99	0
All	All	1216/1256 (96%)	-0.26	29 (2%) 59 62	17, 31, 60, 99	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	279	GLY	7.1
1	D	280	LEU	6.0
1	D	18	LEU	5.1
1	D	272	VAL	4.5
1	D	275	LEU	4.3

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

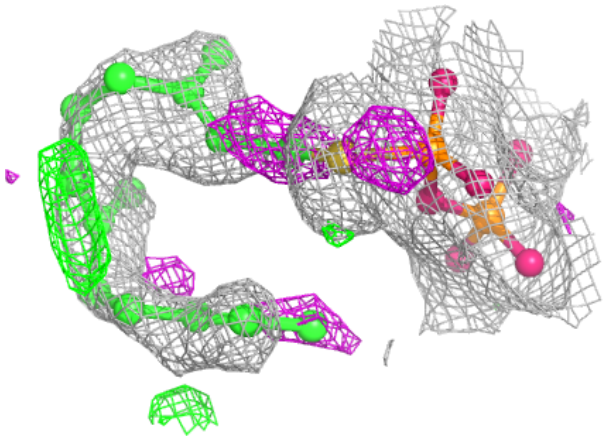
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

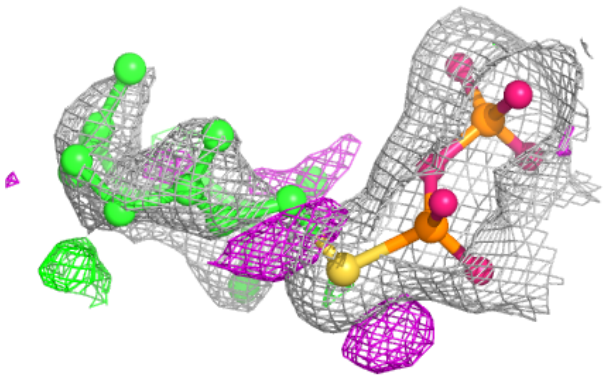
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	GOL	C	704	6/6	0.88	0.17	30,36,48,58	0
2	MG	D	703	1/1	0.91	0.06	44,44,44,44	0
4	GOL	B	402	6/6	0.92	0.11	32,37,37,45	0
2	MG	A	702	1/1	0.92	0.09	22,22,22,22	0
2	MG	D	701	1/1	0.96	0.07	32,32,32,32	0
2	MG	C	703	1/1	0.96	0.04	27,27,27,27	0
2	MG	C	701	1/1	0.97	0.05	31,31,31,31	0
3	FPS	D	704	24/24	0.97	0.15	26,45,64,66	0
2	MG	C	702	1/1	0.97	0.04	28,28,28,28	0
2	MG	D	702	1/1	0.97	0.07	29,29,29,29	0
3	FPS	C	705	24/24	0.98	0.08	25,33,43,47	0
2	MG	B	404	1/1	0.98	0.10	19,19,19,19	0
3	FPS	A	704	24/24	0.98	0.11	16,27,37,41	0
3	FPS	B	405	24/24	0.98	0.11	16,25,31,34	0
2	MG	B	403	1/1	0.99	0.11	18,18,18,18	0
2	MG	A	701	1/1	0.99	0.06	22,22,22,22	0
2	MG	A	703	1/1	1.00	0.05	21,21,21,21	0
2	MG	B	401	1/1	1.00	0.06	19,19,19,19	0

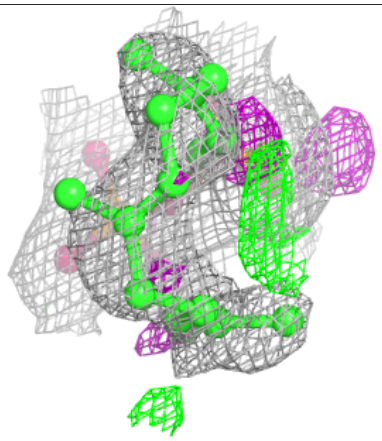
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around FPS D 704:

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

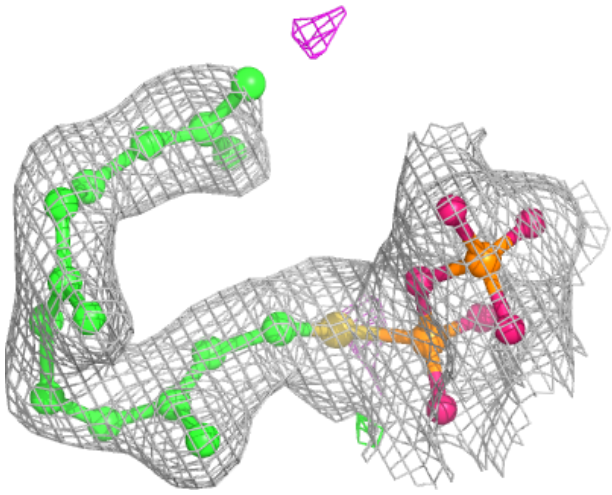


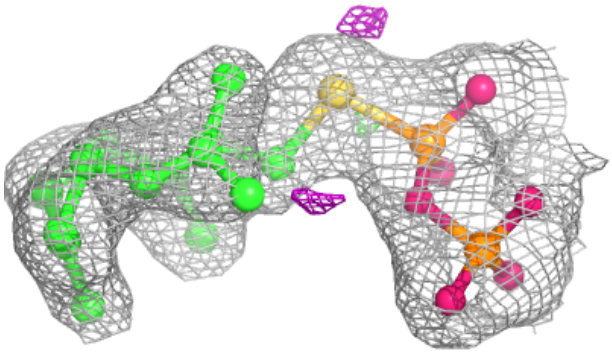


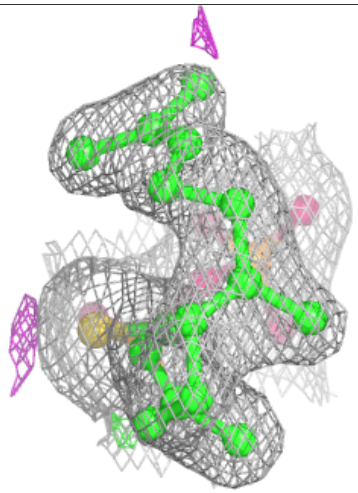


Electron density around FPS C 705:

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

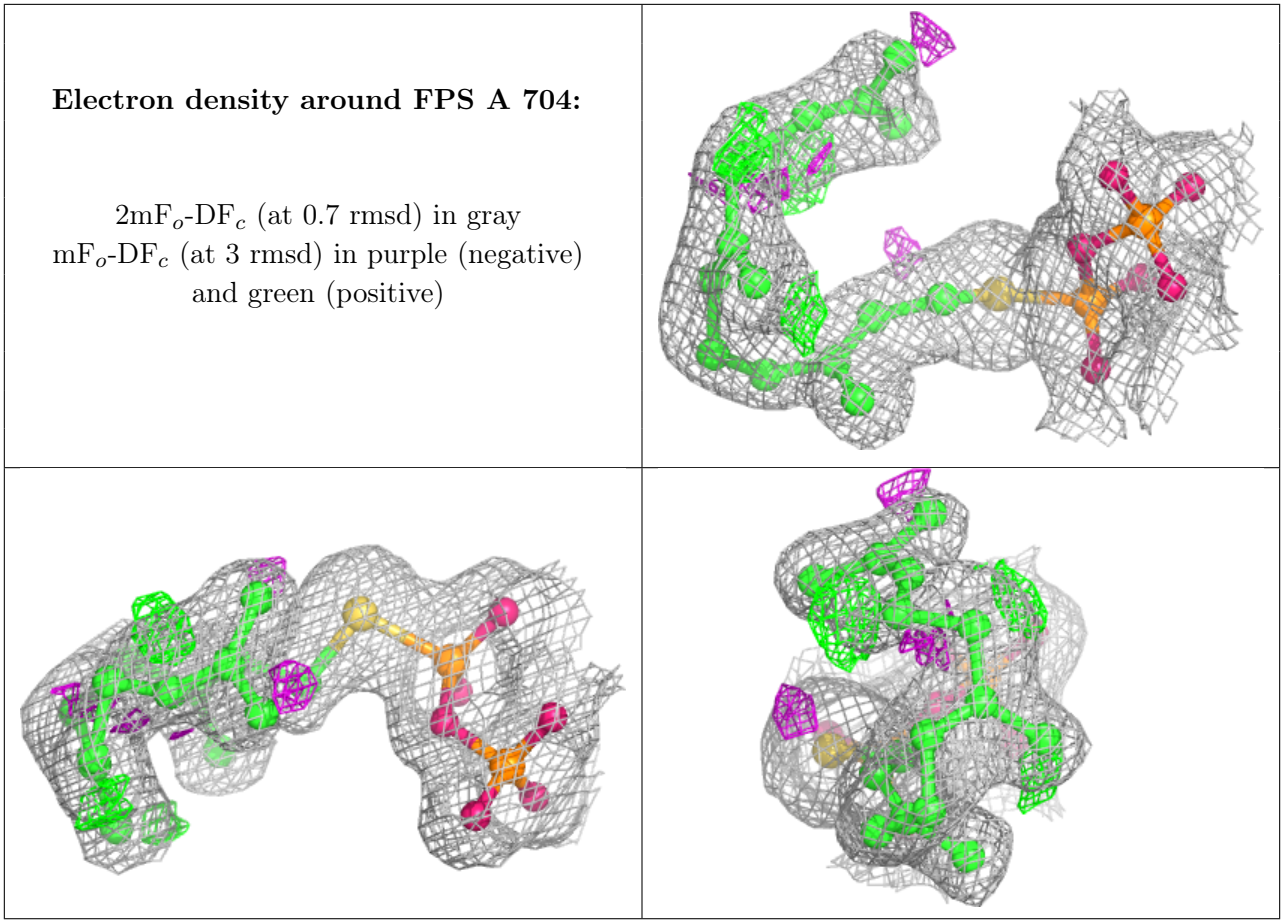






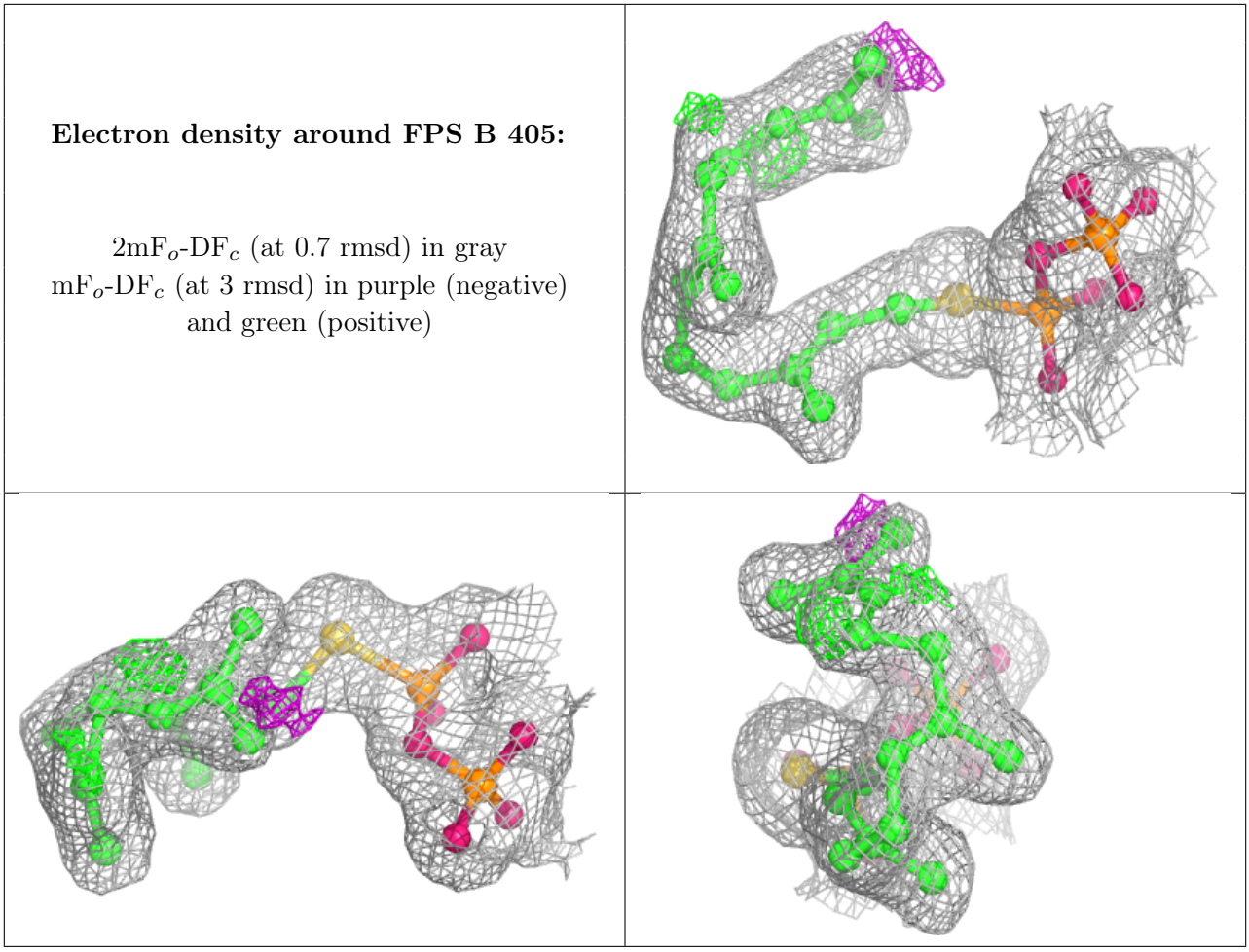
Electron density around FPS A 704:

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



Electron density around FPS B 405:

$2mF_o$-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.