



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 03:34 PM BST

PDB ID : 4NH2  
Title : Crystal structure of AmtB from E. coli bound to phosphatidylglycerol  
Authors : Laganowsky, A.; Reading, E.; Allison, T.M.; Robinson, C.V.  
Deposited on : 2013-11-04  
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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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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 : 2.13.1  
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) : 2.13.1

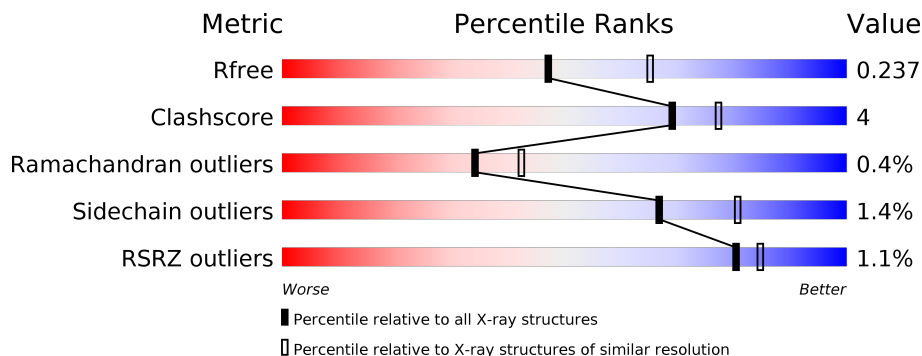
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	406	 81% 7% • 11%
1	B	406	 84% 6% 10%
1	C	406	 82% 8% 9%
1	D	406	 82% 8% 10%
1	E	406	 82% 9% • 9%
1	F	406	 83% 6% 10%

## 2 Entry composition [i](#)

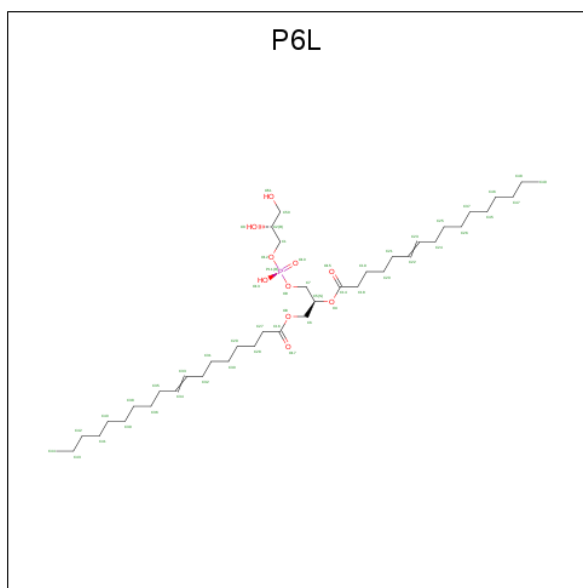
There are 3 unique types of molecules in this entry. The entry contains 16260 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Ammonia channel.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	363	Total 2614	C 1728	N 418	O 449	S 19	0	0	0
1	B	367	Total 2645	C 1751	N 420	O 455	S 19	0	0	0
1	C	368	Total 2657	C 1757	N 423	O 458	S 19	0	0	0
1	D	366	Total 2645	C 1751	N 421	O 454	S 19	0	0	0
1	E	371	Total 2665	C 1762	N 425	O 459	S 19	0	0	0
1	F	364	Total 2630	C 1742	N 419	O 450	S 19	0	0	0

- Molecule 2 is (2S)-3-{{{[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-2-[(6E)-HEXADEC-6-ENOYLOXY]PROPYL (8E)-OCTADEC-8-ENOATE (three-letter code: P6L) (formula: C<sub>40</sub>H<sub>75</sub>O<sub>10</sub>P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			25	14	10	1		
2	B	1	Total	C	O	P	0	0
			23	12	10	1		
2	C	1	Total	C	O	P	0	0
			39	28	10	1		
2	C	1	Total	C	O	P	0	0
			51	40	10	1		
2	D	1	Total	C	O	P	0	0
			34	23	10	1		
2	E	1	Total	C	O	P	0	0
			35	24	10	1		
2	F	1	Total	C	O	P	0	0
			35	24	10	1		
2	F	1	Total	C	O	P	0	0
			51	40	10	1		

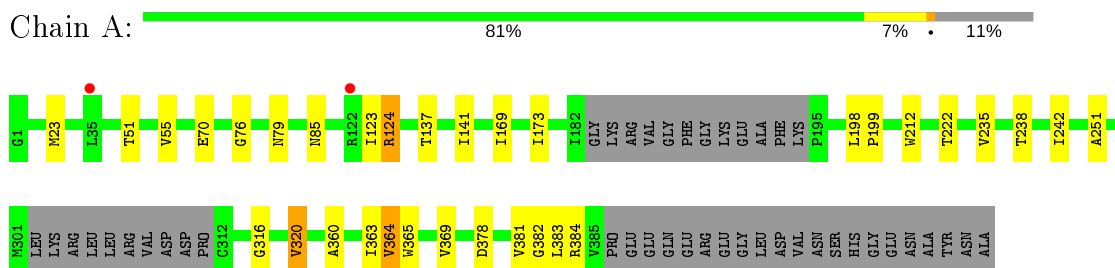
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	19	Total	O	0	0
			19	19		
3	B	19	Total	O	0	0
			19	19		
3	C	17	Total	O	0	0
			17	17		
3	D	17	Total	O	0	0
			17	17		
3	E	19	Total	O	0	0
			19	19		
3	F	20	Total	O	0	0
			20	20		

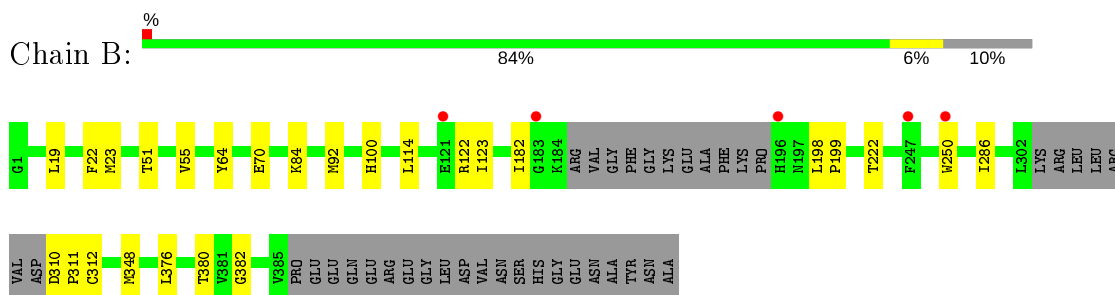
### 3 Residue-property plots

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.

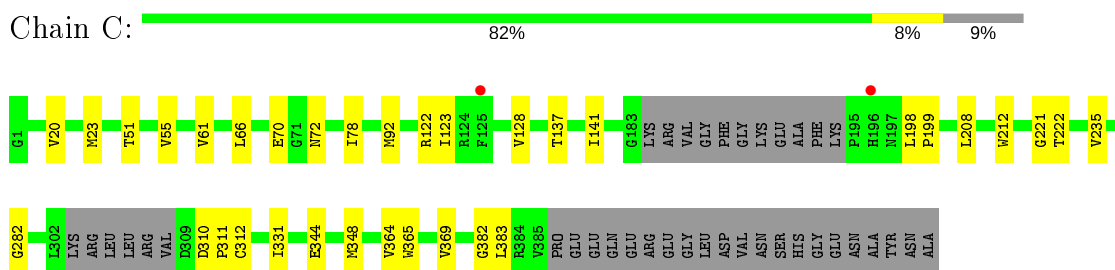
- Molecule 1: Ammonia channel



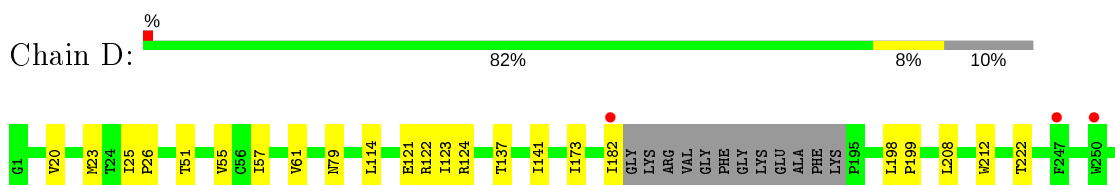
- Molecule 1: Ammonia channel



- Molecule 1: Ammonia channel

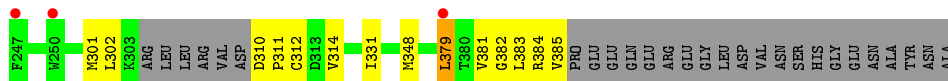
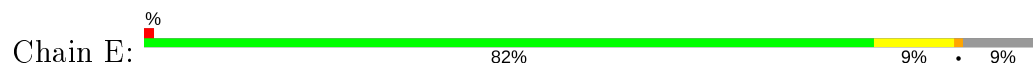


- Molecule 1: Ammonia channel

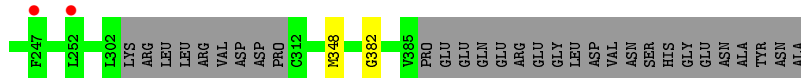
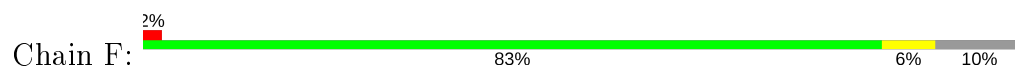




- Molecule 1: Ammonia channel



- Molecule 1: Ammonia channel



## 4 Data and refinement statistics i

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	116.19Å 201.19Å 232.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.74 – 2.30 38.74 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.3 (38.74-2.30) 99.3 (38.74-2.30)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.21 (at 2.29Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.202 , 0.234 0.207 , 0.237	Depositor DCC
$R_{free}$ test set	5989 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.6	Xtriage
Anisotropy	1.119	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 26.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.419 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.435 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
Reported twinning fraction	0.432 for H, K, L 0.287 for -1/2H+1/2K, 3/2H+1/2K, -L 0.281 for -1/2H-1/2K, -3/2H+1/2K, -L	Depositor
Outliers	1 of 119767 reflections (0.001%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	16260	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 19.84 % 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 9.9231e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

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

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: P6L

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	0.79	1/2672 (0.0%)	0.79	3/3646 (0.1%)
1	B	0.78	0/2704	0.79	3/3690 (0.1%)
1	C	0.81	0/2717	0.79	3/3708 (0.1%)
1	D	0.74	0/2705	0.78	4/3692 (0.1%)
1	E	0.82	3/2725 (0.1%)	0.80	4/3721 (0.1%)
1	F	0.78	1/2689 (0.0%)	0.79	2/3669 (0.1%)
All	All	0.79	5/16212 (0.0%)	0.79	19/22126 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	87	GLU	CD-OE1	5.84	1.32	1.25
1	F	72	ASN	CB-CG	-5.77	1.37	1.51
1	E	87	GLU	CG-CD	5.71	1.60	1.51
1	E	126	SER	CB-OG	-5.35	1.35	1.42
1	A	382	GLY	N-CA	5.09	1.53	1.46

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	122	ARG	NE-CZ-NH1	7.34	123.97	120.30
1	C	92	MET	CG-SD-CE	7.03	111.45	100.20
1	B	122	ARG	NE-CZ-NH1	6.93	123.76	120.30
1	F	348	MET	CG-SD-CE	6.59	110.74	100.20
1	F	72	ASN	CB-CA-C	-6.55	97.29	110.40
1	B	23	MET	CG-SD-CE	6.38	110.41	100.20
1	D	124	ARG	CA-CB-CG	6.12	126.85	113.40
1	C	364	VAL	CB-CA-C	5.74	122.30	111.40
1	B	348	MET	CG-SD-CE	5.73	109.37	100.20
1	E	23	MET	CG-SD-CE	5.73	109.37	100.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	379	LEU	CA-CB-CG	5.69	128.39	115.30
1	A	23	MET	CG-SD-CE	5.62	109.20	100.20
1	E	84	LYS	CD-CE-NZ	5.47	124.28	111.70
1	A	124	ARG	CA-CB-CG	5.42	125.32	113.40
1	D	124	ARG	N-CA-CB	-5.31	101.04	110.60
1	A	320	VAL	CB-CA-C	-5.27	101.38	111.40
1	E	143	ILE	CA-CB-CG1	5.17	120.82	111.00
1	C	344	GLU	OE1-CD-OE2	-5.11	117.17	123.30
1	D	320	VAL	CB-CA-C	-5.06	101.79	111.40

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	2614	0	2661	18	0
1	B	2645	0	2694	13	0
1	C	2657	0	2704	21	0
1	D	2645	0	2697	23	0
1	E	2665	0	2697	17	0
1	F	2630	0	2686	20	0
2	A	25	0	20	1	0
2	B	23	0	16	2	0
2	C	90	0	123	9	0
2	D	34	0	36	2	0
2	E	35	0	38	1	0
2	F	86	0	112	8	0
3	A	19	0	0	3	0
3	B	19	0	0	0	0
3	C	17	0	0	2	0
3	D	17	0	0	1	0
3	E	19	0	0	0	0
3	F	20	0	0	1	0
All	All	16260	0	16484	120	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.

All (120) 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)
2:B:501:P6L:H2	2:B:501:P6L:O10	1.77	0.85
1:F:79:ASN:ND2	3:F:615:HOH:O	2.09	0.84
1:D:331:ILE:HG23	1:D:348:MET:HE1	1.66	0.78
1:A:124:ARG:HG3	1:A:384:ARG:O	1.84	0.78
1:F:78:ILE:HD13	2:F:501:P6L:C30	2.14	0.78
1:C:282:GLY:HA3	2:C:502:P6L:H302	1.70	0.72
1:D:173:ILE:CD1	1:D:363:ILE:O	2.39	0.70
1:A:173:ILE:HD11	1:A:363:ILE:HG12	1.72	0.70
1:E:331:ILE:HG12	1:E:348:MET:HE3	1.72	0.70
1:C:331:ILE:HG23	1:C:348:MET:HE1	1.74	0.69
1:E:123:ILE:HD11	1:E:383:LEU:HD22	1.75	0.69
1:C:331:ILE:HG12	1:C:348:MET:HE3	1.74	0.68
1:F:123:ILE:CG2	1:F:182:ILE:HD11	2.23	0.68
1:D:123:ILE:CG2	1:D:182:ILE:HD11	2.24	0.68
1:A:123:ILE:HD11	1:A:383:LEU:HD22	1.76	0.67
1:B:123:ILE:CG2	1:B:182:ILE:HD11	2.25	0.67
1:E:139:SER:O	1:E:143:ILE:HG12	1.95	0.67
1:C:123:ILE:HD11	1:C:383:LEU:HD22	1.75	0.66
1:A:85:ASN:OD1	3:A:602:HOH:O	2.14	0.64
1:D:173:ILE:CD1	1:D:363:ILE:HA	2.27	0.64
1:D:331:ILE:HG12	1:D:348:MET:HE3	1.77	0.64
1:D:57:ILE:O	1:D:61:VAL:HG12	1.97	0.64
1:F:72:ASN:HB3	1:F:74:PHE:H	1.63	0.64
1:D:316:GLY:O	1:D:320:VAL:HG23	1.98	0.63
1:C:122:ARG:NH1	1:C:312:CYS:SG	2.71	0.63
1:B:84:LYS:HD2	2:C:502:P6L:O15	1.99	0.63
1:B:64:TYR:OH	1:B:100:HIS:HD2	1.81	0.62
1:A:316:GLY:O	1:A:320:VAL:HG23	1.99	0.62
2:B:501:P6L:C2	2:B:501:P6L:O10	2.47	0.62
1:D:173:ILE:HD11	1:D:363:ILE:O	1.98	0.62
1:B:286:ILE:HG13	2:F:502:P6L:C22	2.31	0.61
1:E:41:VAL:HG23	1:E:42:LEU:HD12	1.84	0.60
1:D:173:ILE:HD13	1:D:363:ILE:HA	1.83	0.59
2:D:501:P6L:O15	2:D:501:P6L:H71	2.01	0.59
1:A:169:ILE:O	1:A:173:ILE:HD12	2.02	0.59
1:F:72:ASN:CB	1:F:74:PHE:H	2.16	0.58
2:E:501:P6L:C23	2:E:501:P6L:H291	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:20:VAL:O	1:D:23:MET:HG2	2.04	0.58
1:F:20:VAL:O	1:F:23:MET:HG2	2.05	0.57
1:E:331:ILE:HG23	1:E:348:MET:HE1	1.87	0.56
1:C:282:GLY:CA	2:C:502:P6L:H302	2.35	0.55
1:A:378:ASP:O	1:A:381:VAL:O	2.24	0.55
1:C:20:VAL:O	1:C:23:MET:HG2	2.06	0.55
1:C:61:VAL:HG11	2:C:501:P6L:H493	1.89	0.55
1:D:79:ASN:ND2	3:D:604:HOH:O	2.41	0.54
1:A:360:ALA:O	1:A:364:VAL:HG13	2.07	0.54
1:F:121:GLU:HA	1:F:121:GLU:OE1	2.09	0.53
1:E:178:GLY:O	1:E:182:ILE:HG13	2.09	0.53
1:C:331:ILE:HG23	1:C:348:MET:CE	2.38	0.52
1:F:81:LEU:HD12	2:F:502:P6L:H201	1.91	0.52
1:A:173:ILE:CD1	1:A:363:ILE:HG12	2.37	0.52
1:E:331:ILE:HG23	1:E:348:MET:CE	2.39	0.52
1:A:79:ASN:ND2	3:A:616:HOH:O	2.41	0.52
1:B:376:LEU:O	1:B:380:THR:HG23	2.09	0.52
2:C:501:P6L:H282	2:C:501:P6L:C22	2.39	0.52
1:F:78:ILE:CD1	2:F:501:P6L:C30	2.88	0.52
1:F:81:LEU:HD12	2:F:502:P6L:C20	2.40	0.51
1:B:123:ILE:HG23	1:B:182:ILE:HD11	1.92	0.51
1:D:331:ILE:HG23	1:D:348:MET:CE	2.39	0.51
1:C:235:VAL:O	3:C:605:HOH:O	2.19	0.51
1:D:123:ILE:HG23	1:D:182:ILE:HD11	1.91	0.51
1:C:66:LEU:HD21	2:C:501:P6L:H23	1.92	0.50
1:F:123:ILE:HG23	1:F:182:ILE:HD11	1.91	0.50
1:D:23:MET:HB2	1:D:208:LEU:HD23	1.93	0.50
1:E:126:SER:OG	1:E:381:VAL:HG11	2.12	0.50
1:F:23:MET:HB2	1:F:208:LEU:HD23	1.93	0.50
1:C:23:MET:HB2	1:C:208:LEU:HD23	1.93	0.49
1:D:327:ILE:HG23	1:D:352:LEU:HD11	1.95	0.49
1:E:92:MET:SD	1:E:100:HIS:CE1	3.04	0.49
1:B:310:ASP:O	1:B:312:CYS:N	2.46	0.48
1:D:173:ILE:HD11	1:D:363:ILE:HA	1.94	0.48
2:D:501:P6L:O4	2:D:501:P6L:C16	2.61	0.48
2:F:501:P6L:O8	2:F:501:P6L:H182	2.14	0.48
1:C:72:ASN:ND2	2:C:501:P6L:O15	2.46	0.47
1:F:123:ILE:HG22	1:F:182:ILE:HD11	1.96	0.47
1:C:310:ASP:O	1:C:312:CYS:N	2.47	0.47
1:E:301:MET:O	1:E:302:LEU:C	2.52	0.47
1:E:92:MET:SD	1:E:100:HIS:ND1	2.88	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:78:ILE:HD11	2:C:501:P6L:H272	1.97	0.47
1:E:51:THR:O	1:E:55:VAL:HG23	2.15	0.47
1:A:51:THR:O	1:A:55:VAL:HG23	2.16	0.46
1:B:51:THR:O	1:B:55:VAL:HG23	2.16	0.46
1:E:310:ASP:O	1:E:312:CYS:N	2.49	0.46
1:C:198:LEU:N	1:C:199:PRO:CD	2.79	0.46
1:D:310:ASP:O	1:D:312:CYS:N	2.49	0.46
1:F:51:THR:O	1:F:55:VAL:HG23	2.16	0.45
1:B:198:LEU:N	1:B:199:PRO:CD	2.79	0.45
1:D:198:LEU:N	1:D:199:PRO:CD	2.79	0.45
1:E:137:THR:HA	1:E:141:ILE:HD12	1.99	0.45
1:D:51:THR:O	1:D:55:VAL:HG23	2.17	0.45
1:B:123:ILE:HG22	1:B:182:ILE:HD11	1.98	0.45
2:C:502:P6L:H181	2:C:502:P6L:O8	2.17	0.45
1:D:173:ILE:HD11	1:D:366:SER:HB3	1.98	0.44
1:C:51:THR:O	1:C:55:VAL:HG23	2.17	0.44
1:E:384:ARG:HG2	1:E:385:VAL:HG12	1.99	0.44
1:F:43:SER:OG	1:F:121:GLU:HG2	2.17	0.44
1:D:123:ILE:HG22	1:D:182:ILE:HD11	1.98	0.43
2:F:501:P6L:C30	2:F:501:P6L:H372	2.48	0.43
1:B:92:MET:SD	1:B:100:HIS:CD2	3.12	0.43
1:C:221:GLY:O	3:C:616:HOH:O	2.21	0.43
1:A:198:LEU:N	1:A:199:PRO:CD	2.82	0.42
1:C:123:ILE:HG23	1:C:128:VAL:HG23	2.01	0.42
1:A:235:VAL:O	3:A:606:HOH:O	2.21	0.42
1:B:19:LEU:O	1:B:22:PHE:HB3	2.19	0.42
1:E:198:LEU:N	1:E:199:PRO:CD	2.82	0.42
1:F:137:THR:HA	1:F:141:ILE:HD12	2.01	0.42
1:F:81:LEU:CD1	2:F:502:P6L:C22	2.97	0.41
1:A:137:THR:HA	1:A:141:ILE:HD12	2.02	0.41
1:D:137:THR:HA	1:D:141:ILE:HD12	2.03	0.41
1:C:137:THR:HA	1:C:141:ILE:HD12	2.01	0.41
1:C:365:TRP:O	1:C:369:VAL:HG23	2.21	0.41
1:E:19:LEU:O	1:E:22:PHE:HB3	2.21	0.41
1:A:365:TRP:O	1:A:369:VAL:HG23	2.21	0.41
1:F:198:LEU:N	1:F:199:PRO:CD	2.84	0.41
1:A:76:GLY:O	2:A:501:P6L:H72	2.21	0.41
1:D:25:ILE:HA	1:D:26:PRO:HA	1.93	0.41
1:F:72:ASN:HB2	1:F:75:PHE:H	1.86	0.41
1:A:238:THR:O	1:A:242:ILE:HG13	2.21	0.40
1:A:251:ALA:HB1	1:B:250:TRP:CH2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:238:THR:O	1:F:242:ILE:HG13	2.22	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	357/406 (88%)	343 (96%)	14 (4%)	0	100	100
1	B	361/406 (89%)	346 (96%)	13 (4%)	2 (1%)	25	31
1	C	362/406 (89%)	346 (96%)	14 (4%)	2 (1%)	25	31
1	D	360/406 (89%)	343 (95%)	15 (4%)	2 (1%)	25	31
1	E	365/406 (90%)	346 (95%)	17 (5%)	2 (0%)	29	35
1	F	358/406 (88%)	344 (96%)	13 (4%)	1 (0%)	41	50
All	All	2163/2436 (89%)	2068 (96%)	86 (4%)	9 (0%)	34	42

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	311	PRO
1	C	311	PRO
1	D	311	PRO
1	E	311	PRO
1	E	382	GLY
1	F	382	GLY
1	B	382	GLY
1	C	382	GLY
1	D	382	GLY

### 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	257/297 (86%)	253 (98%)	4 (2%)	62	78
1	B	261/297 (88%)	258 (99%)	3 (1%)	73	86
1	C	263/297 (89%)	260 (99%)	3 (1%)	73	86
1	D	262/297 (88%)	258 (98%)	4 (2%)	65	79
1	E	261/297 (88%)	256 (98%)	5 (2%)	57	73
1	F	260/297 (88%)	257 (99%)	3 (1%)	71	84
All	All	1564/1782 (88%)	1542 (99%)	22 (1%)	67	81

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	GLU
1	A	212	TRP
1	A	222	THR
1	A	364	VAL
1	B	70	GLU
1	B	114	LEU
1	B	222	THR
1	C	70	GLU
1	C	212	TRP
1	C	222	THR
1	D	114	LEU
1	D	121	GLU
1	D	212	TRP
1	D	222	THR
1	E	122	ARG
1	E	212	TRP
1	E	222	THR
1	E	314	VAL
1	E	379	LEU
1	F	43	SER
1	F	195	PRO
1	F	222	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	ASN
1	A	100	HIS
1	B	79	ASN
1	B	100	HIS
1	C	40	ASN
1	C	79	ASN
1	D	79	ASN
1	E	79	ASN
1	F	79	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	P6L	F	501	-	34,34,50	1.29	2 (5%)	37,40,56	1.81	7 (18%)
2	P6L	B	501	-	22,22,50	1.78	2 (9%)	25,28,56	1.92	6 (24%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	P6L	C	502	-	50,50,50	1.04	2 (4%)	53,56,56	1.25	3 (5%)
2	P6L	F	502	-	50,50,50	1.33	2 (4%)	53,56,56	1.23	5 (9%)
2	P6L	E	501	-	34,34,50	1.37	2 (5%)	37,40,56	1.47	4 (10%)
2	P6L	C	501	-	38,38,50	1.21	2 (5%)	41,44,56	1.69	8 (19%)
2	P6L	A	501	-	24,24,50	1.27	3 (12%)	27,30,56	1.89	7 (25%)
2	P6L	D	501	-	33,33,50	1.27	2 (6%)	36,39,56	1.45	7 (19%)

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	P6L	F	501	-	-	16/39/39/55	-
2	P6L	B	501	-	-	13/27/27/55	-
2	P6L	C	502	-	-	36/55/55/55	-
2	P6L	F	502	-	-	30/55/55/55	-
2	P6L	E	501	-	-	21/39/39/55	-
2	P6L	C	501	-	-	12/43/43/55	-
2	P6L	A	501	-	-	16/29/29/55	-
2	P6L	D	501	-	-	22/38/38/55	-

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	502	P6L	O4-C14	5.87	1.50	1.34
2	F	501	P6L	O4-C14	5.41	1.49	1.34
2	B	501	P6L	O8-C16	5.40	1.49	1.33
2	D	501	P6L	O4-C14	5.31	1.49	1.34
2	F	502	P6L	O8-C16	5.22	1.48	1.33
2	C	501	P6L	O4-C14	5.03	1.48	1.34
2	B	501	P6L	O4-C14	5.01	1.48	1.34
2	E	501	P6L	O4-C14	4.91	1.48	1.34
2	E	501	P6L	O8-C16	4.54	1.46	1.33
2	C	502	P6L	O8-C16	4.25	1.45	1.33
2	C	502	P6L	O4-C14	4.21	1.46	1.34
2	A	501	P6L	O8-C16	4.02	1.45	1.33
2	C	501	P6L	O8-C16	3.37	1.43	1.33
2	D	501	P6L	O8-C16	3.36	1.43	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	P6L	O4-C14	2.38	1.41	1.34
2	F	501	P6L	O8-C6	-2.22	1.40	1.45
2	A	501	P6L	O8-C6	-2.09	1.40	1.45

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	501	P6L	O4-C14-C18	6.23	124.92	111.50
2	F	501	P6L	O4-C14-C18	6.05	124.54	111.50
2	C	502	P6L	O4-C14-C18	6.01	124.45	111.50
2	B	501	P6L	O8-C16-C27	5.82	126.64	111.38
2	C	501	P6L	O4-C14-C18	5.48	123.32	111.50
2	F	501	P6L	C5-O4-C14	5.37	131.02	117.79
2	F	502	P6L	O4-C14-C18	4.92	122.11	111.50
2	A	501	P6L	O8-C16-O17	-4.41	112.47	123.59
2	C	501	P6L	O8-C16-C27	4.34	125.52	111.91
2	A	501	P6L	O8-C16-C27	4.13	122.20	111.38
2	C	501	P6L	O8-C16-O17	-4.04	113.39	123.59
2	F	502	P6L	O8-C16-C27	3.77	123.75	111.91
2	B	501	P6L	C5-O4-C14	3.76	127.05	117.79
2	D	501	P6L	O4-C14-C18	3.74	119.56	111.50
2	A	501	P6L	O4-C5-C7	3.49	121.03	108.40
2	D	501	P6L	C7-C5-C6	-3.44	103.65	111.79
2	A	501	P6L	O4-C14-C18	3.31	118.63	111.50
2	F	501	P6L	C7-C5-C6	-3.17	104.30	111.79
2	B	501	P6L	O8-C16-O17	-3.08	115.82	123.59
2	B	501	P6L	O4-C14-C18	3.06	119.34	110.80
2	E	501	P6L	O4-C14-O15	-2.99	116.48	123.70
2	C	501	P6L	O4-C5-C7	2.91	118.94	108.40
2	C	502	P6L	O8-C16-C27	2.85	120.84	111.91
2	A	501	P6L	O4-C14-O15	-2.84	116.83	123.70
2	A	501	P6L	O4-C5-C6	-2.77	98.38	108.40
2	B	501	P6L	O3-C2-C50	2.65	120.81	109.12
2	F	501	P6L	O8-C6-C5	-2.64	100.74	108.43
2	D	501	P6L	C5-O4-C14	2.61	124.23	117.79
2	C	501	P6L	C5-O4-C14	2.59	124.17	117.79
2	F	502	P6L	C5-O4-C14	2.58	124.15	117.79
2	D	501	P6L	O8-C16-O17	-2.58	117.09	123.59
2	F	502	P6L	O8-C16-O17	-2.56	117.12	123.59
2	F	501	P6L	O8-C16-O17	-2.56	117.14	123.59
2	B	501	P6L	C6-O8-C16	2.50	126.36	117.12
2	C	502	P6L	O4-C14-O15	-2.46	117.75	123.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	501	P6L	O8-C16-C27	2.44	119.56	111.91
2	D	501	P6L	O4-C5-C7	2.43	117.20	108.40
2	F	501	P6L	C19-C18-C14	-2.40	104.89	113.62
2	C	501	P6L	O13-P11-O10	2.35	123.86	112.24
2	D	501	P6L	O8-C16-C27	2.31	119.15	111.91
2	C	501	P6L	C20-C19-C18	2.28	121.38	113.19
2	F	501	P6L	O4-C14-O15	-2.15	118.51	123.70
2	F	502	P6L	O4-C5-C6	2.13	116.12	108.40
2	E	501	P6L	O13-P11-O10	2.08	122.50	112.24
2	D	501	P6L	O13-P11-O10	2.07	122.48	112.24
2	C	501	P6L	O4-C14-O15	-2.06	118.73	123.70
2	A	501	P6L	C5-O4-C14	2.01	122.74	117.79

There are no chirality outliers.

All (166) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	501	P6L	O15-C14-O4-C5
2	F	501	P6L	C18-C14-O4-C5
2	F	501	P6L	C1-O12-P11-O13
2	B	501	P6L	C2-C1-O12-P11
2	B	501	P6L	O17-C16-O8-C6
2	B	501	P6L	C27-C16-O8-C6
2	C	502	P6L	O12-C1-C2-C50
2	C	502	P6L	C18-C14-O4-C5
2	C	502	P6L	C7-O9-P11-O10
2	C	502	P6L	C1-O12-P11-O9
2	C	502	P6L	C1-O12-P11-O10
2	C	502	P6L	C1-O12-P11-O13
2	F	502	P6L	C1-C2-C50-O51
2	F	502	P6L	C5-C7-O9-P11
2	F	502	P6L	O17-C16-O8-C6
2	F	502	P6L	C27-C16-O8-C6
2	F	502	P6L	C1-O12-P11-O13
2	E	501	P6L	C7-O9-P11-O13
2	E	501	P6L	C1-O12-P11-O10
2	C	501	P6L	O12-C1-C2-O3
2	C	501	P6L	O12-C1-C2-C50
2	A	501	P6L	C7-O9-P11-O13
2	D	501	P6L	C5-C7-O9-P11
2	D	501	P6L	C7-O9-P11-O10
2	A	501	P6L	O17-C16-O8-C6

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Mol	Chain	Res	Type	Atoms
2	E	501	P6L	C27-C16-O8-C6
2	A	501	P6L	C27-C16-O8-C6
2	E	501	P6L	O17-C16-O8-C6
2	D	501	P6L	O17-C16-O8-C6
2	C	502	P6L	O15-C14-O4-C5
2	D	501	P6L	C27-C16-O8-C6
2	C	502	P6L	O12-C1-C2-O3
2	B	501	P6L	O12-C1-C2-C50
2	D	501	P6L	C14-C18-C19-C20
2	D	501	P6L	O3-C2-C50-O51
2	A	501	P6L	O12-C1-C2-O3
2	F	501	P6L	C1-O12-P11-O9
2	B	501	P6L	C7-O9-P11-O12
2	F	502	P6L	C7-O9-P11-O12
2	F	502	P6L	C1-O12-P11-O9
2	E	501	P6L	C7-O9-P11-O12
2	E	501	P6L	C1-O12-P11-O9
2	C	501	P6L	C1-O12-P11-O9
2	A	501	P6L	C7-O9-P11-O12
2	A	501	P6L	O12-C1-C2-C50
2	F	501	P6L	C27-C16-O8-C6
2	D	501	P6L	C25-C26-C37-C45
2	C	502	P6L	C25-C26-C37-C45
2	D	501	P6L	C7-C5-O4-C14
2	E	501	P6L	O12-C1-C2-O3
2	F	502	P6L	C27-C28-C29-C30
2	D	501	P6L	C24-C25-C26-C37
2	C	502	P6L	C26-C37-C45-C46
2	F	501	P6L	C1-C2-C50-O51
2	D	501	P6L	C1-C2-C50-O51
2	D	501	P6L	C19-C20-C21-C22
2	C	502	P6L	C45-C46-C47-C48
2	F	502	P6L	C28-C29-C30-C31
2	F	502	P6L	O3-C2-C50-O51
2	C	502	P6L	C16-C27-C28-C29
2	A	501	P6L	O15-C14-O4-C5
2	E	501	P6L	C18-C19-C20-C21
2	F	502	P6L	C18-C14-O4-C5
2	F	501	P6L	O17-C16-O8-C6
2	F	502	P6L	C26-C37-C45-C46
2	E	501	P6L	C16-C27-C28-C29
2	F	501	P6L	C14-C18-C19-C20

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Mol	Chain	Res	Type	Atoms
2	E	501	P6L	C18-C14-O4-C5
2	A	501	P6L	C18-C14-O4-C5
2	F	501	P6L	C20-C21-C22-C23
2	F	502	P6L	O15-C14-O4-C5
2	C	502	P6L	C23-C24-C25-C26
2	F	502	P6L	C30-C31-C32-C33
2	D	501	P6L	C23-C24-C25-C26
2	F	502	P6L	C25-C26-C37-C45
2	E	501	P6L	O15-C14-O4-C5
2	C	502	P6L	C28-C29-C30-C31
2	C	502	P6L	C7-O9-P11-O12
2	C	502	P6L	C34-C35-C36-C38
2	F	502	P6L	C34-C35-C36-C38
2	E	501	P6L	C19-C20-C21-C22
2	F	501	P6L	C18-C19-C20-C21
2	F	501	P6L	C27-C28-C29-C30
2	C	502	P6L	C39-C40-C41-C42
2	F	501	P6L	O3-C2-C50-O51
2	C	502	P6L	C30-C31-C32-C33
2	F	502	P6L	C35-C36-C38-C39
2	F	502	P6L	C6-C5-O4-C14
2	A	501	P6L	C7-C5-O4-C14
2	C	502	P6L	C2-C1-O12-P11
2	E	501	P6L	O4-C5-C7-O9
2	A	501	P6L	C14-C18-C19-C20
2	C	502	P6L	O4-C5-C6-O8
2	D	501	P6L	C26-C37-C45-C46
2	C	502	P6L	C6-C5-C7-O9
2	D	501	P6L	C6-C5-C7-O9
2	F	502	P6L	C40-C41-C42-C43
2	C	502	P6L	C5-C7-O9-P11
2	C	502	P6L	C7-C5-C6-O8
2	A	501	P6L	C7-C5-C6-O8
2	C	502	P6L	O4-C5-C7-O9
2	C	501	P6L	O15-C14-O4-C5
2	C	501	P6L	C37-C45-C46-C47
2	F	501	P6L	C26-C37-C45-C46
2	F	502	P6L	C24-C25-C26-C37
2	A	501	P6L	C2-C1-O12-P11
2	A	501	P6L	C5-C7-O9-P11
2	C	501	P6L	C18-C14-O4-C5
2	A	501	P6L	C18-C19-C20-C21

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Mol	Chain	Res	Type	Atoms
2	D	501	P6L	C20-C21-C22-C23
2	D	501	P6L	C18-C19-C20-C21
2	C	502	P6L	C37-C45-C46-C47
2	F	502	P6L	C7-C5-C6-O8
2	D	501	P6L	O4-C5-C7-O9
2	E	501	P6L	O12-C1-C2-C50
2	B	501	P6L	O4-C5-C6-O8
2	A	501	P6L	O4-C5-C6-O8
2	F	502	P6L	C37-C45-C46-C47
2	D	501	P6L	C16-C27-C28-C29
2	D	501	P6L	O15-C14-O4-C5
2	F	502	P6L	C39-C40-C41-C42
2	D	501	P6L	C5-C6-O8-C16
2	D	501	P6L	C7-O9-P11-O12
2	B	501	P6L	C7-O9-P11-O10
2	C	502	P6L	C7-O9-P11-O13
2	F	502	P6L	C7-O9-P11-O10
2	E	501	P6L	C1-O12-P11-O13
2	C	501	P6L	C1-O12-P11-O10
2	E	501	P6L	C6-C5-C7-O9
2	B	501	P6L	O4-C5-C7-O9
2	B	501	P6L	O8-C16-C27-C28
2	C	501	P6L	C14-C18-C19-C20
2	C	502	P6L	O8-C16-C27-C28
2	C	501	P6L	O4-C14-C18-C19
2	C	501	P6L	O8-C16-C27-C28
2	C	502	P6L	C18-C19-C20-C21
2	C	502	P6L	C7-C5-O4-C14
2	E	501	P6L	C6-C5-O4-C14
2	C	501	P6L	C7-C5-O4-C14
2	F	501	P6L	C24-C25-C26-C37
2	C	502	P6L	C20-C21-C22-C23
2	E	501	P6L	C27-C28-C29-C30
2	C	501	P6L	C45-C46-C47-C48
2	B	501	P6L	O17-C16-C27-C28
2	F	501	P6L	C5-C7-O9-P11
2	B	501	P6L	O4-C14-C18-C19
2	C	502	P6L	C41-C42-C43-C44
2	C	502	P6L	C27-C16-O8-C6
2	F	502	P6L	C46-C47-C48-C49
2	C	502	P6L	O4-C14-C18-C19
2	C	502	P6L	C36-C38-C39-C40

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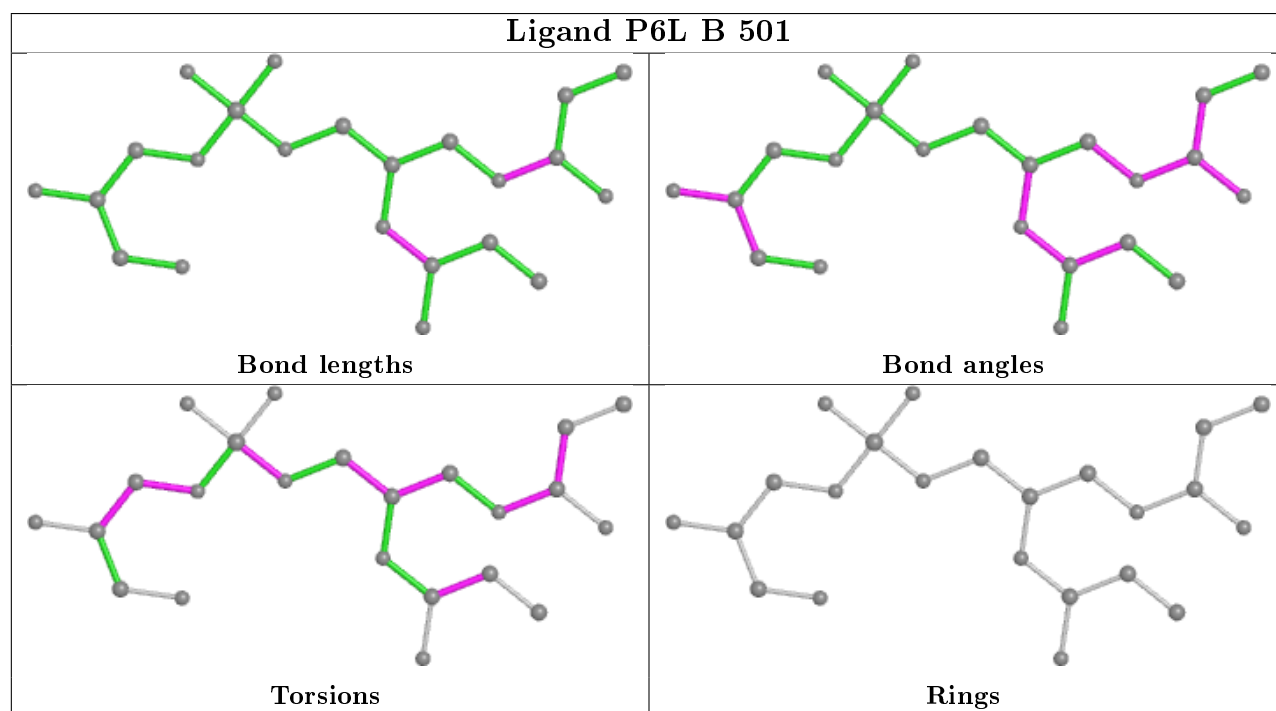
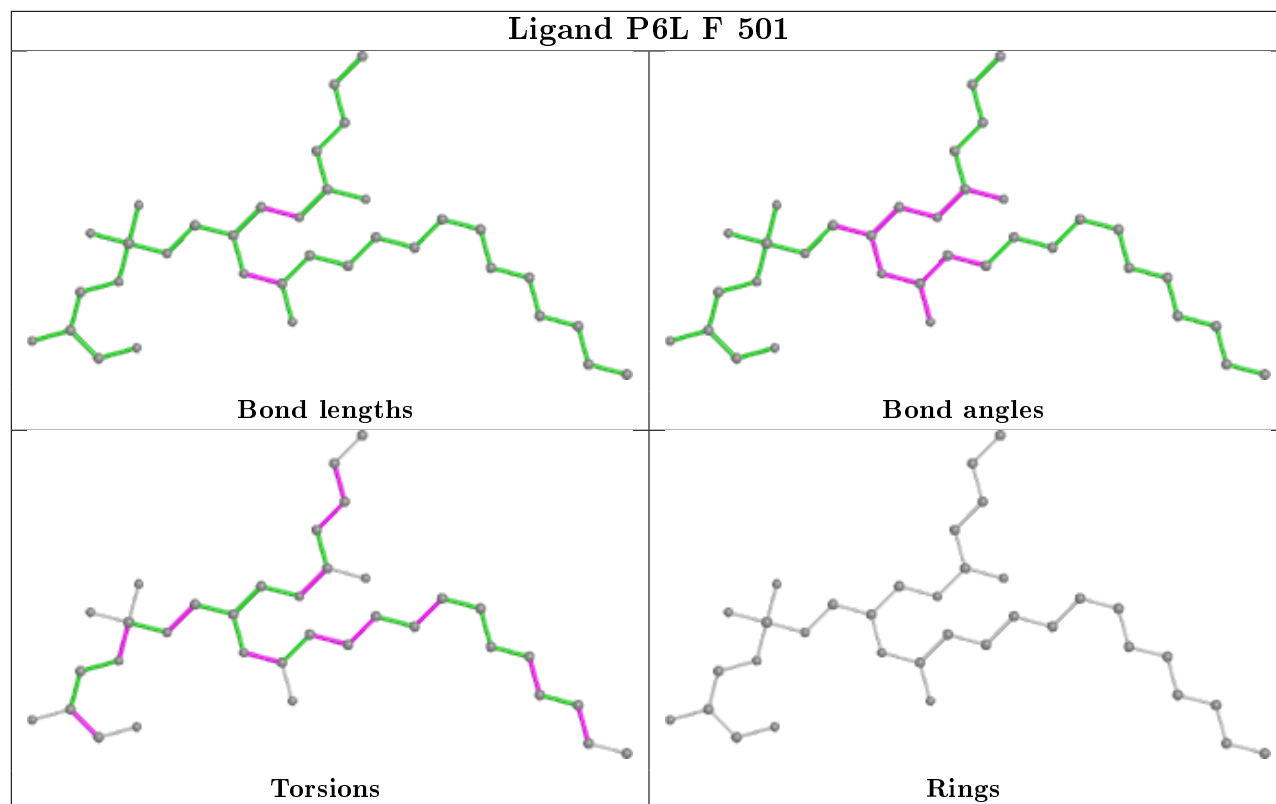
Mol	Chain	Res	Type	Atoms
2	E	501	P6L	O8-C16-C27-C28
2	E	501	P6L	C20-C21-C22-C23
2	B	501	P6L	C7-C5-C6-O8
2	B	501	P6L	C6-C5-C7-O9
2	F	502	P6L	C36-C38-C39-C40
2	D	501	P6L	C18-C14-O4-C5
2	F	501	P6L	C16-C27-C28-C29
2	C	502	P6L	O15-C14-C18-C19
2	C	502	P6L	O17-C16-O8-C6
2	E	501	P6L	O17-C16-C27-C28
2	F	502	P6L	C22-C23-C24-C25
2	A	501	P6L	O4-C14-C18-C19
2	F	502	P6L	C33-C34-C35-C36
2	F	502	P6L	O8-C16-C27-C28
2	F	502	P6L	O17-C16-C27-C28

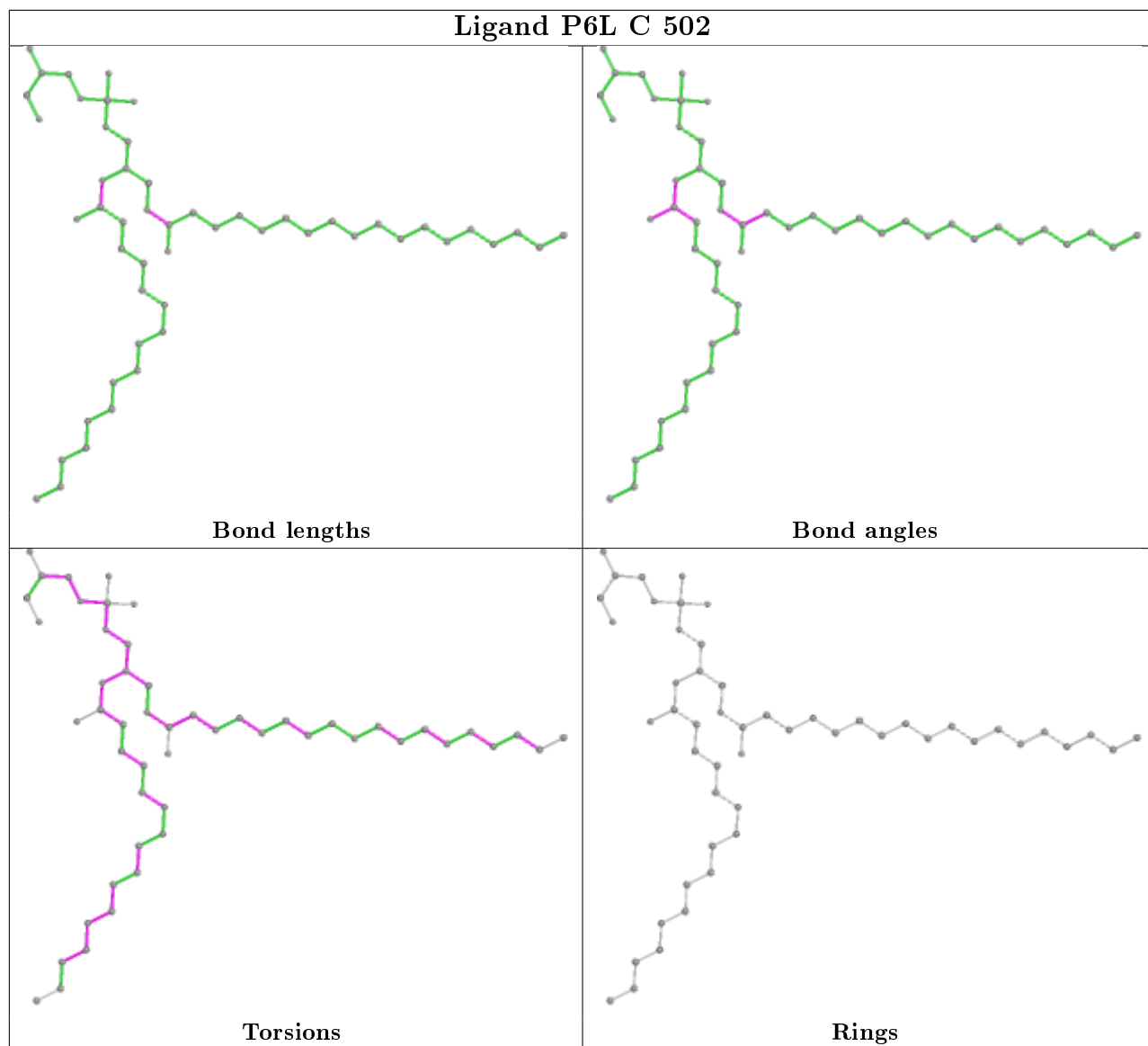
There are no ring outliers.

8 monomers are involved in 23 short contacts:

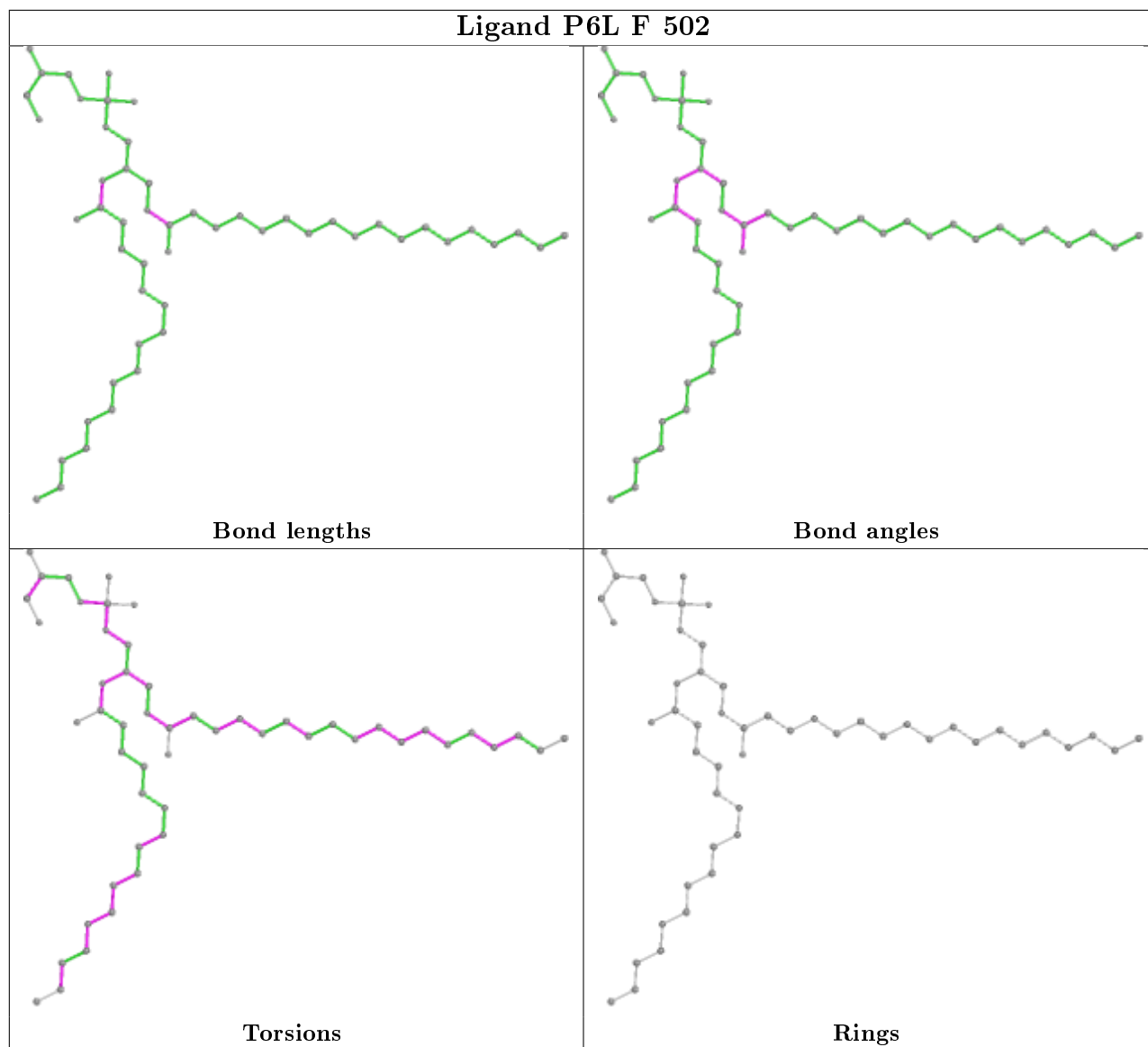
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	501	P6L	4	0
2	B	501	P6L	2	0
2	C	502	P6L	4	0
2	F	502	P6L	4	0
2	E	501	P6L	1	0
2	C	501	P6L	5	0
2	A	501	P6L	1	0
2	D	501	P6L	2	0

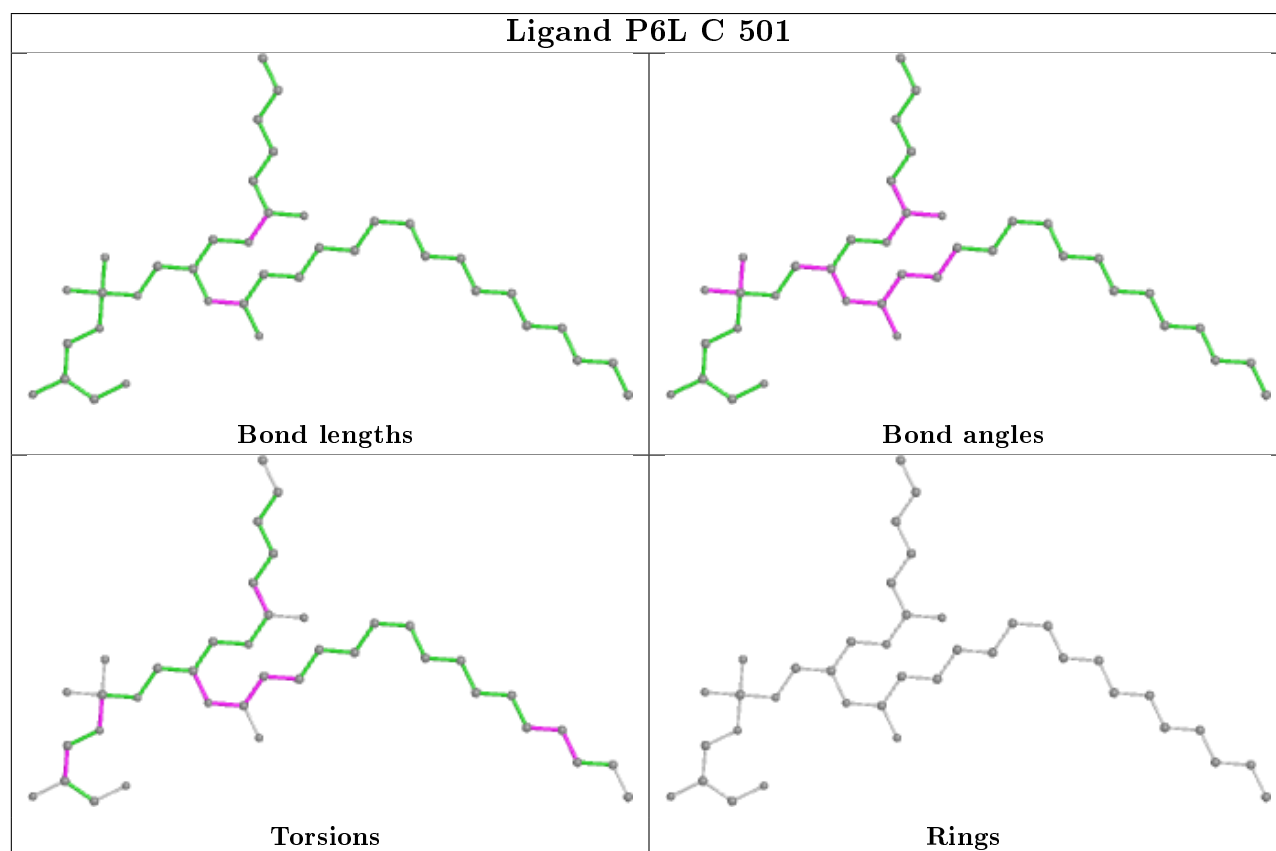
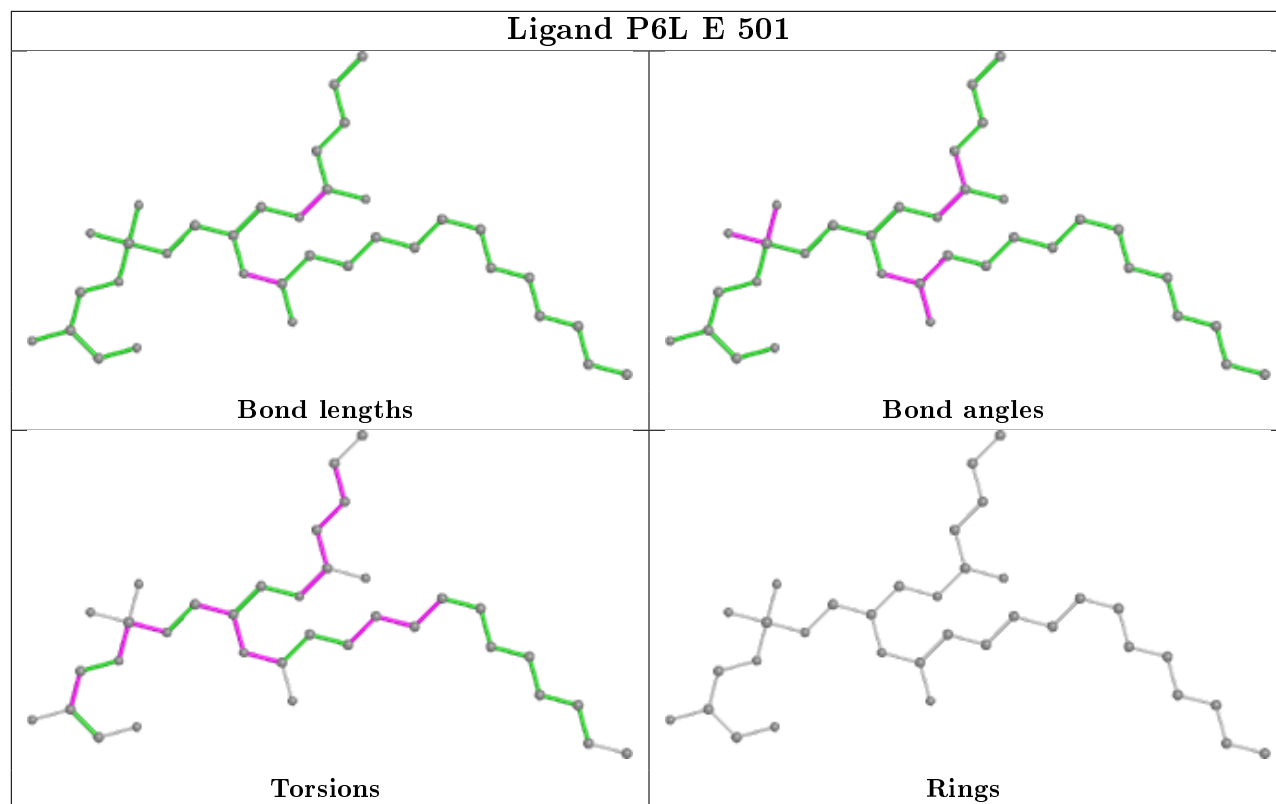
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

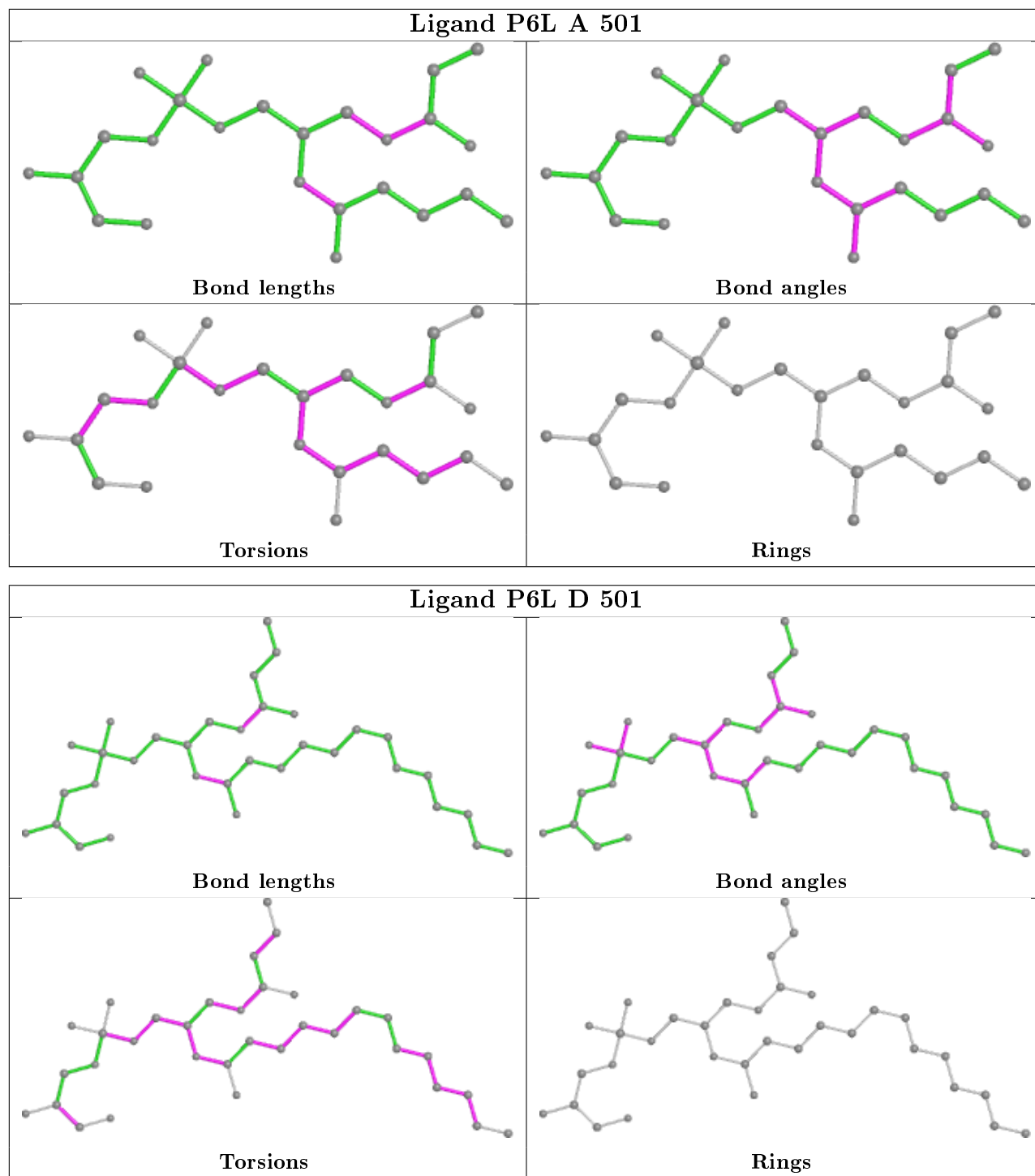












## 5.7 Other polymers [\(i\)](#)

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

### 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<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	363/406 (89%)	-0.24	2 (0%) 89 92	21, 40, 72, 91	0
1	B	367/406 (90%)	-0.16	5 (1%) 75 80	23, 42, 74, 99	0
1	C	368/406 (90%)	-0.19	2 (0%) 91 94	21, 41, 77, 96	0
1	D	366/406 (90%)	-0.23	3 (0%) 86 89	25, 43, 77, 103	0
1	E	371/406 (91%)	-0.16	5 (1%) 77 81	21, 41, 72, 92	0
1	F	364/406 (89%)	-0.18	7 (1%) 66 73	22, 40, 77, 93	0
All	All	2199/2436 (90%)	-0.19	24 (1%) 80 85	21, 41, 76, 103	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	250	TRP	4.2
1	D	247	PHE	3.8
1	B	250	TRP	3.8
1	B	121	GLU	3.1
1	E	250	TRP	3.0
1	E	379	LEU	2.7
1	F	247	PHE	2.7
1	F	252	LEU	2.7
1	A	122	ARG	2.7
1	B	183	GLY	2.6
1	E	247	PHE	2.6
1	B	196	HIS	2.6
1	D	182	ILE	2.6
1	F	195	PRO	2.5
1	B	247	PHE	2.5
1	F	121	GLU	2.4
1	F	119	LEU	2.4
1	F	181	LEU	2.3
1	A	35	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	196	HIS	2.2
1	F	35	LEU	2.2
1	E	183	GLY	2.2
1	E	180	TYR	2.0
1	C	125	PHE	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](#)

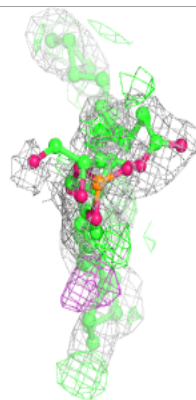
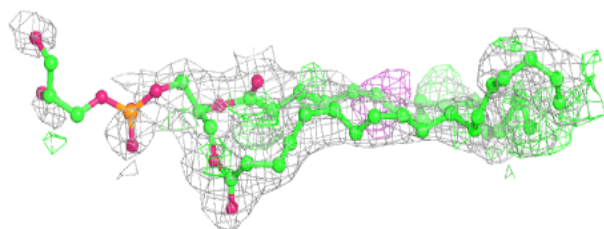
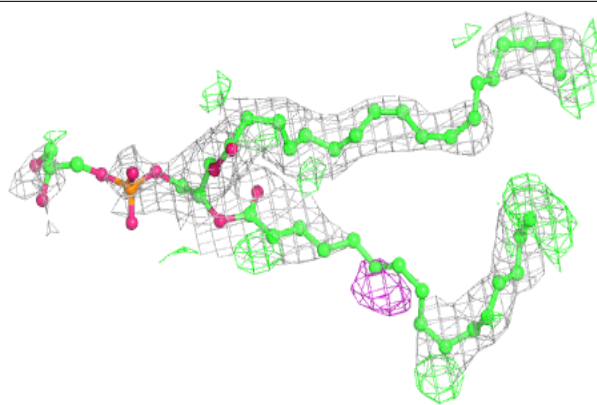
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	P6L	F	502	51/51	0.63	0.25	47,66,127,139	0
2	P6L	C	502	51/51	0.78	0.19	44,63,108,123	0
2	P6L	A	501	25/51	0.85	0.16	32,53,65,79	0
2	P6L	E	501	35/51	0.87	0.24	43,68,80,81	0
2	P6L	C	501	39/51	0.87	0.20	38,62,77,77	0
2	P6L	F	501	35/51	0.87	0.23	44,57,71,73	0
2	P6L	D	501	34/51	0.90	0.14	40,61,73,75	0
2	P6L	B	501	23/51	0.91	0.17	43,58,68,71	0

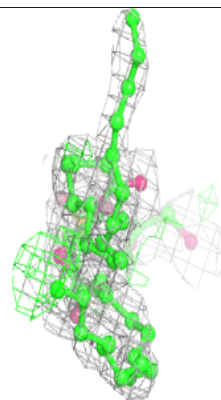
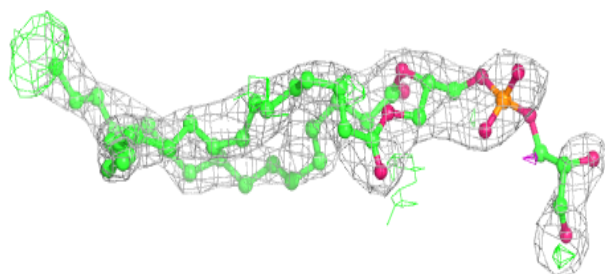
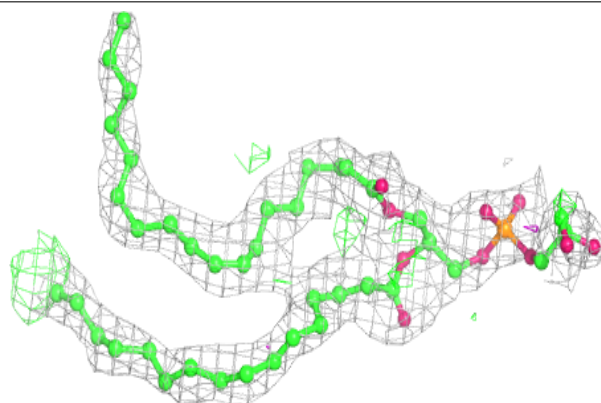
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around P6L F 502:**

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

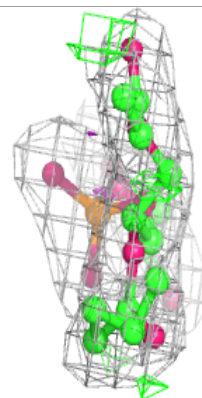
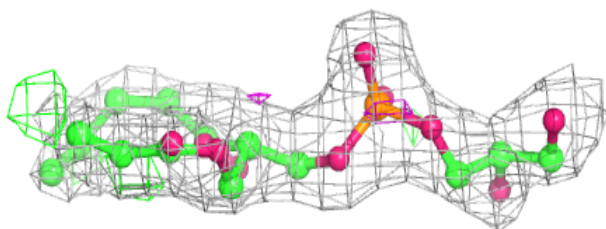
**Electron density around P6L C 502:**

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

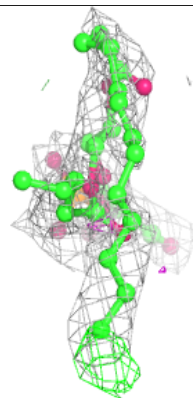
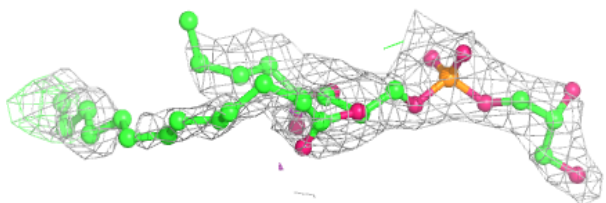
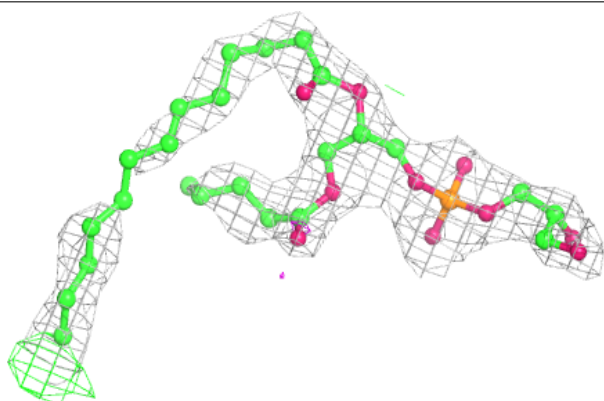


**Electron density around P6L A 501:**

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

**Electron density around P6L E 501:**

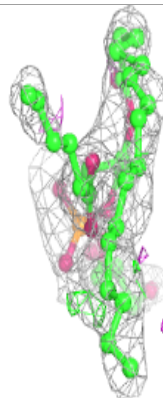
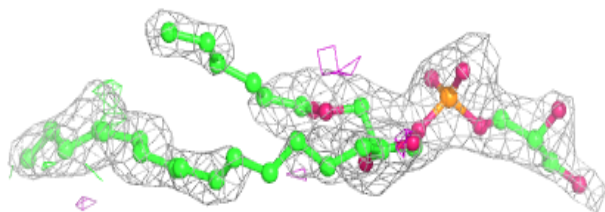
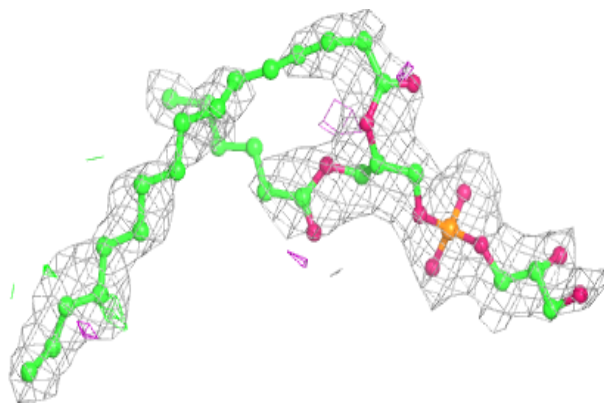
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



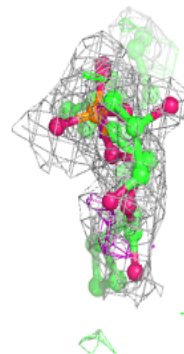
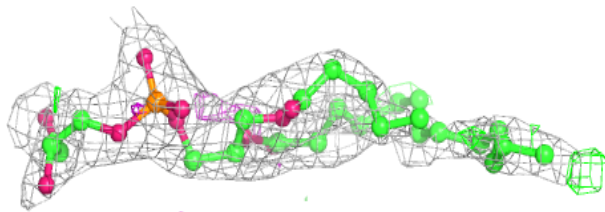
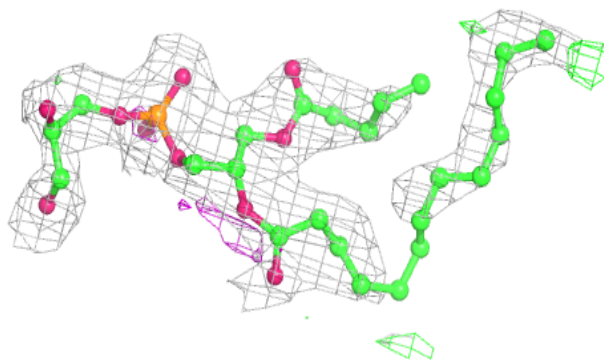


**Electron density around P6L C 501:**

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

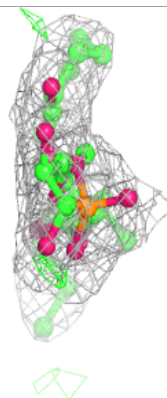
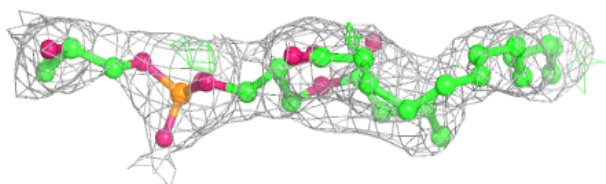
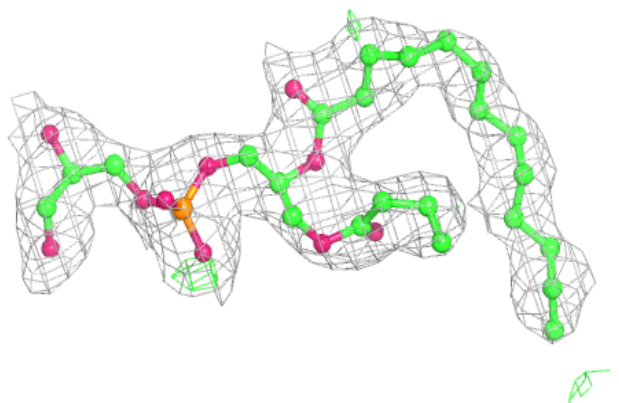
**Electron density around P6L F 501:**

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

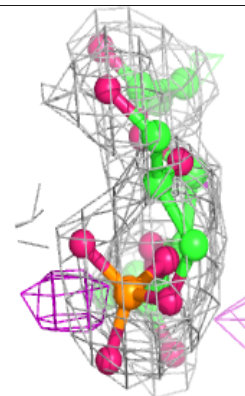
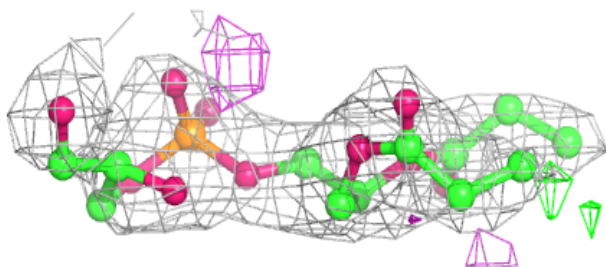
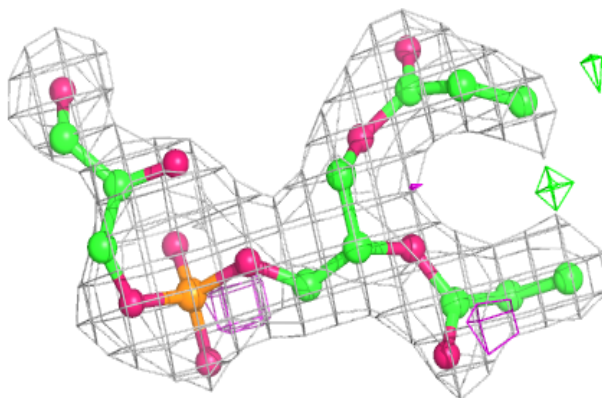


**Electron density around P6L D 501:**

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

**Electron density around P6L B 501:**

$2mF_o-DF_c$  (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.