wwPDB X-ray Structure Validation Summary Report (i)

Sep 25, 2023 – 08:45 AM EDT

PDB ID	:	5VCB
Title	:	Crystal structure of holo-(acyl-carrier-protein) synthase:holo(acyl-carrier-protein) complex from Escherichia Coli.
Authors	:	Marcella, A.M.; Barb, A.W.
Deposited on	:	2017-03-31
Resolution	:	4.10 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:

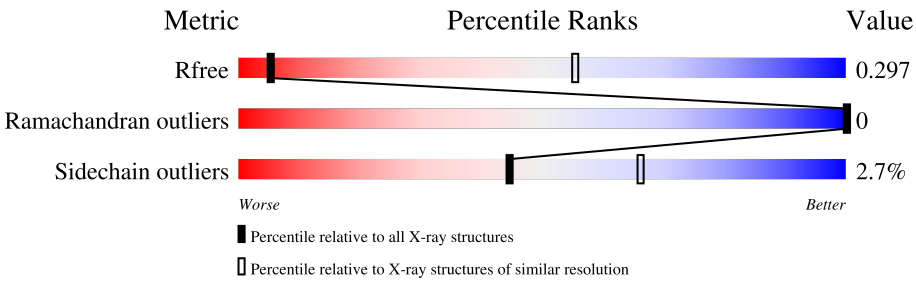
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & 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 4.10 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	1193 (4.50-3.70)
Ramachandran outliers	138981	1005 (4.48-3.72)
Sidechain outliers	138945	1199 (4.50-3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Mol	Chain	Length	Quality of chain
1	A	126	94% • •
1	B	126	90% • 6%
1	C	126	94% • 6%
1	G	126	92% • •
1	H	126	94% • 5%
1	I	126	94% • •
1	M	126	97% • •
1	N	126	92% 5% •

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Mol	Chain	Length	Quality of chain
1	O	126	90% 5%
1	S	126	93%
1	T	126	92%
1	U	126	94% 5%
1	a	126	94%
1	b	126	93%
1	c	126	95% 5%
2	D	79	91% 6%
2	E	79	96%
2	F	79	96%
2	J	79	91% 6%
2	K	79	96%
2	L	79	96%
2	P	79	96%
2	Q	79	92%
2	R	79	95%
2	V	79	95%
2	W	79	97%
2	X	79	94%
2	d	79	97%
2	e	79	97%
2	f	79	95%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 23422 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 Holo-[acyl-carrier-protein] synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	b	121	955	611	176	166	2	0	1	0
1	a	122	966	617	180	167	2	0	1	0
1	c	120	955	612	177	164	2	0	2	0
1	G	121	955	611	176	166	2	0	1	0
1	I	122	966	617	180	167	2	0	1	0
1	H	120	955	612	177	164	2	0	2	0
1	O	121	955	611	176	166	2	0	1	0
1	N	122	966	617	180	167	2	0	1	0
1	M	123	962	616	175	169	2	0	2	0
1	B	119	943	605	173	163	2	0	1	0
1	A	122	966	617	180	167	2	0	1	0
1	C	119	951	610	176	163	2	0	2	0
1	T	121	955	611	176	166	2	0	1	0
1	S	122	966	617	180	167	2	0	1	0
1	U	120	955	612	177	164	2	0	2	0

- Molecule 2 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	f	77	596	368	92	135	1	0	0	0
2	e	77	596	368	92	135	1	0	0	0
2	d	77	596	368	92	135	1	0	0	0
2	K	77	596	368	92	135	1	0	0	0
2	J	77	596	368	92	135	1	0	0	0
2	L	77	596	368	92	135	1	0	0	0
2	F	77	596	368	92	135	1	0	0	0
2	E	77	596	368	92	135	1	0	0	0
2	D	77	596	368	92	135	1	0	0	0
2	P	77	596	368	92	135	1	0	0	0
2	R	77	596	368	92	135	1	0	0	0
2	Q	77	596	368	92	135	1	0	0	0
2	X	77	596	368	92	135	1	0	0	0
2	W	77	596	368	92	135	1	0	0	0
2	V	77	596	368	92	135	1	0	0	0

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
f	-1	MET	-	initiating methionine	UNP B7MJ81
f	0	GLY	-	expression tag	UNP B7MJ81
e	-1	MET	-	initiating methionine	UNP B7MJ81
e	0	GLY	-	expression tag	UNP B7MJ81
d	-1	MET	-	initiating methionine	UNP B7MJ81
d	0	GLY	-	expression tag	UNP B7MJ81
K	-1	MET	-	initiating methionine	UNP B7MJ81
K	0	GLY	-	expression tag	UNP B7MJ81
J	-1	MET	-	initiating methionine	UNP B7MJ81
J	0	GLY	-	expression tag	UNP B7MJ81

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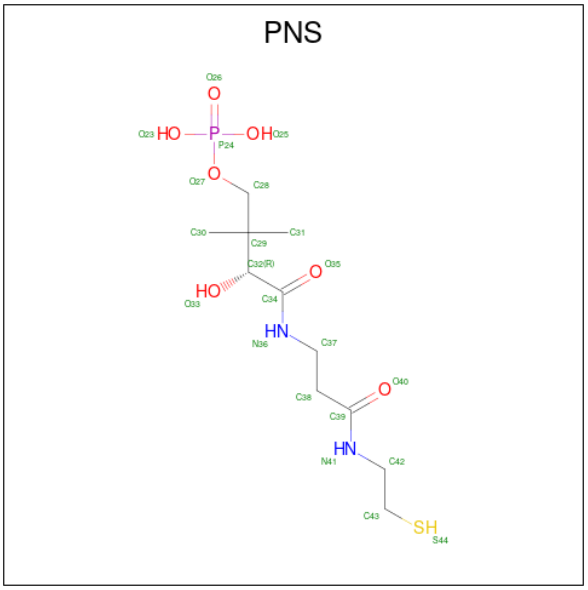
Chain	Residue	Modelled	Actual	Comment	Reference
L	-1	MET	-	initiating methionine	UNP B7MJ81
L	0	GLY	-	expression tag	UNP B7MJ81
F	-1	MET	-	initiating methionine	UNP B7MJ81
F	0	GLY	-	expression tag	UNP B7MJ81
E	-1	MET	-	initiating methionine	UNP B7MJ81
E	0	GLY	-	expression tag	UNP B7MJ81
D	-1	MET	-	initiating methionine	UNP B7MJ81
D	0	GLY	-	expression tag	UNP B7MJ81
P	-1	MET	-	initiating methionine	UNP B7MJ81
P	0	GLY	-	expression tag	UNP B7MJ81
R	-1	MET	-	initiating methionine	UNP B7MJ81
R	0	GLY	-	expression tag	UNP B7MJ81
Q	-1	MET	-	initiating methionine	UNP B7MJ81
Q	0	GLY	-	expression tag	UNP B7MJ81
X	-1	MET	-	initiating methionine	UNP B7MJ81
X	0	GLY	-	expression tag	UNP B7MJ81
W	-1	MET	-	initiating methionine	UNP B7MJ81
W	0	GLY	-	expression tag	UNP B7MJ81
V	-1	MET	-	initiating methionine	UNP B7MJ81
V	0	GLY	-	expression tag	UNP B7MJ81

- Molecule 3 is 4'-PHOSPHOPANTETHEINE (three-letter code: PNS) (formula: $C_{11}H_{23}N_2O_7PS$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	f	1	13	6	1	5	1	0	0

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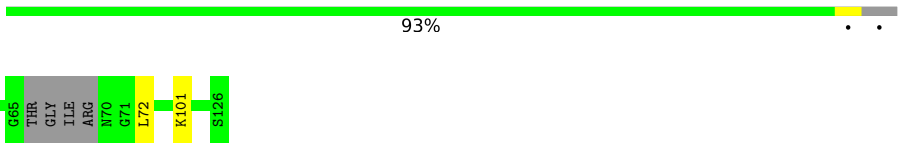
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	e	1	Total C O P 5 1 3 1	0	0
3	d	1	Total C N O P 15 8 1 5 1	0	0
3	J	1	Total C O P 5 1 3 1	0	0
3	L	1	Total C O P 5 1 3 1	0	0
3	F	1	Total C O P 10 5 4 1	0	0
3	E	1	Total C O P 5 1 3 1	0	0
3	D	1	Total C O P 10 5 4 1	0	0
3	P	1	Total C O P 9 5 3 1	0	0
3	R	1	Total C O P 8 4 3 1	0	0
3	Q	1	Total O P 4 3 1	0	0
3	X	1	Total C N O P 13 6 1 5 1	0	0
3	W	1	Total C O P 5 1 3 1	0	0
3	V	1	Total O P 4 3 1	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

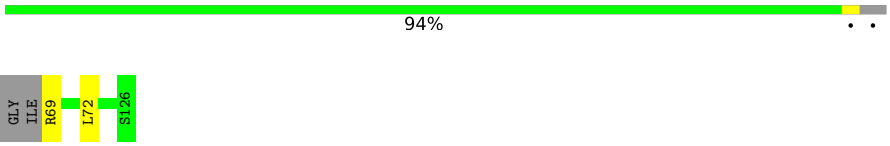
- Molecule 1: Holo-[acyl-carrier-protein] synthase

Chain b:



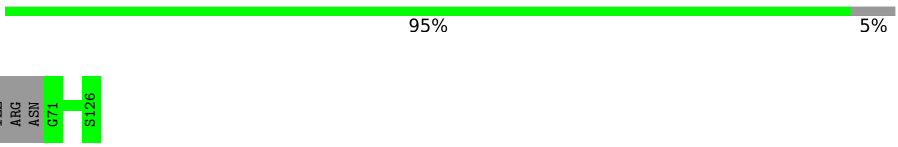
- Molecule 1: Holo-[acyl-carrier-protein] synthase

Chain a:



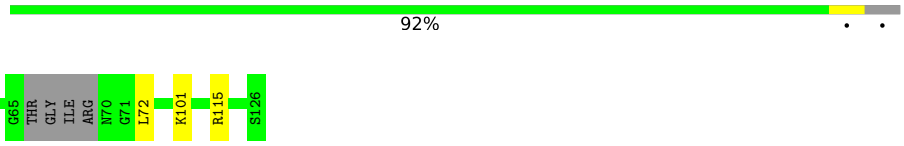
- Molecule 1: Holo-[acyl-carrier-protein] synthase

Chain c:



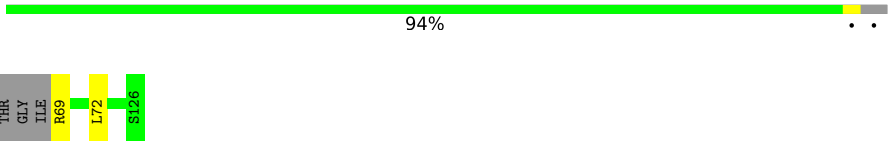
- Molecule 1: Holo-[acyl-carrier-protein] synthase

Chain G:



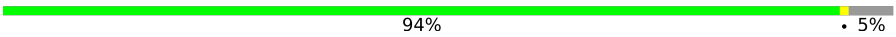
- Molecule 1: Holo-[acyl-carrier-protein] synthase

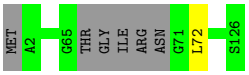
Chain I:



- Molecule 1: Holo-[acyl-carrier-protein] synthase

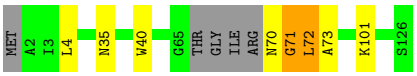
Chain H:





• Molecule 1: Holo-[acyl-carrier-protein] synthase

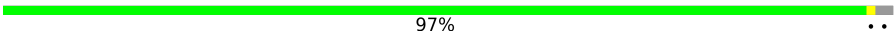
Chain O:

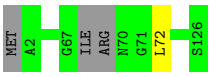


• Molecule 1: Holo-[acyl-carrier-protein] synthase

Chain N:

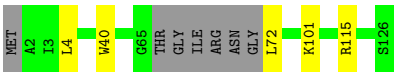
• Molecule 1: Holo-[acyl-carrier-protein] synthase

Chain M: 

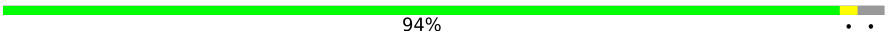


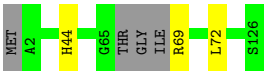
• Molecule 1: Holo-[acyl-carrier-protein] synthase

Chain B:

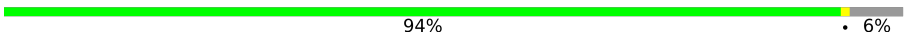


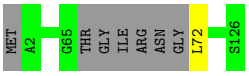
• Molecule 1: Holo-[acyl-carrier-protein] synthase

Chain A: 



• Molecule 1: Holo-[acyl-carrier-protein] synthase

Chain C: 



• Molecule 1: Holo-[acyl-carrier-protein] synthase

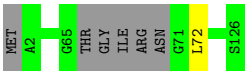
Chain T:

• Molecule 1: Holo-[acyl-carrier-protein] synthase

Chain S: 93%

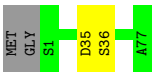
• Molecule 1: Holo-[acyl-carrier-protein] synthase

Chain U: 94% 5%



• Molecule 2: Acyl carrier protein

Chain f: 95%



• Molecule 2: Acyl carrier protein

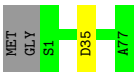
Chain e: 97%

• Molecule 2: Acyl carrier protein

Chain d: 97%

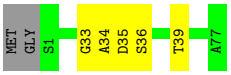
• Molecule 2: Acyl carrier protein

Chain K: 96%



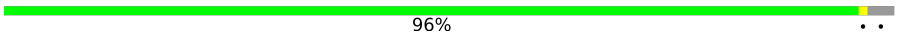
• Molecule 2: Acyl carrier protein

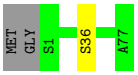
Chain J: 91% 6%



• Molecule 2: Acyl carrier protein

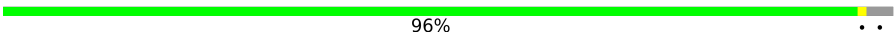
Chain L:

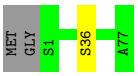




• Molecule 2: Acyl carrier protein

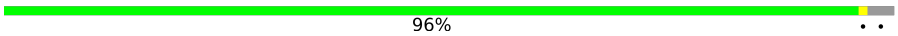
Chain F:

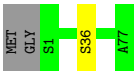




• Molecule 2: Acyl carrier protein

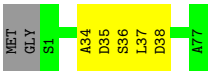
Chain E:





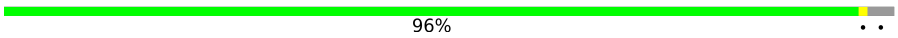
• Molecule 2: Acyl carrier protein

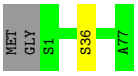
Chain D:



• Molecule 2: Acyl carrier protein

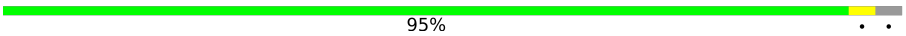
Chain P:

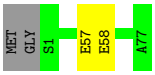




• Molecule 2: Acyl carrier protein

Chain R:



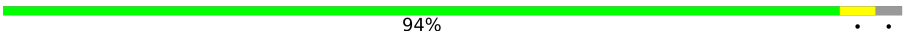


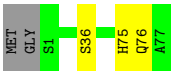
• Molecule 2: Acyl carrier protein

Chain Q:

• Molecule 2: Acyl carrier protein

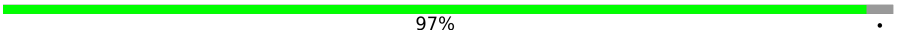
Chain X:





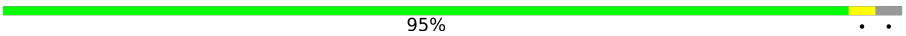
• Molecule 2: Acyl carrier protein

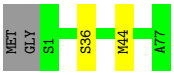
Chain W:



• Molecule 2: Acyl carrier protein

Chain V:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α, β, γ	251.42Å 251.42Å 58.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.31 – 4.10 49.31 – 4.10	Depositor EDS
% Data completeness (in resolution range)	96.2 (49.31-4.10) 96.2 (49.31-4.10)	Depositor EDS
R_{merge}	0.25	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.49 (at 4.14Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.278 , 0.297 0.278 , 0.297	Depositor DCC
R_{free} test set	1396 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å^2)	171.0	Xtriage
Anisotropy	0.112	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.25 , 165.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.43$, $< L^2 > = 0.25$	Xtriage
Estimated twinning fraction	0.060 for h,-k,-l	Xtriage
F_o,F_c correlation	0.87	EDS
Total number of atoms	23422	wwPDB-VP
Average B, all atoms (Å^2)	255.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.81% 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: PNS

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	0.27	0/987	0.49	0/1330
1	B	0.28	0/964	0.49	0/1300
1	C	0.27	0/975	0.46	0/1314
1	G	0.28	0/976	0.49	0/1316
1	H	0.26	0/979	0.47	0/1319
1	I	0.27	0/987	0.48	0/1330
1	M	0.27	0/986	0.46	0/1331
1	N	0.29	0/987	0.47	0/1330
1	O	0.27	0/976	1.01	7/1316 (0.5%)
1	S	0.28	0/987	0.52	0/1330
1	T	0.27	0/976	0.49	0/1316
1	U	0.27	0/979	0.47	0/1319
1	a	0.27	0/987	0.48	0/1330
1	b	0.28	0/976	0.48	0/1316
1	c	0.27	0/979	0.46	0/1319
2	D	0.29	0/600	1.17	9/810 (1.1%)
2	E	0.27	0/600	0.43	0/810
2	F	0.29	0/600	0.48	0/810
2	J	0.26	0/600	0.96	5/810 (0.6%)
2	K	0.29	0/600	0.46	0/810
2	L	0.26	0/600	0.45	0/810
2	P	0.26	0/600	0.42	0/810
2	Q	0.28	0/600	0.78	3/810 (0.4%)
2	R	0.35	1/600 (0.2%)	0.68	4/810 (0.5%)
2	V	0.27	0/600	0.46	0/810
2	W	0.27	0/600	0.54	0/810
2	X	0.33	0/600	0.51	0/810
2	d	0.27	0/600	0.49	0/810
2	e	0.25	0/600	0.42	0/810
2	f	0.29	0/600	0.63	1/810 (0.1%)
All	All	0.28	1/23701 (0.0%)	0.57	29/31966 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	O	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	R	57	GLU	CA-C	5.58	1.67	1.52

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	O	70	ASN	CB-CA-C	19.58	149.57	110.40
2	D	35	ASP	N-CA-C	16.21	154.76	111.00
1	O	71	GLY	C-N-CA	15.28	159.89	121.70
2	J	36	SER	N-CA-CB	-13.24	90.64	110.50
2	J	35	ASP	N-CA-C	-11.95	78.74	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	O	71	GLY	Peptide

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	119/126 (94%)	118 (99%)	1 (1%)	0	100	100
1	B	116/126 (92%)	115 (99%)	1 (1%)	0	100	100
1	C	117/126 (93%)	117 (100%)	0	0	100	100
1	G	118/126 (94%)	115 (98%)	3 (2%)	0	100	100
1	H	118/126 (94%)	118 (100%)	0	0	100	100
1	I	119/126 (94%)	118 (99%)	1 (1%)	0	100	100
1	M	121/126 (96%)	121 (100%)	0	0	100	100
1	N	119/126 (94%)	118 (99%)	1 (1%)	0	100	100
1	O	118/126 (94%)	117 (99%)	1 (1%)	0	100	100
1	S	119/126 (94%)	118 (99%)	1 (1%)	0	100	100
1	T	118/126 (94%)	118 (100%)	0	0	100	100
1	U	118/126 (94%)	118 (100%)	0	0	100	100
1	a	119/126 (94%)	117 (98%)	2 (2%)	0	100	100
1	b	118/126 (94%)	118 (100%)	0	0	100	100
1	c	118/126 (94%)	118 (100%)	0	0	100	100
2	D	75/79 (95%)	71 (95%)	4 (5%)	0	100	100
2	E	75/79 (95%)	71 (95%)	4 (5%)	0	100	100
2	F	75/79 (95%)	71 (95%)	4 (5%)	0	100	100
2	J	75/79 (95%)	71 (95%)	4 (5%)	0	100	100
2	K	75/79 (95%)	69 (92%)	6 (8%)	0	100	100
2	L	75/79 (95%)	71 (95%)	4 (5%)	0	100	100
2	P	75/79 (95%)	70 (93%)	5 (7%)	0	100	100
2	Q	75/79 (95%)	73 (97%)	2 (3%)	0	100	100
2	R	75/79 (95%)	71 (95%)	4 (5%)	0	100	100
2	V	75/79 (95%)	71 (95%)	4 (5%)	0	100	100
2	W	75/79 (95%)	71 (95%)	4 (5%)	0	100	100
2	X	75/79 (95%)	72 (96%)	3 (4%)	0	100	100
2	d	75/79 (95%)	73 (97%)	2 (3%)	0	100	100
2	e	75/79 (95%)	72 (96%)	3 (4%)	0	100	100
2	f	75/79 (95%)	72 (96%)	3 (4%)	0	100	100
All	All	2900/3075 (94%)	2833 (98%)	67 (2%)	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	96/98 (98%)	93 (97%)	3 (3%)	40	63
1	B	94/98 (96%)	89 (95%)	5 (5%)	22	51
1	C	95/98 (97%)	94 (99%)	1 (1%)	73	84
1	G	95/98 (97%)	90 (95%)	5 (5%)	22	51
1	H	95/98 (97%)	94 (99%)	1 (1%)	73	84
1	I	96/98 (98%)	93 (97%)	3 (3%)	40	63
1	M	95/98 (97%)	94 (99%)	1 (1%)	73	84
1	N	96/98 (98%)	90 (94%)	6 (6%)	18	46
1	O	95/98 (97%)	90 (95%)	5 (5%)	22	51
1	S	96/98 (98%)	91 (95%)	5 (5%)	23	51
1	T	95/98 (97%)	90 (95%)	5 (5%)	22	51
1	U	95/98 (97%)	94 (99%)	1 (1%)	73	84
1	a	96/98 (98%)	93 (97%)	3 (3%)	40	63
1	b	95/98 (97%)	91 (96%)	4 (4%)	30	56
1	c	95/98 (97%)	95 (100%)	0	100	100
2	D	65/67 (97%)	64 (98%)	1 (2%)	65	79
2	E	65/67 (97%)	64 (98%)	1 (2%)	65	79
2	F	65/67 (97%)	64 (98%)	1 (2%)	65	79
2	J	65/67 (97%)	64 (98%)	1 (2%)	65	79
2	K	65/67 (97%)	64 (98%)	1 (2%)	65	79
2	L	65/67 (97%)	64 (98%)	1 (2%)	65	79
2	P	65/67 (97%)	64 (98%)	1 (2%)	65	79
2	Q	65/67 (97%)	62 (95%)	3 (5%)	27	54
2	R	65/67 (97%)	65 (100%)	0	100	100
2	V	65/67 (97%)	63 (97%)	2 (3%)	40	63
2	W	65/67 (97%)	65 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	X	65/67 (97%)	62 (95%)	3 (5%)	27	54
2	d	65/67 (97%)	65 (100%)	0	100	100
2	e	65/67 (97%)	65 (100%)	0	100	100
2	f	65/67 (97%)	64 (98%)	1 (2%)	65	79
All	All	2404/2475 (97%)	2340 (97%)	64 (3%)	44	66

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	S	101	LYS
2	X	36	SER
1	O	101	LYS
1	O	72	LEU
2	X	75	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	44	HIS
2	Q	14	GLN
2	R	14	GLN
1	T	43	HIS
2	J	14	GLN

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)

14 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	$\#\|Z\| > 2$
3	PNS	e	101	2	1,4,21	1.82	0	0,4,29	-	-
3	PNS	d	101	2	8,14,21	0.45	0	11,19,29	1.85	4 (36%)
3	PNS	f	101	2	7,12,21	0.84	0	11,17,29	1.03	1 (9%)
3	PNS	J	101	-	1,4,21	1.57	0	0,4,29	-	-
3	PNS	R	201	2	5,7,21	0.23	0	3,8,29	0.55	0
3	PNS	D	101	-	6,9,21	0.42	0	7,12,29	0.36	0
3	PNS	Q	101	2	0,3,21	-	-	0,3,29	-	-
3	PNS	F	101	2	6,9,21	0.49	0	7,12,29	0.66	0
3	PNS	X	101	2	7,12,21	0.72	0	11,17,29	1.40	2 (18%)
3	PNS	E	101	2	1,4,21	1.63	0	0,4,29	-	-
3	PNS	P	101	-	5,8,21	0.90	0	6,11,29	0.14	0
3	PNS	W	101	2	1,4,21	0.48	0	0,4,29	-	-
3	PNS	V	101	2	0,3,21	-	-	0,3,29	-	-
3	PNS	L	101	2	1,4,21	1.52	0	0,4,29	-	-

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	PNS	e	101	2	-	0/0/2/27	-
3	PNS	d	101	2	-	5/17/19/27	-
3	PNS	f	101	2	-	4/13/16/27	-
3	PNS	J	101	-	-	0/0/2/27	-
3	PNS	R	201	2	-	2/3/5/27	-
3	PNS	D	101	-	-	0/7/9/27	-
3	PNS	F	101	2	-	6/7/9/27	-
3	PNS	X	101	2	-	10/13/16/27	-
3	PNS	E	101	2	-	0/0/2/27	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PNS	P	101	-	-	0/4/6/27	-
3	PNS	W	101	2	-	0/0/2/27	-
3	PNS	L	101	2	-	0/0/2/27	-

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	d	101	PNS	C30-C29-C32	-3.91	102.04	108.82
3	d	101	PNS	C31-C29-C32	-2.89	103.81	108.82
3	X	101	PNS	C31-C29-C28	2.80	112.80	108.23
3	X	101	PNS	O33-C32-C34	-2.66	106.05	110.93
3	f	101	PNS	O33-C32-C34	-2.38	106.56	110.93

There are no chirality outliers.

5 of 27 torsion outliers are listed below:

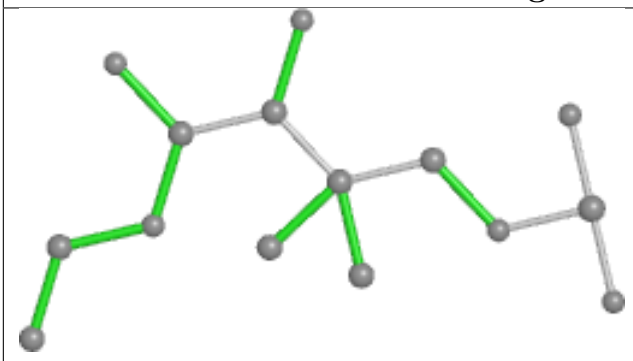
Mol	Chain	Res	Type	Atoms
3	f	101	PNS	O27-C28-C29-C32
3	f	101	PNS	C29-C32-C34-O35
3	d	101	PNS	O27-C28-C29-C32
3	d	101	PNS	C32-C34-N36-C37
3	F	101	PNS	C29-C28-O27-P24

There are no ring outliers.

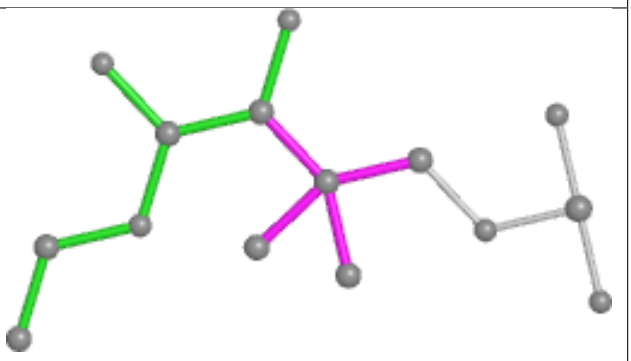
No monomer is involved in short contacts.

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.

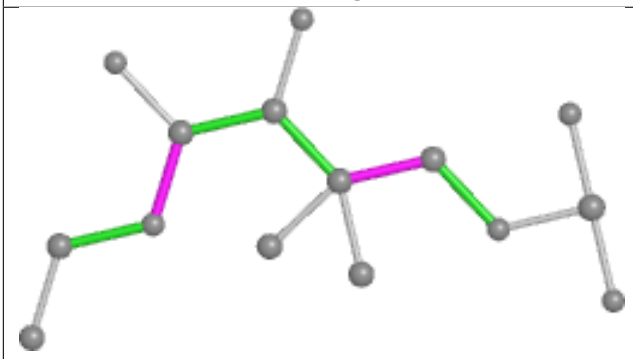
Ligand PNS d 101



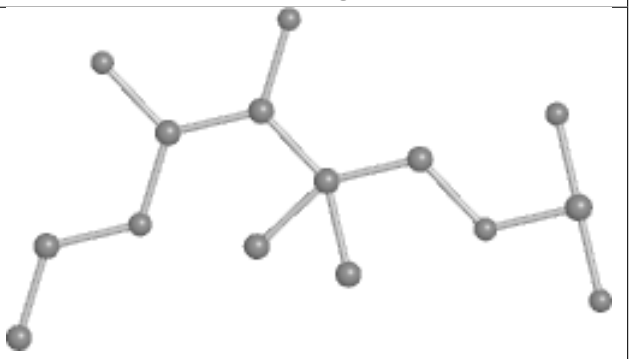
Bond lengths



Bond angles

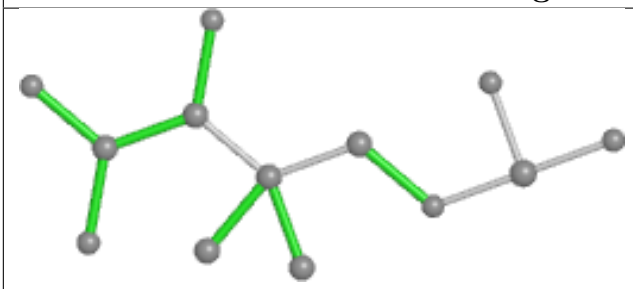


Torsions

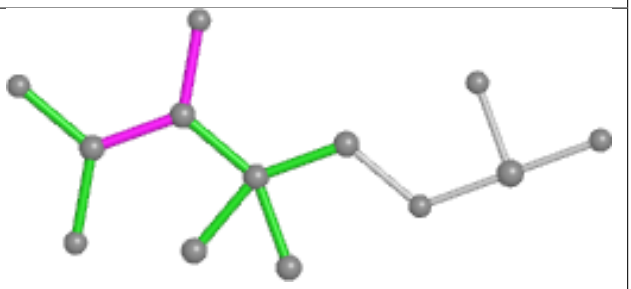


Rings

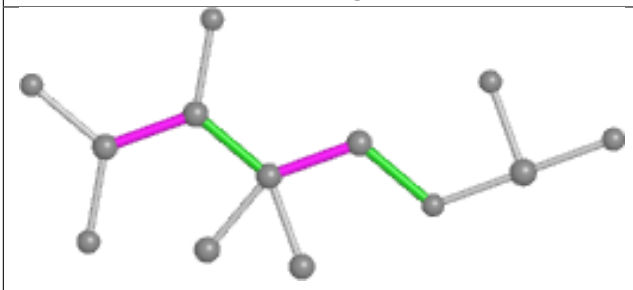
Ligand PNS f 101



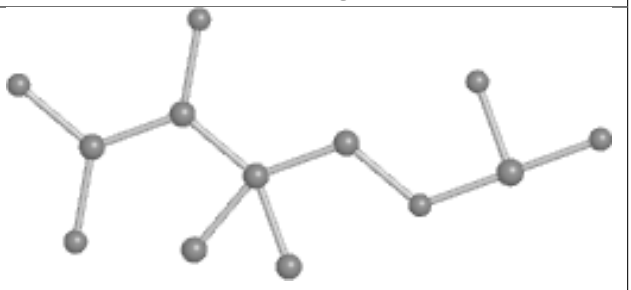
Bond lengths



Bond angles

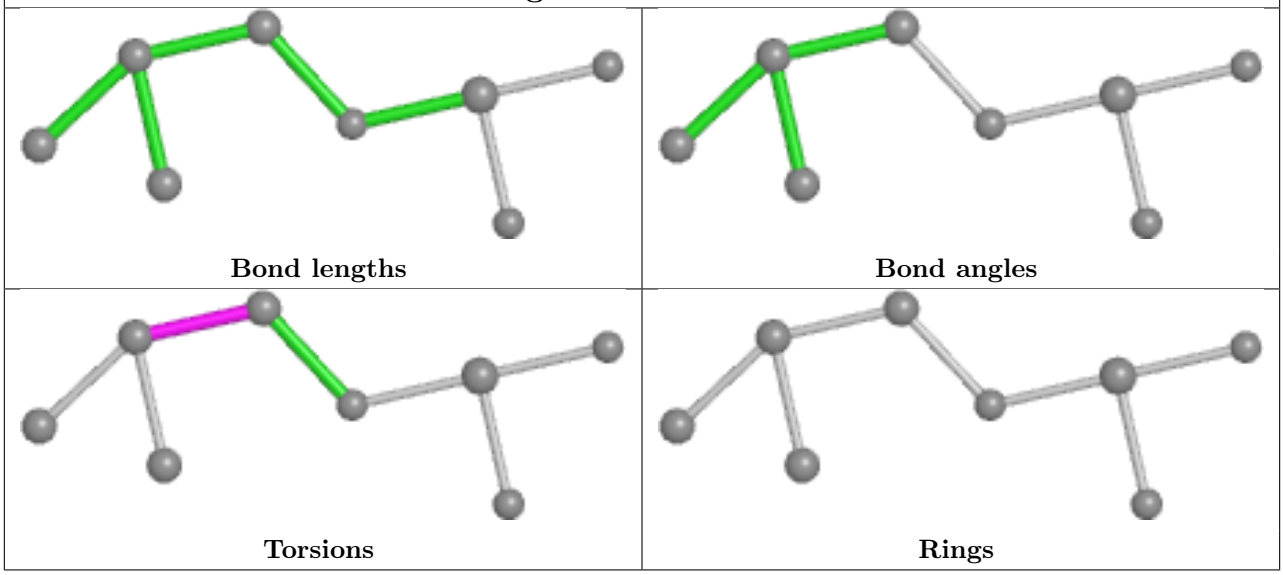


Torsions

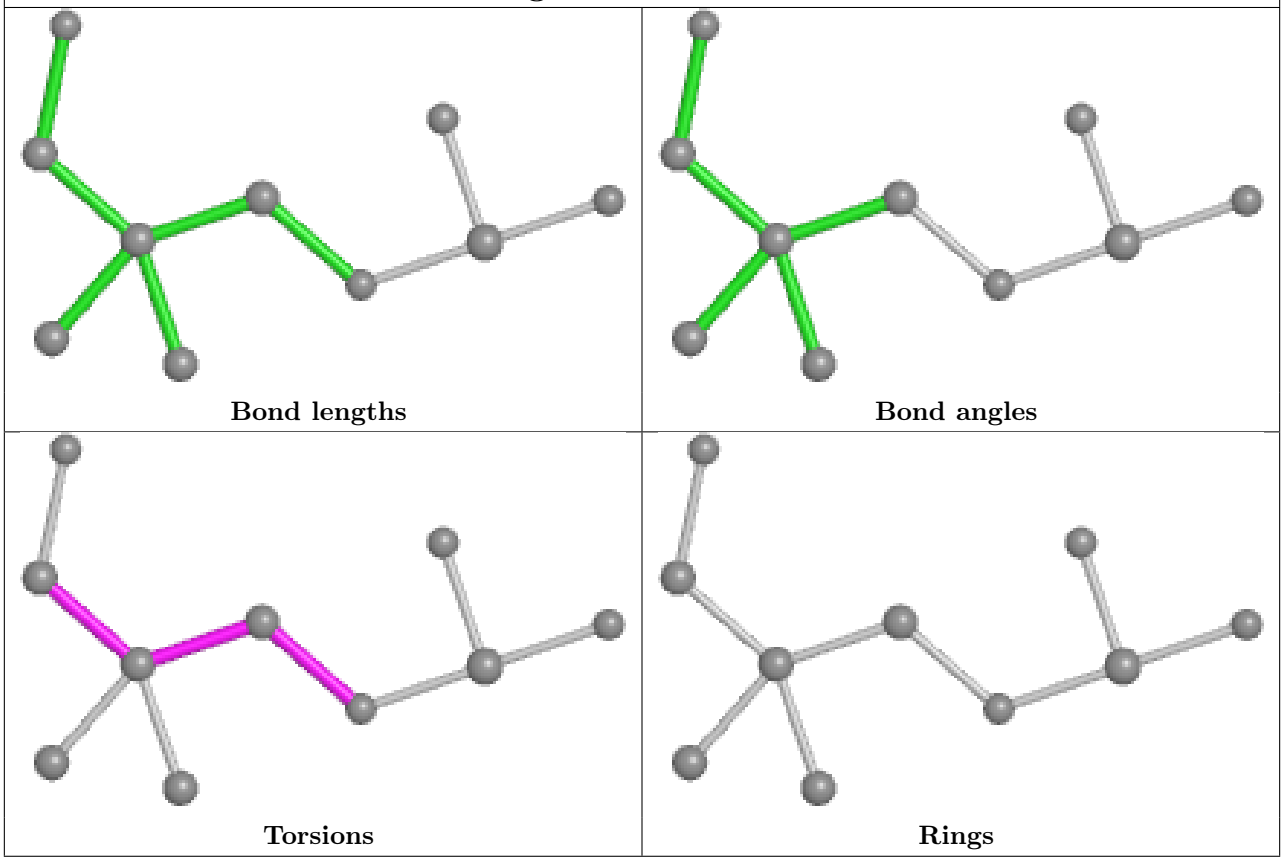


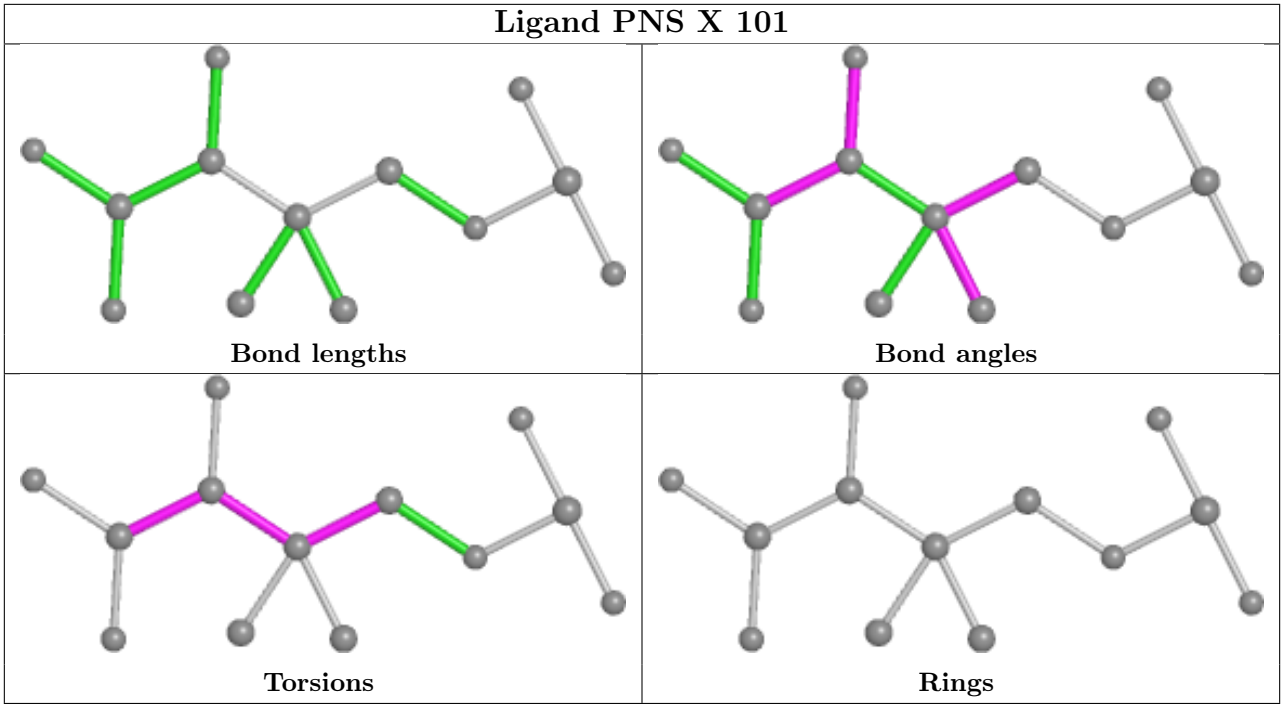
Rings

Ligand PNS R 201



Ligand PNS F 101





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)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

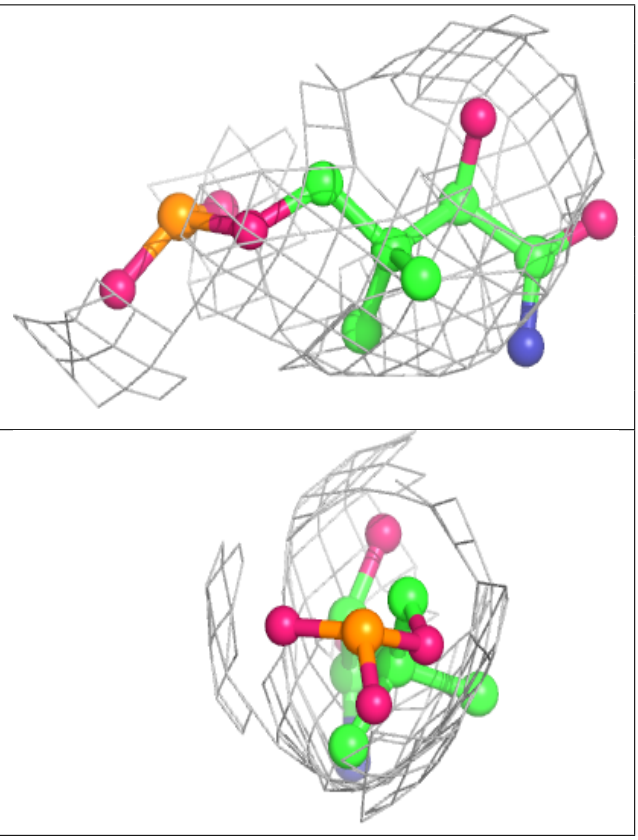
6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

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.

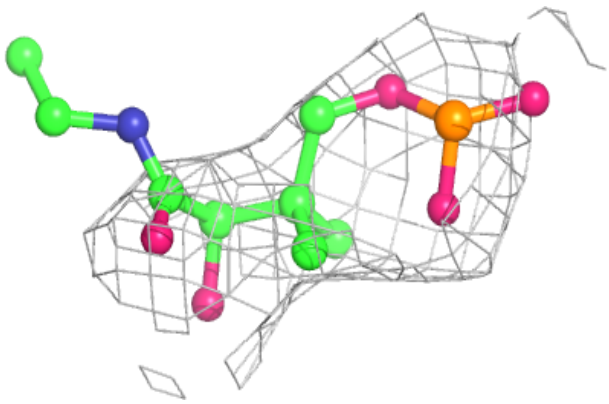
Electron density around PNS f 101:

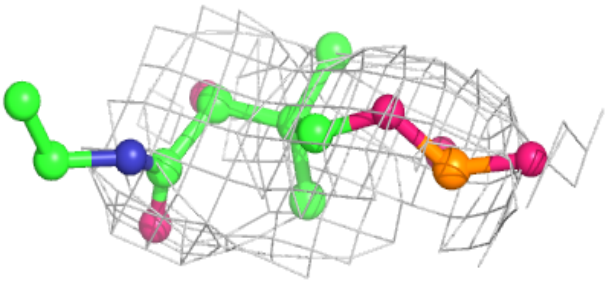
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

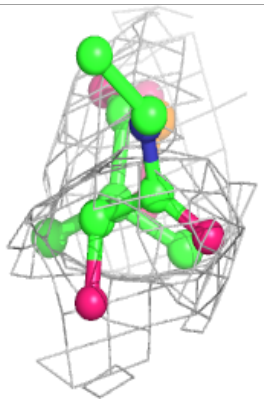


Electron density around PNS d 101:

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

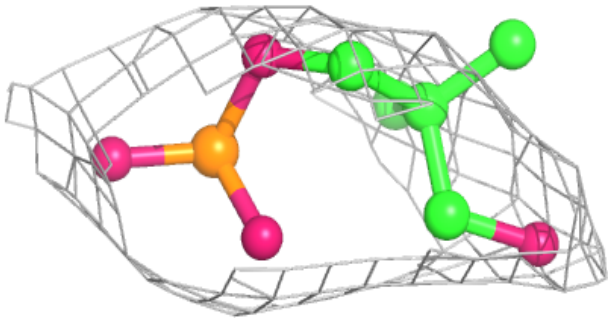


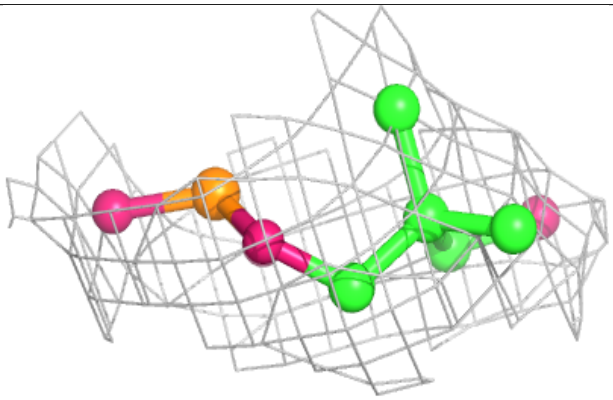


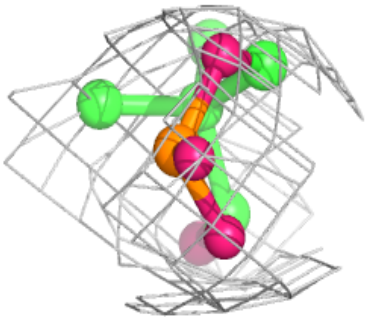


Electron density around PNS F 101:

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

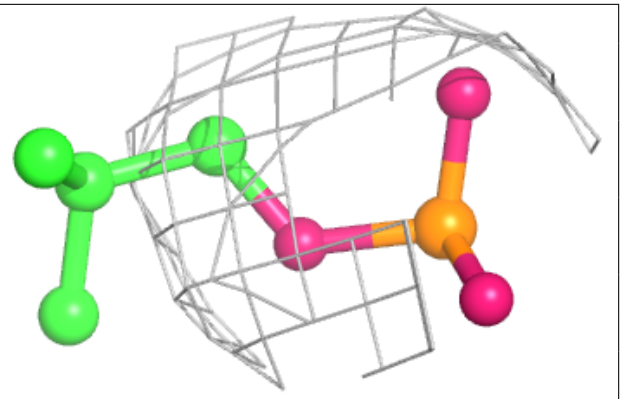


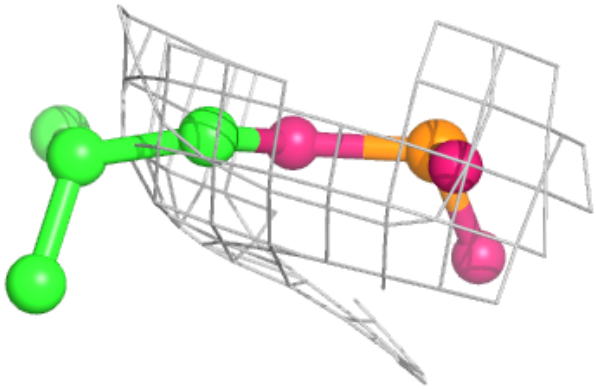


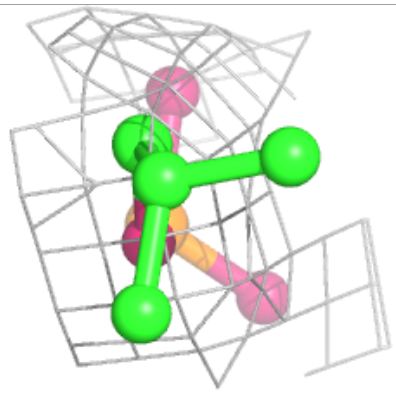


Electron density around PNS R 201:

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

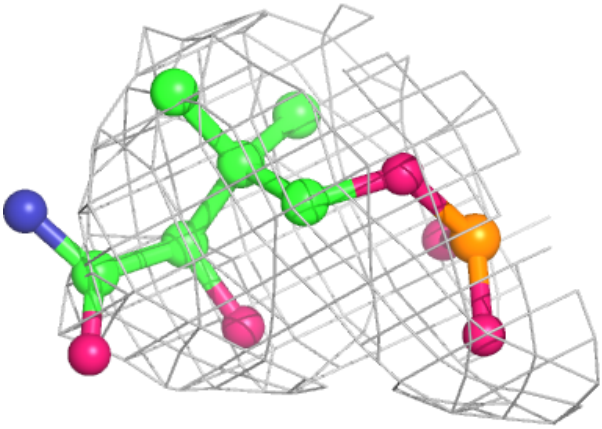


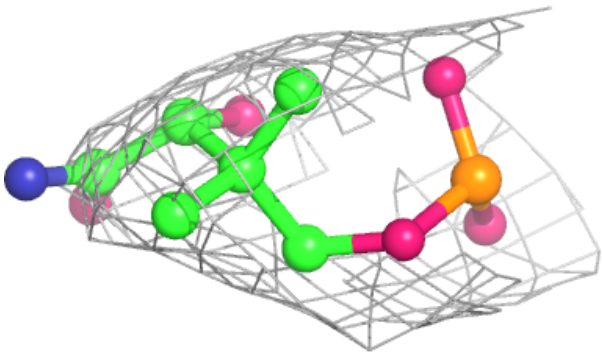


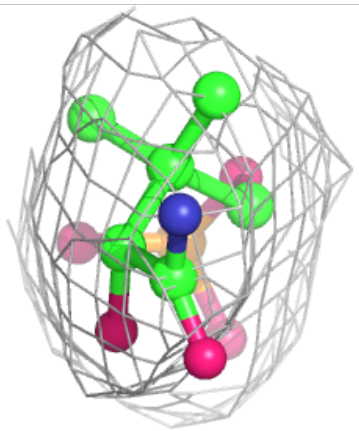


Electron density around PNS X 101:

$2mF_o$-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)

Unable to reproduce the depositors R factor - this section is therefore empty.