



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:19 AM UTC

PDB ID : 6SND / pdb_00006snd
Title : crystal structure of LN01 Fab in complex with an HIV-1 gp41 peptide
Authors : Caillat, C.; Pinto, D.; Corti, D.; Fenwick, C.; Pantaleo, G.; Weissenhorn, W.
Deposited on : 2019-08-23
Resolution : 3.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

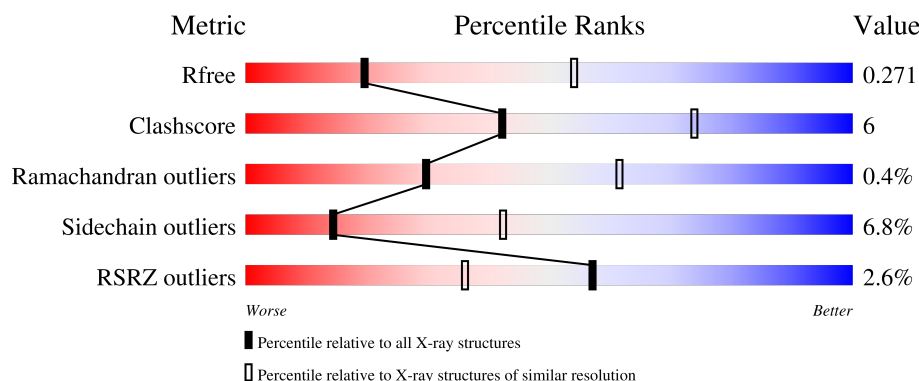
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	213	 4% 85% 14% .
1	L	213	 82% 15% .
2	B	235	 2% 75% 21% . .
2	H	235	 3% 76% 17% . 5%
3	C	25	 8% 64% 12% 24%

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Mol	Chain	Length	Quality of chain
3	P	25	 A horizontal bar chart showing the quality of chain P. The bar is divided into four segments: a small red segment at the beginning labeled '4%', followed by a green segment labeled '52%', a yellow segment labeled '24%', and a grey segment at the end labeled '24%'.

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7209 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 LN01 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	213	Total	C	N	O	S	0	0	0
			1635	1026	276	328	5			
1	L	213	Total	C	N	O	S	0	0	0
			1635	1026	276	328	5			

- Molecule 2 is a protein called LN01 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	230	Total	C	N	O	S	0	0	0
			1762	1126	294	337	5			
2	H	224	Total	C	N	O	S	0	0	0
			1727	1107	287	328	5			

- Molecule 3 is a protein called Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	19	Total	C	N	O	S	0	0	0
			179	128	25	25	1			
3	P	19	Total	C	N	O	S	0	0	0
			179	128	25	25	1			

There are 12 discrepancies between the modelled and reference sequences:

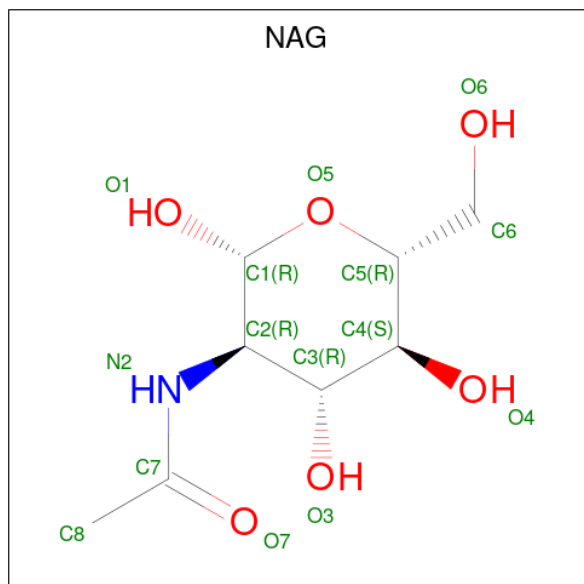
Chain	Residue	Modelled	Actual	Comment	Reference
C	690	LYS	-	expression tag	UNP G3DH64
C	691	LYS	-	expression tag	UNP G3DH64
C	692	LYS	-	expression tag	UNP G3DH64
C	693	LYS	-	expression tag	UNP G3DH64
C	694	LYS	-	expression tag	UNP G3DH64
C	695	LYS	-	expression tag	UNP G3DH64
P	690	LYS	-	expression tag	UNP G3DH64
P	691	LYS	-	expression tag	UNP G3DH64

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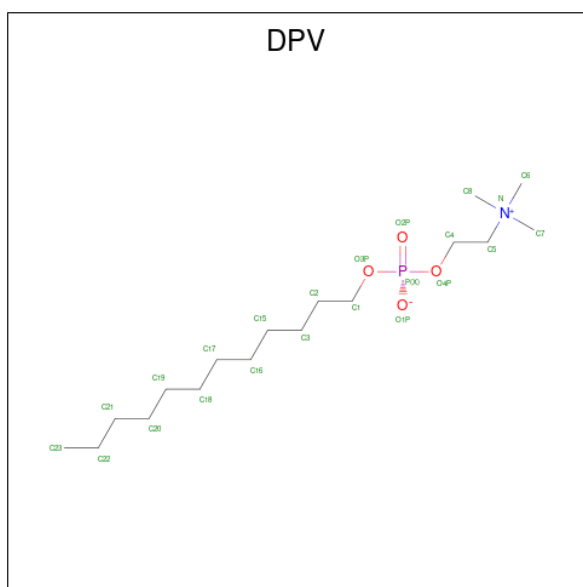
Chain	Residue	Modelled	Actual	Comment	Reference
P	692	LYS	-	expression tag	UNP G3DH64
P	693	LYS	-	expression tag	UNP G3DH64
P	694	LYS	-	expression tag	UNP G3DH64
P	695	LYS	-	expression tag	UNP G3DH64

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



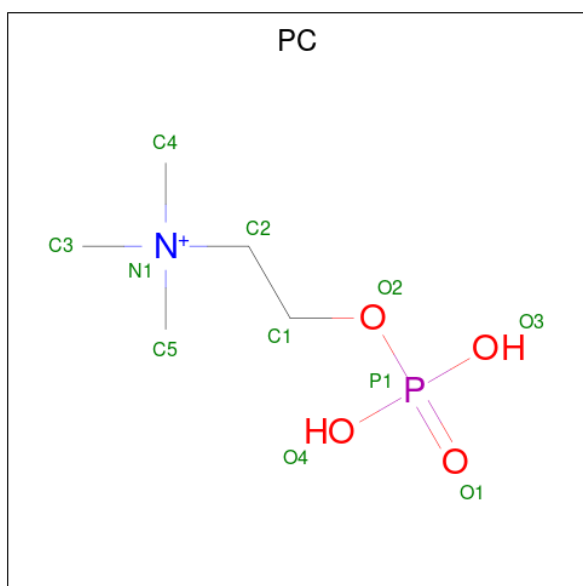
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	L	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is dodecyl 2-(trimethylammonio)ethyl phosphate (CCD ID: DPV) (formula: $C_{17}H_{38}NO_4P$) (labeled as "Ligand of Interest" by depositor).



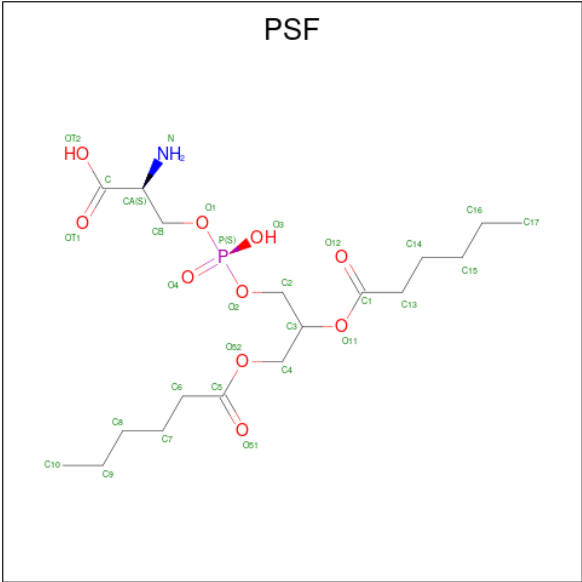
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			23	17	1	4	1		

- Molecule 6 is PHOSPHOCHOLINE (CCD ID: PC) (formula: $C_5H_{15}NO_4P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	L	1	Total	C	N	O	P	0	0
			11	5	1	4	1		

- Molecule 7 is 1,2-DICAPROYL-SN-PHOSPHATIDYL-L-SERINE (CCD ID: PSF) (formula: $C_{18}H_{34}NO_{10}P$) (labeled as "Ligand of Interest" by depositor).

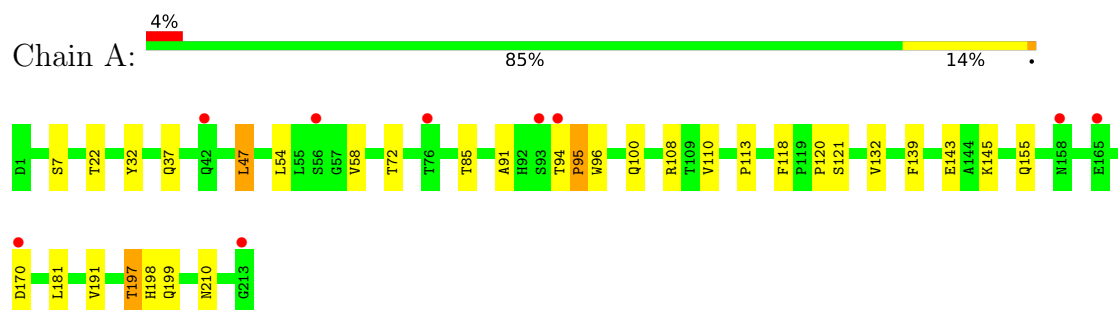


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	H	1	Total	C	N	O	P	0	0
			30	18	1	10	1		

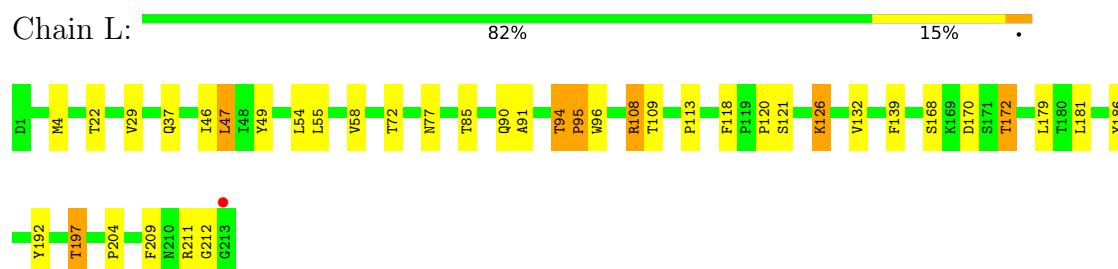
3 Residue-property plots [i](#)

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.

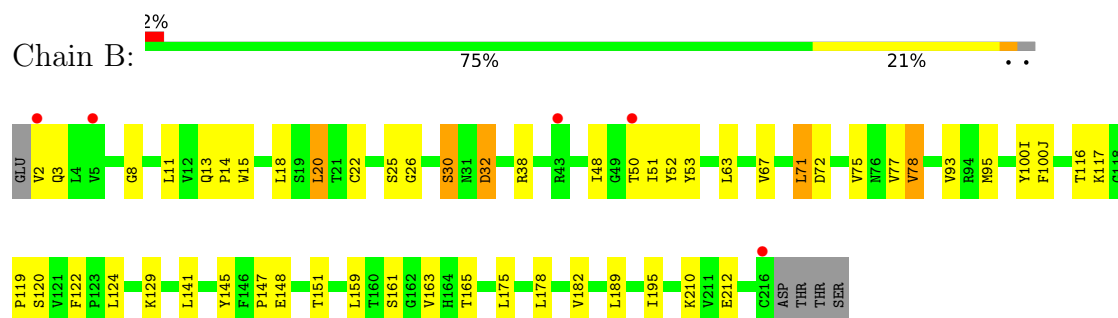
- Molecule 1: LN01 light chain



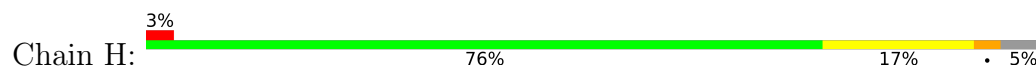
- Molecule 1: LN01 light chain

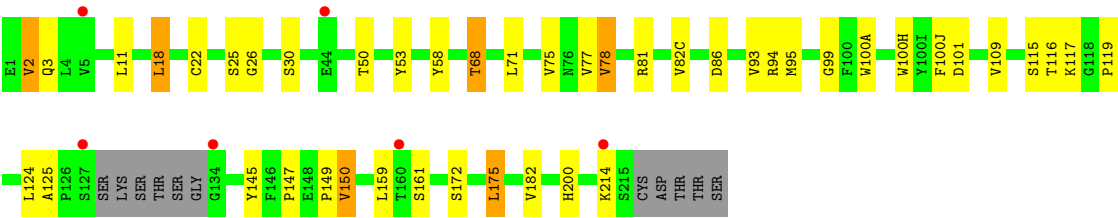


- Molecule 2: LN01 heavy chain

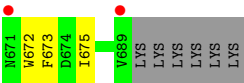


- Molecule 2: LN01 heavy chain

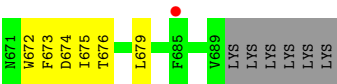




• Molecule 3: Envelope glycoprotein gp160



• Molecule 3: Envelope glycoprotein gp160



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	137.71Å 137.71Å 146.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.17 – 3.10 47.17 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.7 (47.17-3.10) 99.6 (47.17-3.10)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.76 (at 3.12Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.238 , 0.267 0.243 , 0.271	Depositor DCC
R_{free} test set	1337 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	76.6	Xtriage
Anisotropy	0.078	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 34.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7209	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.68% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PSF, NAG, DPV, PC

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	0.14	0/1673	0.52	0/2278
1	L	0.14	0/1673	0.50	0/2278
2	B	0.16	0/1815	0.50	0/2486
2	H	0.14	0/1779	0.43	0/2437
3	C	0.16	0/187	0.40	0/256
3	P	0.15	0/187	0.34	0/256
All	All	0.15	0/7314	0.48	0/9991

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	1635	0	1581	15	0
1	L	1635	0	1581	22	0
2	B	1762	0	1705	26	0
2	H	1727	0	1670	26	0
3	C	179	0	176	3	0
3	P	179	0	176	5	0
4	A	14	0	13	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	L	14	0	13	0	0
5	A	23	0	38	0	0
6	L	11	0	13	2	0
7	H	30	0	32	5	0
All	All	7209	0	6998	89	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 6.

All (89) 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:L:94:THR:HG23	1:L:95:PRO:HD3	1.54	0.90
1:A:94:THR:HG23	1:A:95:PRO:HD3	1.57	0.85
2:H:68:THR:HG21	2:H:81:ARG:HH21	1.47	0.79
2:B:3:GLN:HB2	2:B:25:SER:HB2	1.70	0.71
2:B:51:ILE:HD13	2:B:71:LEU:HD13	1.74	0.69
2:B:38:ARG:HD3	2:B:48:ILE:HD11	1.76	0.67
1:A:120:PRO:HD3	1:A:132:VAL:HG12	1.77	0.66
2:B:159:LEU:HD11	2:B:182:VAL:HG21	1.78	0.65
2:H:75:VAL:HG13	2:H:77:VAL:HG13	1.78	0.64
2:B:15:TRP:NE1	6:L:302:PC:O1	2.30	0.64
1:L:209:PHE:HD1	1:L:211:ARG:H	1.45	0.63
2:B:119:PRO:HB3	2:B:145:TYR:HB3	1.81	0.62
2:B:75:VAL:HG23	2:B:77:VAL:HG13	1.82	0.62
1:L:49:TYR:HD2	1:L:55:LEU:HD11	1.65	0.61
2:B:72:ASP:HB3	2:B:77:VAL:HG22	1.83	0.61
2:H:50:THR:HG22	2:H:58:TYR:HB3	1.83	0.60
1:L:197:THR:HG23	1:L:204:PRO:HG3	1.83	0.59
2:B:22:CYS:HB3	2:B:78:VAL:HG13	1.84	0.59
2:H:22:CYS:HB3	2:H:78:VAL:HG13	1.86	0.58
1:L:113:PRO:HB3	1:L:139:PHE:HB3	1.85	0.58
1:L:4:MET:HE3	1:L:90:GLN:HB3	1.85	0.57
1:L:96:TRP:CH2	2:H:95:MET:HE1	2.38	0.57
2:H:3:GLN:HB2	2:H:25:SER:HB2	1.88	0.56
2:H:100(A):TRP:HZ2	7:H:301:PSF:H71	1.70	0.56
1:L:37:GLN:HB2	1:L:47:LEU:HD21	1.87	0.56
2:B:50:THR:HG21	3:C:673:PHE:HZ	1.70	0.55
2:H:95:MET:HE2	2:H:100(H):TRP:HB3	1.88	0.55
1:A:113:PRO:HB3	1:A:139:PHE:HB3	1.89	0.55
1:L:91:ALA:HA	1:L:96:TRP:CD1	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:120:PRO:HD3	1:L:132:VAL:HG22	1.88	0.54
2:H:30:SER:HA	2:H:53:TYR:HB2	1.88	0.54
1:L:4:MET:HE3	1:L:90:GLN:HG2	1.89	0.54
1:L:46:ILE:HG21	2:H:101:ASP:HA	1.89	0.53
1:A:37:GLN:HB2	1:A:47:LEU:HD21	1.91	0.53
2:B:210:LYS:NZ	2:B:212:GLU:OE2	2.41	0.52
2:H:11:LEU:HB2	2:H:147:PRO:HG3	1.91	0.52
2:H:18:LEU:HD12	2:H:109:VAL:HG11	1.91	0.52
1:L:170:ASP:HB3	1:L:172:THR:HG23	1.90	0.51
2:B:2:VAL:HA	2:B:26:GLY:HA3	1.93	0.51
2:B:50:THR:HG21	3:C:673:PHE:CZ	2.46	0.51
2:H:100(A):TRP:CZ2	7:H:301:PSF:H71	2.45	0.50
3:C:672:TRP:HA	3:C:675:ILE:HD12	1.93	0.50
2:H:2:VAL:HG11	2:H:94:ARG:HH12	1.77	0.49
2:H:93:VAL:HG11	2:H:100(J):PHE:HB3	1.94	0.49
2:B:95:MET:HG3	2:B:100(I):TYR:O	2.13	0.49
2:H:150:VAL:HG12	2:H:200:HIS:HD2	1.77	0.49
7:H:301:PSF:H161	7:H:301:PSF:H72	1.95	0.49
1:A:191:VAL:HG22	1:A:210:ASN:OD1	2.12	0.48
1:L:118:PHE:CD2	2:H:124:LEU:HB3	2.48	0.48
1:A:145:LYS:HB3	1:A:197:THR:OG1	2.13	0.48
3:P:672:TRP:O	3:P:676:THR:HG23	2.14	0.48
1:A:47:LEU:HA	1:A:58:VAL:HG21	1.95	0.47
2:B:8:GLY:HA3	2:B:20:LEU:HD12	1.95	0.47
2:B:117:LYS:HD2	2:B:175:LEU:HD13	1.97	0.47
2:H:2:VAL:HA	2:H:26:GLY:HA3	1.95	0.47
1:A:143:GLU:O	1:A:198:HIS:HD2	1.98	0.46
1:A:118:PHE:CD2	2:B:124:LEU:HB3	2.51	0.46
2:B:11:LEU:HB2	2:B:147:PRO:HG3	1.97	0.46
2:B:93:VAL:HG11	2:B:100(J):PHE:HB3	1.95	0.46
2:B:32:ASP:HB2	2:B:53:TYR:CE1	2.51	0.46
3:P:675:ILE:HG22	3:P:679:LEU:HG	1.97	0.46
2:H:50:THR:HG21	3:P:673:PHE:CE2	2.51	0.46
2:H:95:MET:CE	2:H:100(H):TRP:HB3	2.45	0.46
2:B:13:GLN:HG3	2:B:14:PRO:HD2	1.97	0.46
1:A:32:TYR:HB3	1:A:91:ALA:HB3	1.98	0.45
1:L:108:ARG:NE	1:L:109:THR:O	2.50	0.45
1:L:94:THR:HB	3:P:674:ASP:OD2	2.16	0.45
2:H:119:PRO:HB3	2:H:145:TYR:HB3	1.99	0.45
1:A:181:LEU:HD23	1:A:181:LEU:HA	1.87	0.45
6:L:302:PC:H52	6:L:302:PC:H11	1.69	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:47:LEU:HA	1:L:58:VAL:HG21	1.99	0.44
2:H:100(A):TRP:NE1	7:H:301:PSF:O51	2.43	0.43
1:L:186:TYR:HA	1:L:192:TYR:OH	2.18	0.43
3:P:672:TRP:HA	3:P:675:ILE:HD12	1.99	0.43
1:A:121:SER:OG	2:B:122:PHE:HB3	2.19	0.43
2:H:125:ALA:HB3	2:H:214:LYS:HE2	2.01	0.42
1:A:100:GLN:HG3	1:L:77:ASN:OD1	2.20	0.42
1:L:4:MET:HE1	1:L:29:VAL:HG21	2.01	0.42
2:B:51:ILE:HG12	2:B:52:TYR:N	2.35	0.41
1:L:29:VAL:HG12	1:L:29:VAL:O	2.21	0.41
2:H:117:LYS:HG2	2:H:175:LEU:HD22	2.03	0.41
1:A:91:ALA:HA	1:A:96:TRP:CD1	2.55	0.41
2:B:30:SER:HA	2:B:53:TYR:HB2	2.03	0.41
2:H:99:GLY:HA3	7:H:301:PSF:HB2	2.02	0.41
1:A:198:HIS:ND1	1:A:199:GLN:O	2.54	0.41
2:B:141:LEU:HD12	2:B:178:LEU:O	2.21	0.41
2:B:63:LEU:O	2:B:67:VAL:HG12	2.22	0.40
2:H:82(C):VAL:HG23	2:H:86:ASP:HB2	2.03	0.40
1:L:126:LYS:HE3	1:L:126:LYS:HB2	1.45	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	211/213 (99%)	199 (94%)	11 (5%)	1 (0%)	24	57
1	L	211/213 (99%)	199 (94%)	10 (5%)	2 (1%)	14	44
2	B	228/235 (97%)	219 (96%)	9 (4%)	0	100	100
2	H	220/235 (94%)	215 (98%)	4 (2%)	1 (0%)	24	57
3	C	17/25 (68%)	17 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	P	17/25 (68%)	17 (100%)	0	0	100	100
All	All	904/946 (96%)	866 (96%)	34 (4%)	4 (0%)	30	61

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	212	GLY
1	L	95	PRO
1	A	95	PRO
2	H	149	PRO

5.3.2 Protein sidechains ⓘ

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	184/184 (100%)	173 (94%)	11 (6%)	17	47
1	L	184/184 (100%)	170 (92%)	14 (8%)	12	39
2	B	199/205 (97%)	183 (92%)	16 (8%)	11	37
2	H	194/205 (95%)	181 (93%)	13 (7%)	15	43
3	C	19/25 (76%)	19 (100%)	0	100	100
3	P	19/25 (76%)	19 (100%)	0	100	100
All	All	799/828 (96%)	745 (93%)	54 (7%)	14	42

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	SER
1	A	22	THR
1	A	47	LEU
1	A	54	LEU
1	A	72	THR
1	A	85	THR
1	A	108	ARG

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Mol	Chain	Res	Type
1	A	110	VAL
1	A	155	GLN
1	A	170	ASP
1	A	197	THR
2	B	18	LEU
2	B	20	LEU
2	B	30	SER
2	B	32	ASP
2	B	71	LEU
2	B	78	VAL
2	B	116	THR
2	B	120	SER
2	B	129	LYS
2	B	148	GLU
2	B	151	THR
2	B	161	SER
2	B	163	VAL
2	B	165	THR
2	B	189	LEU
2	B	195	ILE
1	L	22	THR
1	L	47	LEU
1	L	54	LEU
1	L	72	THR
1	L	85	THR
1	L	94	THR
1	L	108	ARG
1	L	121	SER
1	L	126	LYS
1	L	168	SER
1	L	172	THR
1	L	179	LEU
1	L	181	LEU
1	L	197	THR
2	H	2	VAL
2	H	18	LEU
2	H	68	THR
2	H	71	LEU
2	H	78	VAL
2	H	115	SER
2	H	116	THR
2	H	150	VAL

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Mol	Chain	Res	Type
2	H	159	LEU
2	H	161	SER
2	H	172	SER
2	H	175	LEU
2	H	182	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	92	HIS
1	A	103	HIS
2	B	3	GLN
1	L	103	HIS
2	H	39	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 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
4	NAG	L	301	1	14,14,15	0.48	0	17,19,21	0.48	0
5	DPV	A	302	-	22,22,22	0.97	0	26,27,27	0.70	0
4	NAG	A	301	1	14,14,15	0.57	0	17,19,21	0.50	0
7	PSF	H	301	-	28,29,29	1.22	3 (10%)	30,36,36	1.39	3 (10%)
6	PC	L	302	-	10,10,10	1.45	1 (10%)	15,15,15	0.58	0

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
4	NAG	L	301	1	-	1/6/23/26	0/1/1/1
5	DPV	A	302	-	-	11/22/22/22	-
4	NAG	A	301	1	-	2/6/23/26	0/1/1/1
7	PSF	H	301	-	-	15/35/35/35	-
6	PC	L	302	-	-	3/8/8/8	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	H	301	PSF	O52-C5	2.59	1.40	1.33
7	H	301	PSF	O11-C3	-2.47	1.40	1.46
7	H	301	PSF	O11-C1	2.45	1.41	1.34
6	L	302	PC	C2-N1	-2.14	1.45	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	H	301	PSF	O11-C1-C13	4.61	121.45	111.48
7	H	301	PSF	O52-C5-C6	3.07	121.18	111.83
7	H	301	PSF	O1-CB-CA	2.58	110.30	108.06

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	L	302	PC	C1-O2-P1-O3
6	L	302	PC	C1-O2-P1-O4
7	H	301	PSF	CB-O1-P-O4

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Mol	Chain	Res	Type	Atoms
7	H	301	PSF	O12-C1-O11-C3
7	H	301	PSF	C13-C1-O11-C3
7	H	301	PSF	N-CA-CB-O1
4	A	301	NAG	C4-C5-C6-O6
4	A	301	NAG	O5-C5-C6-O6
7	H	301	PSF	C1-C13-C14-C15
7	H	301	PSF	C6-C7-C8-C9
5	A	302	DPV	C17-C18-C19-C20
4	L	301	NAG	O5-C5-C6-O6
5	A	302	DPV	O3P-C1-C2-C3
6	L	302	PC	C1-O2-P1-O1
5	A	302	DPV	C15-C16-C17-C18
5	A	302	DPV	C16-C17-C18-C19
7	H	301	PSF	O2-C2-C3-O11
7	H	301	PSF	C7-C8-C9-C10
5	A	302	DPV	C5-C4-O4P-P
5	A	302	DPV	O4P-C4-C5-N
5	A	302	DPV	C20-C21-C22-C23
7	H	301	PSF	O2-C2-C3-C4
5	A	302	DPV	C4-O4P-P-O1P
5	A	302	DPV	C4-O4P-P-O2P
5	A	302	DPV	C4-O4P-P-O3P
7	H	301	PSF	CB-O1-P-O2
7	H	301	PSF	C5-C6-C7-C8
7	H	301	PSF	C14-C15-C16-C17
5	A	302	DPV	C19-C20-C21-C22
7	H	301	PSF	CA-CB-O1-P
7	H	301	PSF	C3-C2-O2-P
7	H	301	PSF	O11-C1-C13-C14

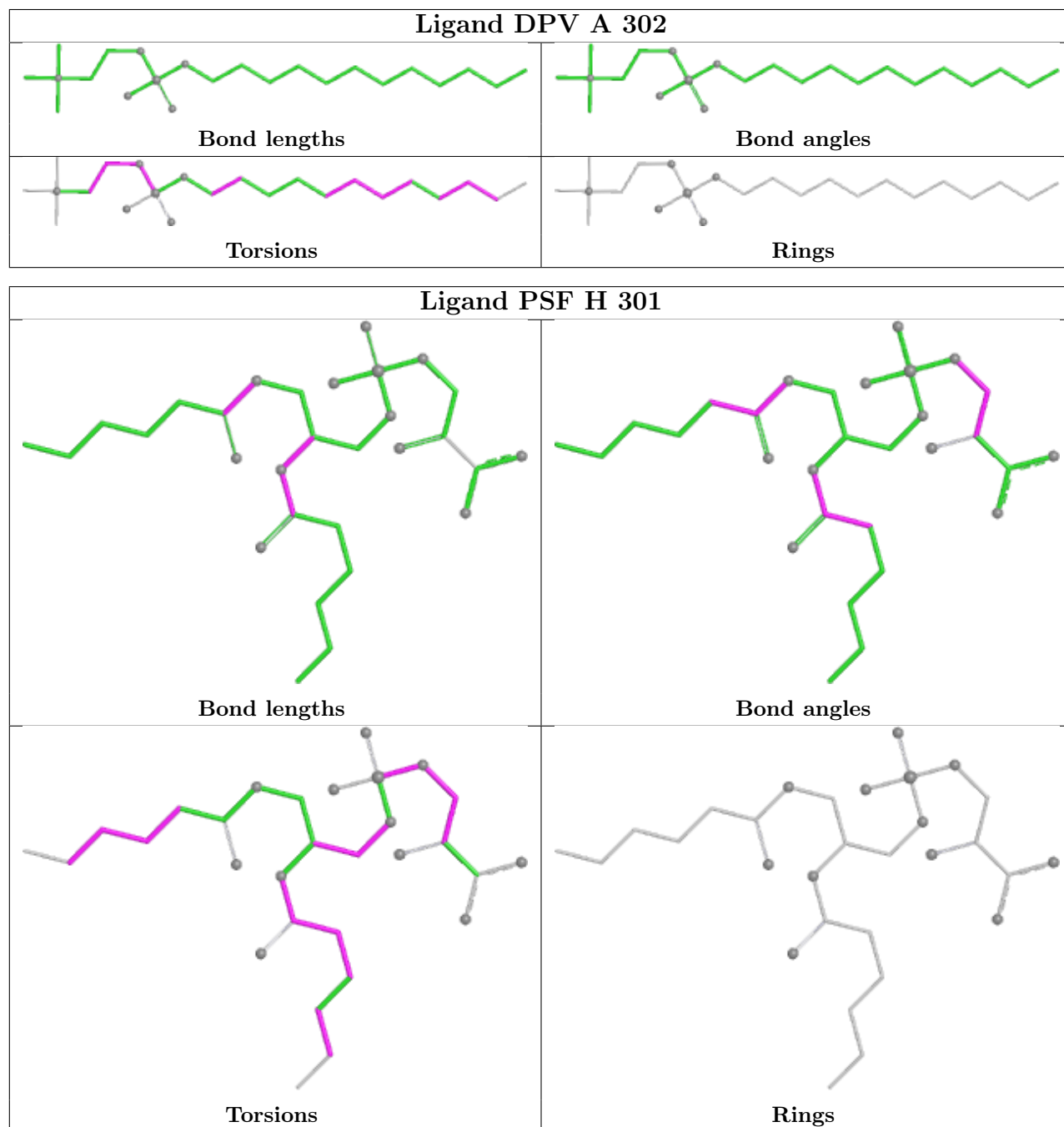
There are no ring outliers.

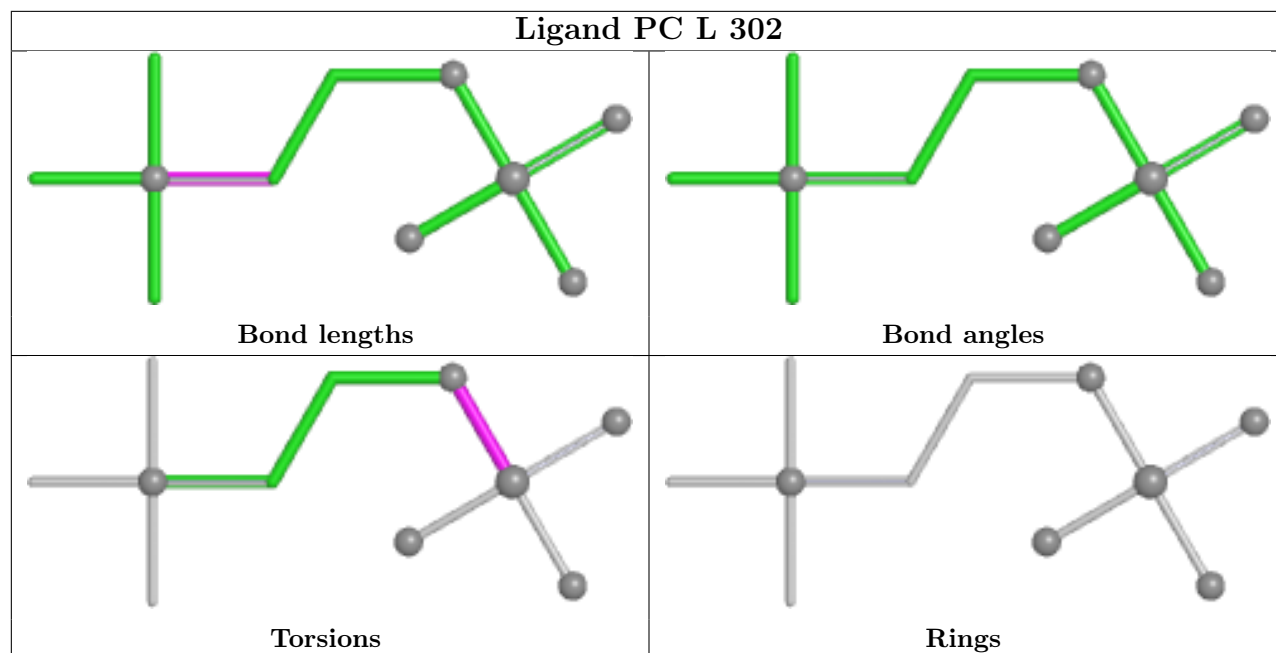
2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	H	301	PSF	5	0
6	L	302	PC	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 [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	213/213 (100%)	0.18	9 (4%) 40 22	40, 61, 99, 111	0
1	L	213/213 (100%)	0.16	1 (0%) 87 73	42, 64, 108, 126	0
2	B	230/235 (97%)	0.22	5 (2%) 62 41	42, 67, 92, 109	0
2	H	224/235 (95%)	0.31	6 (2%) 56 35	44, 70, 93, 102	0
3	C	19/25 (76%)	0.42	2 (10%) 11 6	57, 77, 93, 95	0
3	P	19/25 (76%)	0.71	1 (5%) 32 17	63, 82, 103, 103	0
All	All	918/946 (97%)	0.23	24 (2%) 57 36	40, 67, 100, 126	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	127	SER	4.0
2	B	216	CYS	3.7
1	L	213	GLY	3.4
2	B	50	THR	3.1
1	A	94	THR	3.0
1	A	165	GLU	2.6
1	A	213	GLY	2.6
2	B	5	VAL	2.6
3	P	685	PHE	2.5
1	A	42	GLN	2.5
1	A	170	ASP	2.5
1	A	56	SER	2.4
1	A	158	ASN	2.4
2	H	160	THR	2.4
3	C	689	VAL	2.4
2	B	43	ARG	2.4
2	H	214	LYS	2.3
1	A	93	SER	2.3
2	H	5	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
3	C	671	ASN	2.3
2	H	134	GLY	2.2
1	A	76	THR	2.0
2	B	2	VAL	2.0
2	H	44	GLU	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

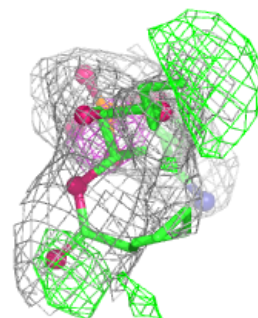
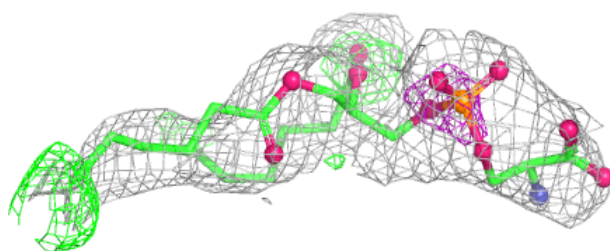
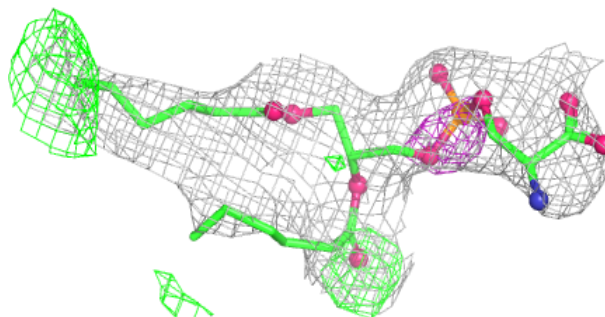
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	A	301	14/15	0.62	0.13	54,62,65,65	0
4	NAG	L	301	14/15	0.62	0.14	51,60,65,65	0
7	PSF	H	301	30/30	0.66	0.23	104,104,104,104	0
6	PC	L	302	11/11	0.78	0.19	78,78,78,78	0
5	DPV	A	302	23/23	0.89	0.16	78,78,78,78	0

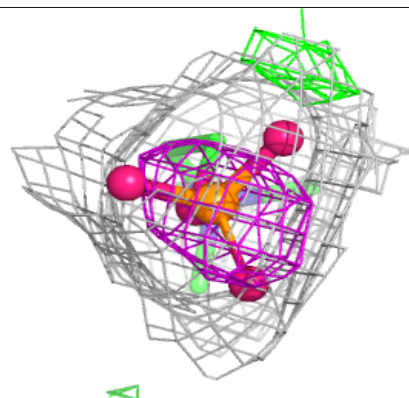
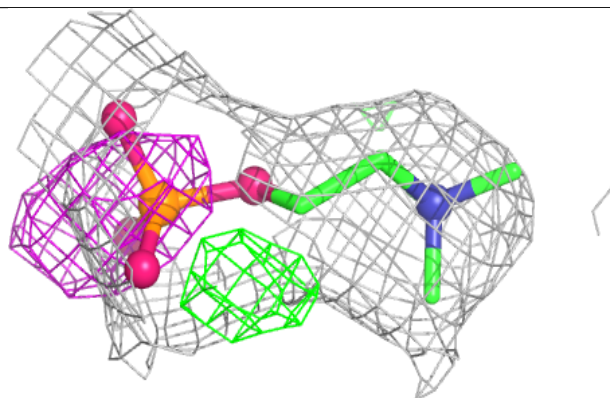
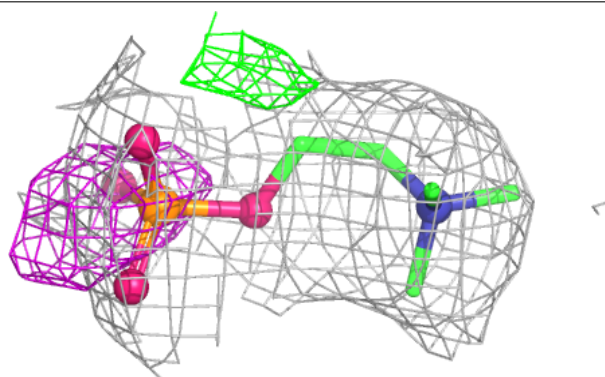
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around PSF H 301:

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

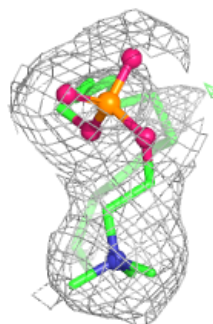
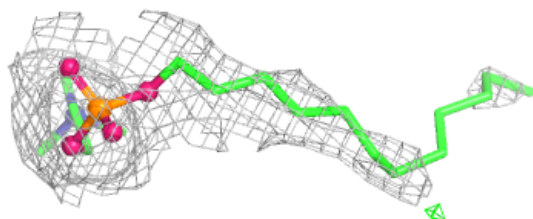
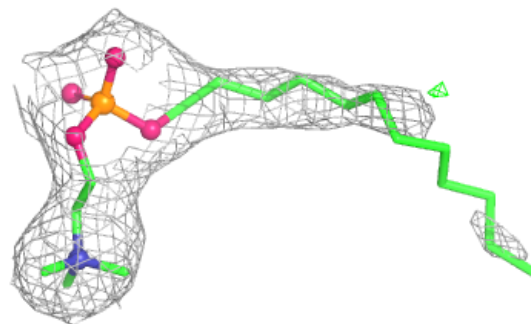
**Electron density around PC L 302:**

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



Electron density around DPV A 302:

$2mF_o-DF_c$ (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.