



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 05:55 AM UTC

PDB ID : 7SNQ / pdb_00007snq
Title : Hexamer HIV-1 CA in complex with CPSF6 peptide and IP6 ligand
Authors : Bester, S.M.; Kvaratskhelia, M.
Deposited on : 2021-10-28
Resolution : 2.81 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 ⓘ 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

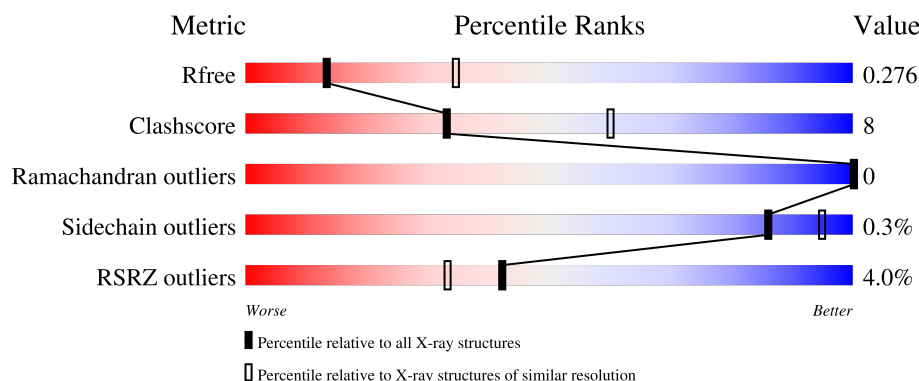
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.81 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	4591 (2.84-2.80)
Clashscore	190562	5010 (2.84-2.80)
Ramachandran outliers	187476	4916 (2.84-2.80)
Sidechain outliers	187428	4918 (2.84-2.80)
RSRZ outliers	180081	4594 (2.84-2.80)

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	231	0% 76% 14% 10%
1	B	231	5% 71% 16% 13%
1	C	231	2% 69% 21% 10%
1	D	231	5% 72% 18% 10%
1	E	231	3% 72% 20% 8%

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Mol	Chain	Length	Quality of chain
1	F	231	
1	G	231	
1	H	231	
1	I	231	
1	J	231	
1	K	231	
1	L	231	
2	M	15	
2	N	15	
2	O	15	
2	P	15	
2	Q	15	
2	R	15	
2	S	15	
2	T	15	
2	U	15	
2	V	15	
2	W	15	
2	X	15	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 20569 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 Capsid protein p24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	209	Total	C	N	O	S	0	1	0
			1619	1014	285	307	13			
1	B	201	Total	C	N	O	S	0	1	0
			1527	961	266	287	13			
1	C	207	Total	C	N	O	S	0	2	0
			1598	1005	281	299	13			
1	D	209	Total	C	N	O	S	0	3	0
			1612	1017	277	305	13			
1	E	213	Total	C	N	O	S	0	1	0
			1633	1027	284	308	14			
1	F	212	Total	C	N	O	S	0	1	0
			1616	1018	278	306	14			
1	G	201	Total	C	N	O	S	0	0	0
			1534	966	267	287	14			
1	H	209	Total	C	N	O	S	0	0	0
			1592	997	280	302	13			
1	I	209	Total	C	N	O	S	0	0	0
			1592	1002	278	298	14			
1	J	208	Total	C	N	O	S	0	0	0
			1551	972	273	293	13			
1	K	209	Total	C	N	O	S	0	1	0
			1604	1010	278	302	14			
1	L	206	Total	C	N	O	S	0	1	0
			1595	1000	283	298	14			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	6	LEU	ILE	conflict	UNP P03366
A	14	CYS	ALA	engineered mutation	UNP P03366
A	45	CYS	GLU	engineered mutation	UNP P03366
A	83	LEU	VAL	conflict	UNP P03366
A	120	HIS	ASN	conflict	UNP P03366

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Chain	Residue	Modelled	Actual	Comment	Reference
A	184	ALA	TRP	engineered mutation	UNP P03366
A	185	ALA	MET	engineered mutation	UNP P03366
A	208	GLY	ALA	conflict	UNP P03366
B	6	LEU	ILE	conflict	UNP P03366
B	14	CYS	ALA	engineered mutation	UNP P03366
B	45	CYS	GLU	engineered mutation	UNP P03366
B	83	LEU	VAL	conflict	UNP P03366
B	120	HIS	ASN	conflict	UNP P03366
B	184	ALA	TRP	engineered mutation	UNP P03366
B	185	ALA	MET	engineered mutation	UNP P03366
B	208	GLY	ALA	conflict	UNP P03366
C	6	LEU	ILE	conflict	UNP P03366
C	14	CYS	ALA	engineered mutation	UNP P03366
C	45	CYS	GLU	engineered mutation	UNP P03366
C	83	LEU	VAL	conflict	UNP P03366
C	120	HIS	ASN	conflict	UNP P03366
C	184	ALA	TRP	engineered mutation	UNP P03366
C	185	ALA	MET	engineered mutation	UNP P03366
C	208	GLY	ALA	conflict	UNP P03366
D	6	LEU	ILE	conflict	UNP P03366
D	14	CYS	ALA	engineered mutation	UNP P03366
D	45	CYS	GLU	engineered mutation	UNP P03366
D	83	LEU	VAL	conflict	UNP P03366
D	120	HIS	ASN	conflict	UNP P03366
D	184	ALA	TRP	engineered mutation	UNP P03366
D	185	ALA	MET	engineered mutation	UNP P03366
D	208	GLY	ALA	conflict	UNP P03366
E	6	LEU	ILE	conflict	UNP P03366
E	14	CYS	ALA	engineered mutation	UNP P03366
E	45	CYS	GLU	engineered mutation	UNP P03366
E	83	LEU	VAL	conflict	UNP P03366
E	120	HIS	ASN	conflict	UNP P03366
E	184	ALA	TRP	engineered mutation	UNP P03366
E	185	ALA	MET	engineered mutation	UNP P03366
E	208	GLY	ALA	conflict	UNP P03366
F	6	LEU	ILE	conflict	UNP P03366
F	14	CYS	ALA	engineered mutation	UNP P03366
F	45	CYS	GLU	engineered mutation	UNP P03366
F	83	LEU	VAL	conflict	UNP P03366
F	120	HIS	ASN	conflict	UNP P03366
F	184	ALA	TRP	engineered mutation	UNP P03366
F	185	ALA	MET	engineered mutation	UNP P03366

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Chain	Residue	Modelled	Actual	Comment	Reference
F	208	GLY	ALA	conflict	UNP P03366
G	6	LEU	ILE	conflict	UNP P03366
G	14	CYS	ALA	engineered mutation	UNP P03366
G	45	CYS	GLU	engineered mutation	UNP P03366
G	83	LEU	VAL	conflict	UNP P03366
G	120	HIS	ASN	conflict	UNP P03366
G	184	ALA	TRP	engineered mutation	UNP P03366
G	185	ALA	MET	engineered mutation	UNP P03366
G	208	GLY	ALA	conflict	UNP P03366
H	6	LEU	ILE	conflict	UNP P03366
H	14	CYS	ALA	engineered mutation	UNP P03366
H	45	CYS	GLU	engineered mutation	UNP P03366
H	83	LEU	VAL	conflict	UNP P03366
H	120	HIS	ASN	conflict	UNP P03366
H	184	ALA	TRP	engineered mutation	UNP P03366
H	185	ALA	MET	engineered mutation	UNP P03366
H	208	GLY	ALA	conflict	UNP P03366
I	6	LEU	ILE	conflict	UNP P03366
I	14	CYS	ALA	engineered mutation	UNP P03366
I	45	CYS	GLU	engineered mutation	UNP P03366
I	83	LEU	VAL	conflict	UNP P03366
I	120	HIS	ASN	conflict	UNP P03366
I	184	ALA	TRP	engineered mutation	UNP P03366
I	185	ALA	MET	engineered mutation	UNP P03366
I	208	GLY	ALA	conflict	UNP P03366
J	6	LEU	ILE	conflict	UNP P03366
J	14	CYS	ALA	engineered mutation	UNP P03366
J	45	CYS	GLU	engineered mutation	UNP P03366
J	83	LEU	VAL	conflict	UNP P03366
J	120	HIS	ASN	conflict	UNP P03366
J	184	ALA	TRP	engineered mutation	UNP P03366
J	185	ALA	MET	engineered mutation	UNP P03366
J	208	GLY	ALA	conflict	UNP P03366
K	6	LEU	ILE	conflict	UNP P03366
K	14	CYS	ALA	engineered mutation	UNP P03366
K	45	CYS	GLU	engineered mutation	UNP P03366
K	83	LEU	VAL	conflict	UNP P03366
K	120	HIS	ASN	conflict	UNP P03366
K	184	ALA	TRP	engineered mutation	UNP P03366
K	185	ALA	MET	engineered mutation	UNP P03366
K	208	GLY	ALA	conflict	UNP P03366
L	6	LEU	ILE	conflict	UNP P03366

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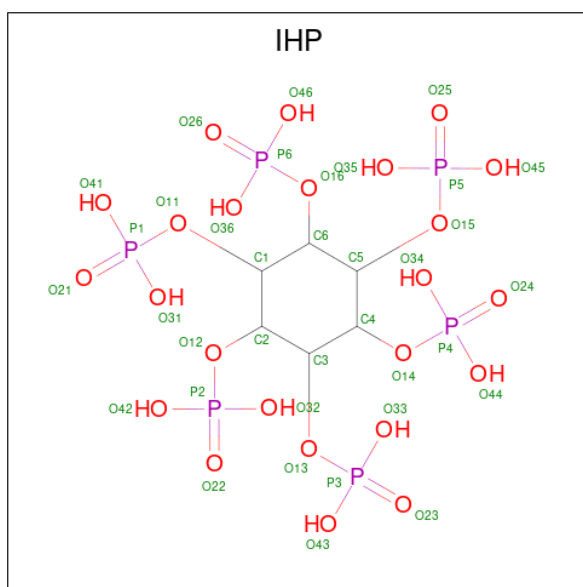
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Chain	Residue	Modelled	Actual	Comment	Reference
L	14	CYS	ALA	engineered mutation	UNP P03366
L	45	CYS	GLU	engineered mutation	UNP P03366
L	83	LEU	VAL	conflict	UNP P03366
L	120	HIS	ASN	conflict	UNP P03366
L	184	ALA	TRP	engineered mutation	UNP P03366
L	185	ALA	MET	engineered mutation	UNP P03366
L	208	GLY	ALA	conflict	UNP P03366

- Molecule 2 is a protein called Cleavage and polyadenylation specificity factor subunit 6.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	M	14	Total	C	N	O	0	0	0
			103	71	16	16			
2	N	13	Total	C	N	O	0	0	0
			90	64	13	13			
2	O	14	Total	C	N	O	0	0	0
			103	71	16	16			
2	P	13	Total	C	N	O	0	0	0
			98	68	15	15			
2	Q	13	Total	C	N	O	0	0	0
			98	68	15	15			
2	R	14	Total	C	N	O	0	0	0
			103	71	16	16			
2	S	13	Total	C	N	O	0	0	0
			95	67	14	14			
2	T	14	Total	C	N	O	0	0	0
			106	74	16	16			
2	U	13	Total	C	N	O	0	0	0
			94	66	14	14			
2	V	12	Total	C	N	O	0	0	0
			91	63	14	14			
2	W	14	Total	C	N	O	0	0	0
			104	72	16	16			
2	X	13	Total	C	N	O	0	0	0
			94	66	14	14			

- Molecule 3 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: C₆H₁₈O₂₄P₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	O	P	0	0
			36	6	24	6		
3	E	1	Total	C	O	P	0	0
			36	6	24	6		
3	G	1	Total	C	O	P	0	0
			36	6	24	6		
3	K	1	Total	C	O	P	0	0
			36	6	24	6		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	1	Total	Cl	0	0
			1	1		
4	G	1	Total	Cl	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	27	Total	O	0	0
			27	27		
5	B	17	Total	O	0	0
			17	17		
5	C	11	Total	O	0	0
			11	11		

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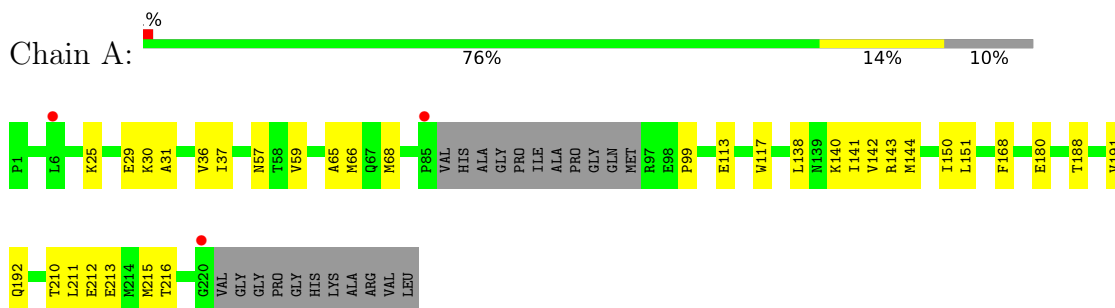
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	10	Total 10	O 10	0	0
5	E	17	Total 17	O 17	0	0
5	F	23	Total 23	O 23	0	0
5	G	6	Total 6	O 6	0	0
5	H	11	Total 11	O 11	0	0
5	I	5	Total 5	O 5	0	0
5	J	8	Total 8	O 8	0	0
5	K	11	Total 11	O 11	0	0
5	L	23	Total 23	O 23	0	0
5	M	1	Total 1	O 1	0	0
5	S	1	Total 1	O 1	0	0

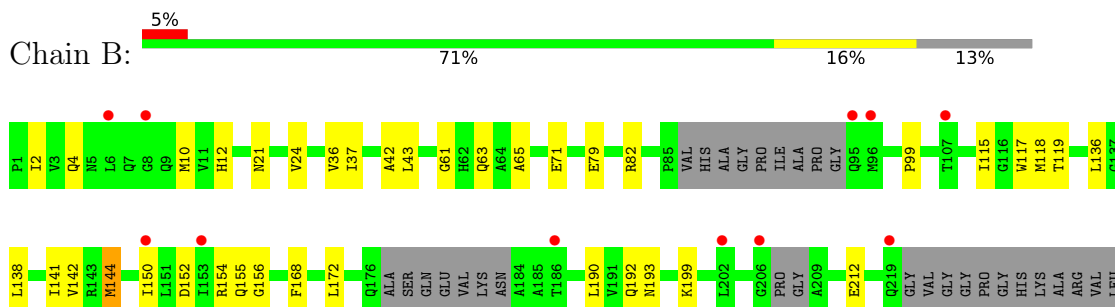
3 Residue-property plots [i](#)

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 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.

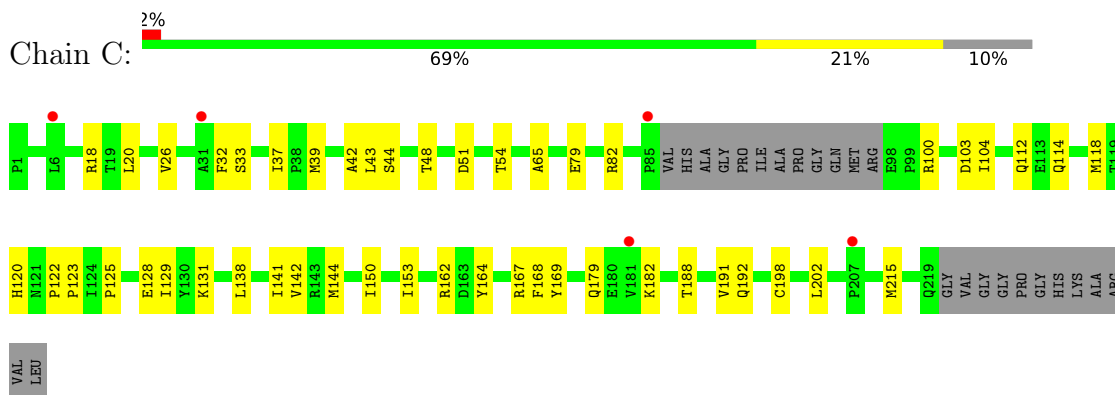
- Molecule 1: Capsid protein p24



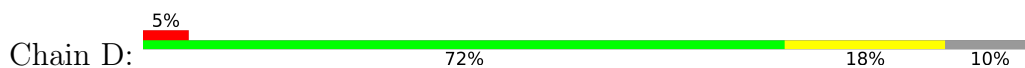
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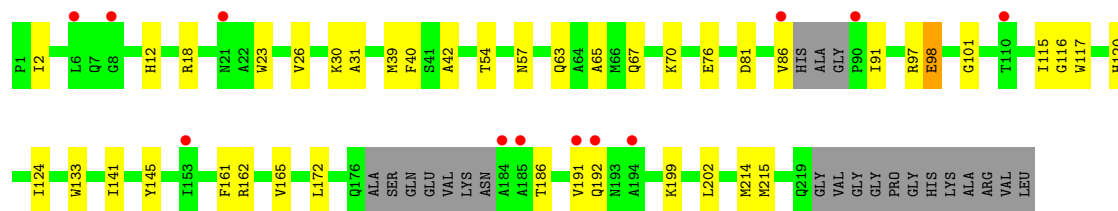


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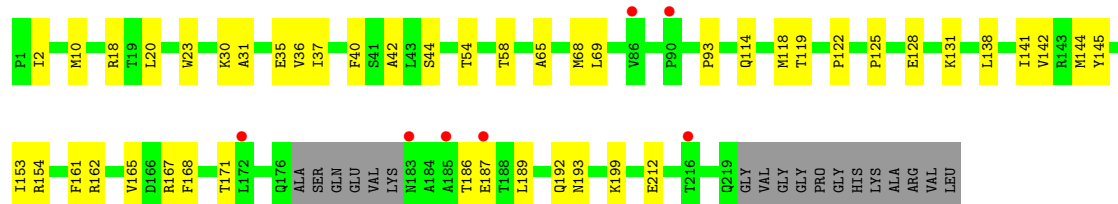
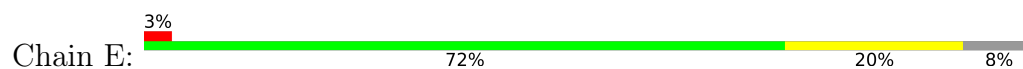


- Molecule 1: Capsid protein p24

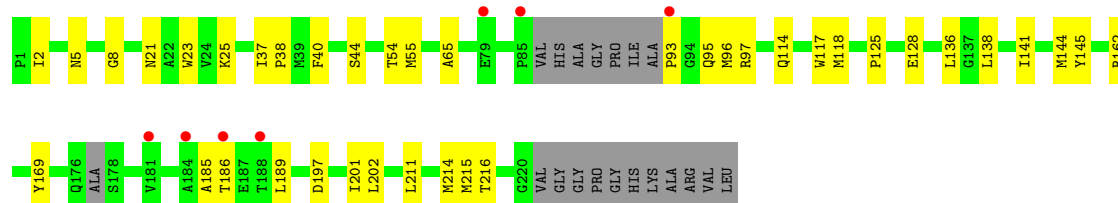
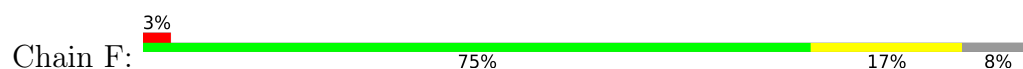




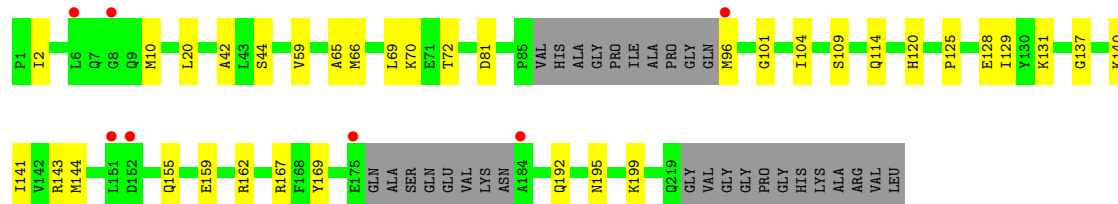
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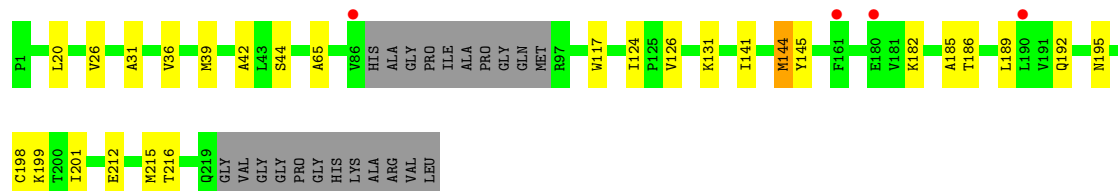
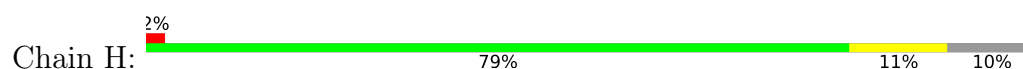
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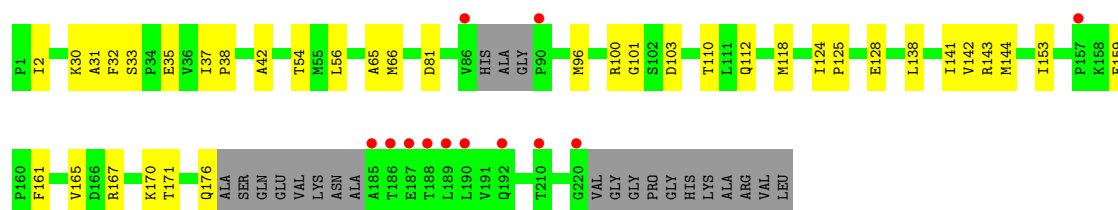
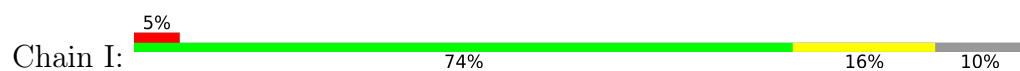
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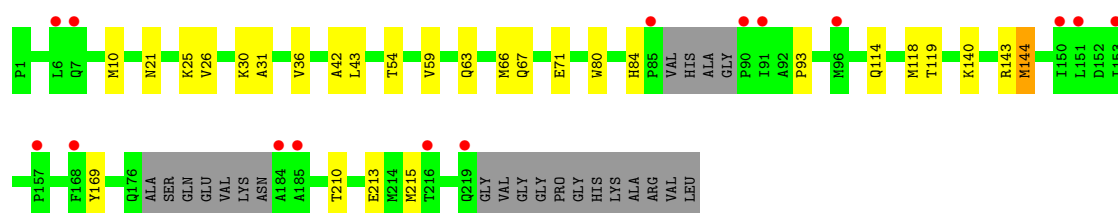
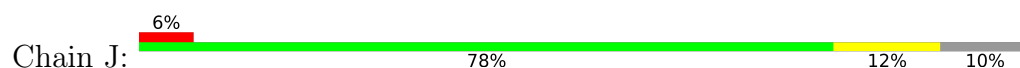
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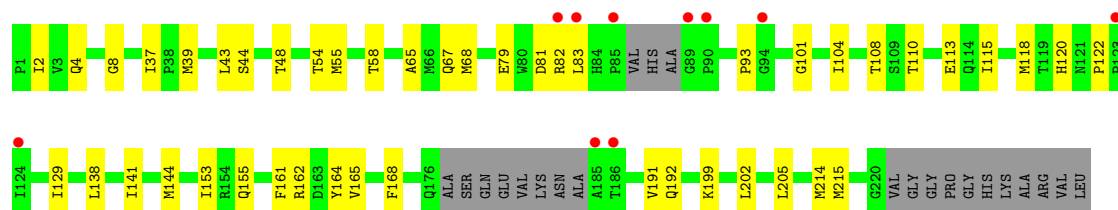
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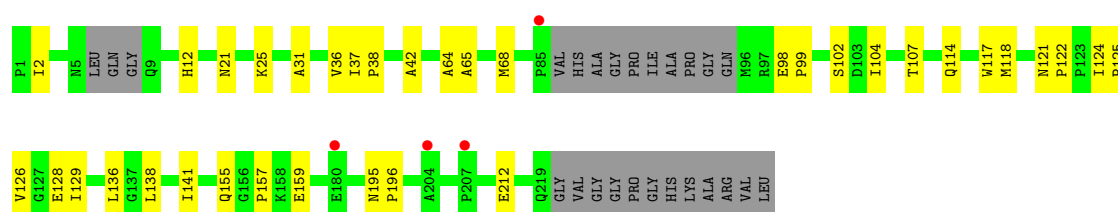
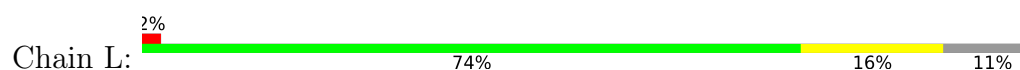
- Molecule 1: Capsid protein p24



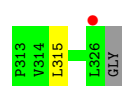
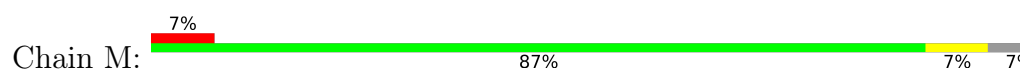
- Molecule 1: Capsid protein p24



- Molecule 1: Capsid protein p24

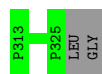


- Molecule 2: Cleavage and polyadenylation specificity factor subunit 6

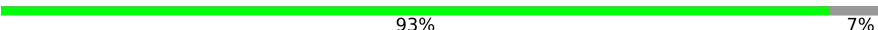


- Molecule 2: Cleavage and polyadenylation specificity factor subunit 6

Chain N:  87% 13%



- Molecule 2: Cleavage and polyadenylation specificity factor subunit 6

Chain O:  93% 7%



- Molecule 2: Cleavage and polyadenylation specificity factor subunit 6

Chain P:  67% 20% 13%



- Molecule 2: Cleavage and polyadenylation specificity factor subunit 6

Chain Q:  87% 13%



- Molecule 2: Cleavage and polyadenylation specificity factor subunit 6

Chain R:  67% 27% 7%



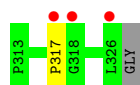
- Molecule 2: Cleavage and polyadenylation specificity factor subunit 6

Chain S:  7% 80% 7% 13%



- Molecule 2: Cleavage and polyadenylation specificity factor subunit 6

Chain T:  20% 87% 7% 7%



- Molecule 2: Cleavage and polyadenylation specificity factor subunit 6

Chain U:  80% 7% 13%



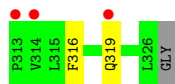
- Molecule 2: Cleavage and polyadenylation specificity factor subunit 6

Chain V:  80% 20%



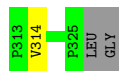
- Molecule 2: Cleavage and polyadenylation specificity factor subunit 6

Chain W:  20% 80% 13% 7%



- Molecule 2: Cleavage and polyadenylation specificity factor subunit 6

Chain X:  80% 7% 13%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	133.92Å 135.67Å 212.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.24 – 2.81 44.24 – 2.81	Depositor EDS
% Data completeness (in resolution range)	99.2 (44.24-2.81) 99.2 (44.24-2.81)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.229 , 0.282 0.226 , 0.276	Depositor DCC
R_{free} test set	4739 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	71.3	Xtriage
Anisotropy	0.282	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 51.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.023 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	20569	wwPDB-VP
Average B, all atoms (Å ²)	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.68% 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: IHP, CL

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	0.42	0/1652	0.60	0/2245
1	B	0.45	0/1557	0.68	0/2116
1	C	0.39	0/1634	0.59	0/2222
1	D	0.41	0/1646	0.59	0/2241
1	E	0.43	0/1669	0.64	0/2273
1	F	0.44	0/1649	0.66	0/2241
1	G	0.41	0/1566	0.62	0/2127
1	H	0.40	0/1625	0.59	0/2210
1	I	0.42	0/1626	0.60	0/2211
1	J	0.36	0/1585	0.56	0/2160
1	K	0.41	0/1638	0.59	0/2226
1	L	0.43	0/1627	0.61	0/2209
2	M	0.42	0/109	0.61	0/150
2	N	0.33	0/96	0.73	0/133
2	O	0.34	0/109	0.52	0/150
2	P	0.41	0/104	0.55	0/143
2	Q	0.30	0/104	0.48	0/143
2	R	0.53	0/109	0.64	0/150
2	S	0.34	0/101	0.57	0/139
2	T	0.35	0/112	0.52	0/154
2	U	0.49	0/100	0.60	0/138
2	V	0.32	0/96	0.47	0/131
2	W	0.33	0/110	0.47	0/151
2	X	0.33	0/100	0.44	0/138
All	All	0.41	0/20724	0.61	0/28201

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	1619	0	1589	27	0
1	B	1527	0	1466	32	0
1	C	1598	0	1574	37	0
1	D	1612	0	1571	29	0
1	E	1633	0	1594	36	0
1	F	1616	0	1576	30	0
1	G	1534	0	1489	25	0
1	H	1592	0	1538	20	0
1	I	1592	0	1549	29	0
1	J	1551	0	1468	20	0
1	K	1604	0	1570	33	0
1	L	1595	0	1562	28	0
2	M	103	0	97	1	0
2	N	90	0	83	0	0
2	O	103	0	97	0	0
2	P	98	0	95	3	0
2	Q	98	0	95	0	0
2	R	103	0	97	2	0
2	S	95	0	91	1	0
2	T	106	0	106	1	0
2	U	94	0	89	1	0
2	V	91	0	88	0	0
2	W	104	0	99	1	0
2	X	94	0	89	1	0
3	B	36	0	6	0	0
3	E	36	0	6	2	0
3	G	36	0	6	0	0
3	K	36	0	6	0	0
4	E	1	0	0	0	0
4	G	1	0	0	0	0
5	A	27	0	0	1	0
5	B	17	0	0	0	0
5	C	11	0	0	1	0
5	D	10	0	0	0	0
5	E	17	0	0	0	0
5	F	23	0	0	1	0
5	G	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	H	11	0	0	0	0
5	I	5	0	0	0	0
5	J	8	0	0	0	0
5	K	11	0	0	0	0
5	L	23	0	0	0	0
5	M	1	0	0	0	0
5	S	1	0	0	0	0
All	All	20569	0	19696	312	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 8.

The worst 5 of 312 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:I:2:ILE:HG12	1:I:118:MET:HE2	1.65	0.78
1:E:162:ARG:HD2	1:F:145:TYR:CE1	2.22	0.75
1:B:212:GLU:HG3	1:C:144:MET:HE1	1.70	0.74
1:A:212:GLU:HB2	1:B:144:MET:HE1	1.70	0.72
1:L:37:ILE:HD12	1:L:138:LEU:HB3	1.72	0.71

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	206/231 (89%)	203 (98%)	3 (2%)	0	100	100
1	B	194/231 (84%)	188 (97%)	6 (3%)	0	100	100
1	C	205/231 (89%)	199 (97%)	6 (3%)	0	100	100
1	D	206/231 (89%)	201 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	210/231 (91%)	204 (97%)	6 (3%)	0	100	100
1	F	207/231 (90%)	204 (99%)	3 (1%)	0	100	100
1	G	195/231 (84%)	187 (96%)	8 (4%)	0	100	100
1	H	205/231 (89%)	200 (98%)	5 (2%)	0	100	100
1	I	203/231 (88%)	199 (98%)	4 (2%)	0	100	100
1	J	202/231 (87%)	192 (95%)	10 (5%)	0	100	100
1	K	204/231 (88%)	200 (98%)	4 (2%)	0	100	100
1	L	201/231 (87%)	199 (99%)	2 (1%)	0	100	100
2	M	12/15 (80%)	12 (100%)	0	0	100	100
2	N	11/15 (73%)	11 (100%)	0	0	100	100
2	O	12/15 (80%)	12 (100%)	0	0	100	100
2	P	11/15 (73%)	11 (100%)	0	0	100	100
2	Q	11/15 (73%)	11 (100%)	0	0	100	100
2	R	12/15 (80%)	12 (100%)	0	0	100	100
2	S	11/15 (73%)	11 (100%)	0	0	100	100
2	T	12/15 (80%)	12 (100%)	0	0	100	100
2	U	11/15 (73%)	11 (100%)	0	0	100	100
2	V	10/15 (67%)	10 (100%)	0	0	100	100
2	W	12/15 (80%)	11 (92%)	1 (8%)	0	100	100
2	X	11/15 (73%)	11 (100%)	0	0	100	100
All	All	2574/2952 (87%)	2511 (98%)	63 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	174/193 (90%)	173 (99%)	1 (1%)	78	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	158/193 (82%)	157 (99%)	1 (1%)	78	92
1	C	171/193 (89%)	170 (99%)	1 (1%)	78	92
1	D	172/193 (89%)	171 (99%)	1 (1%)	78	92
1	E	174/193 (90%)	174 (100%)	0	100	100
1	F	172/193 (89%)	172 (100%)	0	100	100
1	G	161/193 (83%)	161 (100%)	0	100	100
1	H	167/193 (86%)	166 (99%)	1 (1%)	78	92
1	I	168/193 (87%)	168 (100%)	0	100	100
1	J	158/193 (82%)	157 (99%)	1 (1%)	78	92
1	K	171/193 (89%)	171 (100%)	0	100	100
1	L	170/193 (88%)	170 (100%)	0	100	100
2	M	11/12 (92%)	11 (100%)	0	100	100
2	N	9/12 (75%)	9 (100%)	0	100	100
2	O	11/12 (92%)	11 (100%)	0	100	100
2	P	11/12 (92%)	11 (100%)	0	100	100
2	Q	11/12 (92%)	11 (100%)	0	100	100
2	R	11/12 (92%)	11 (100%)	0	100	100
2	S	10/12 (83%)	10 (100%)	0	100	100
2	T	12/12 (100%)	12 (100%)	0	100	100
2	U	10/12 (83%)	10 (100%)	0	100	100
2	V	10/12 (83%)	10 (100%)	0	100	100
2	W	11/12 (92%)	11 (100%)	0	100	100
2	X	10/12 (83%)	10 (100%)	0	100	100
All	All	2143/2460 (87%)	2137 (100%)	6 (0%)	86	95

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	98	GLU
1	H	144	MET
1	J	144	MET
1	B	144	MET
1	A	191	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	4	GLN
1	L	50	GLN
2	R	319	GLN
1	L	84	HIS
1	L	4	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](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	IHP	G	301	-	36,36,36	1.28	0	60,60,60	0.59	0
3	IHP	K	301	-	36,36,36	1.27	2 (5%)	60,60,60	0.56	0
3	IHP	E	301	-	36,36,36	1.23	0	60,60,60	0.56	0
3	IHP	B	301	-	36,36,36	1.34	4 (11%)	60,60,60	0.81	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
3	IHP	G	301	-	-	0/30/54/54	0/1/1/1
3	IHP	K	301	-	-	0/30/54/54	0/1/1/1
3	IHP	E	301	-	-	0/30/54/54	0/1/1/1
3	IHP	B	301	-	-	0/30/54/54	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	K	301	IHP	P3-O43	2.06	1.62	1.54
3	B	301	IHP	P5-O45	2.04	1.62	1.54
3	K	301	IHP	P3-O33	2.02	1.62	1.54
3	B	301	IHP	P5-O35	2.01	1.62	1.54
3	B	301	IHP	P6-O36	2.01	1.62	1.54

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

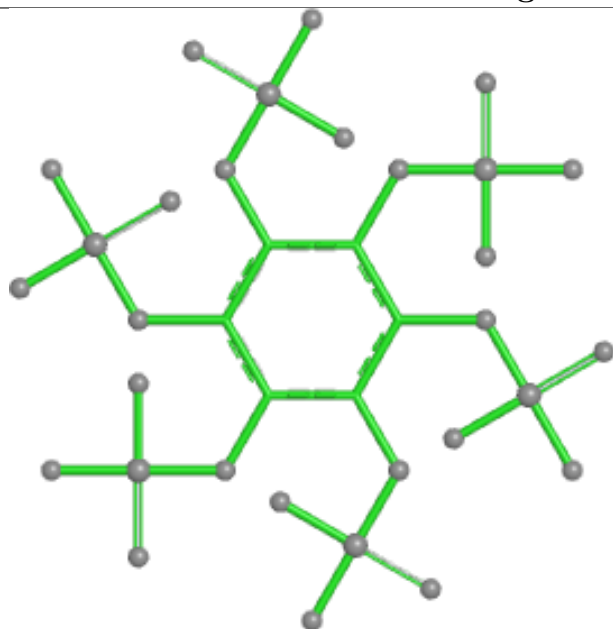
There are no ring outliers.

1 monomer is involved in 2 short contacts:

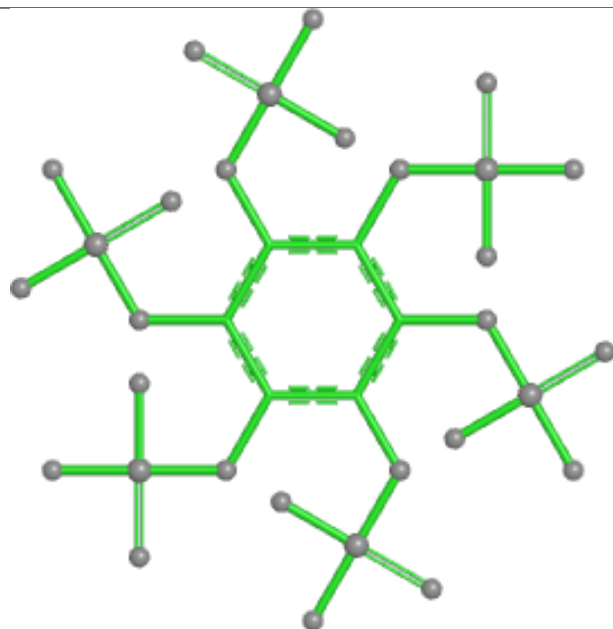
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	301	IHP	2	0

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.

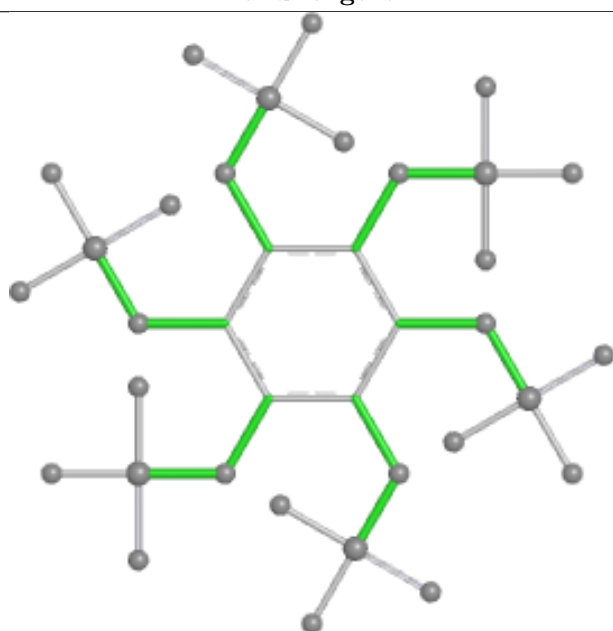
Ligand IHP G 301



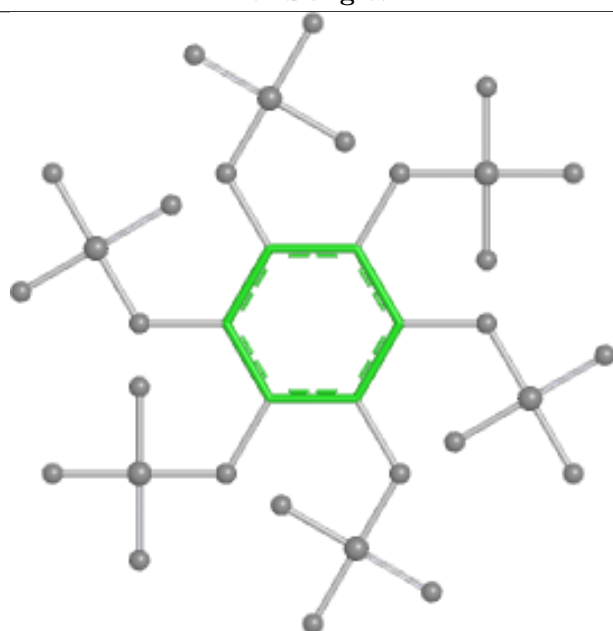
Bond lengths



Bond angles

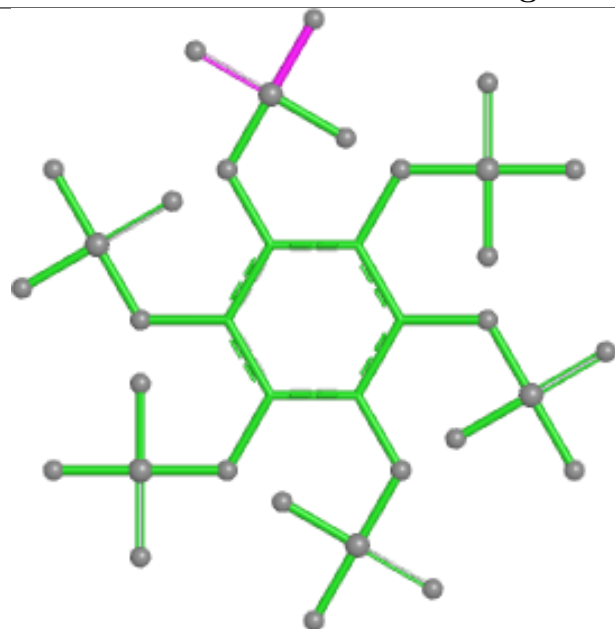


Torsions

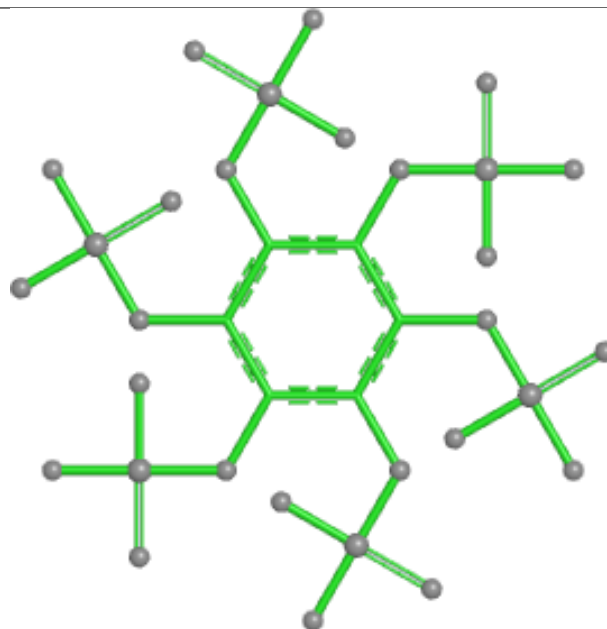


Rings

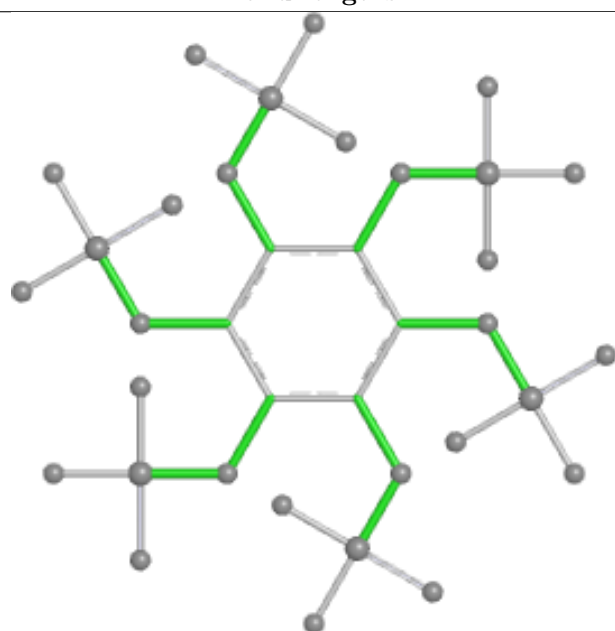
Ligand IHP K 301



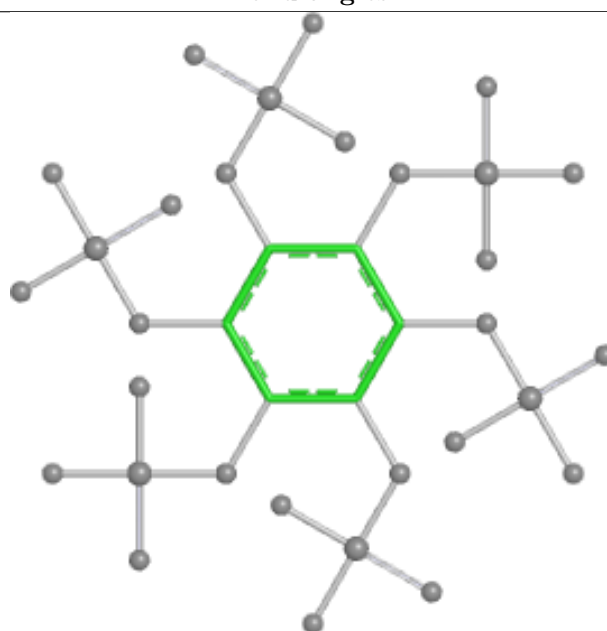
Bond lengths



Bond angles

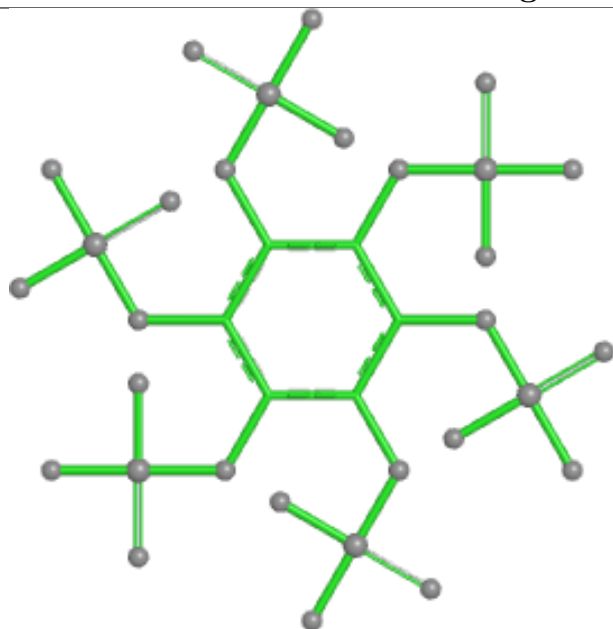


Torsions

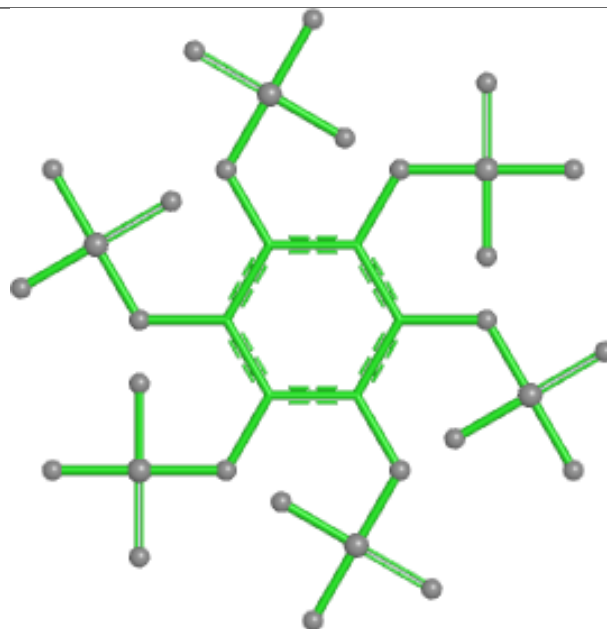


Rings

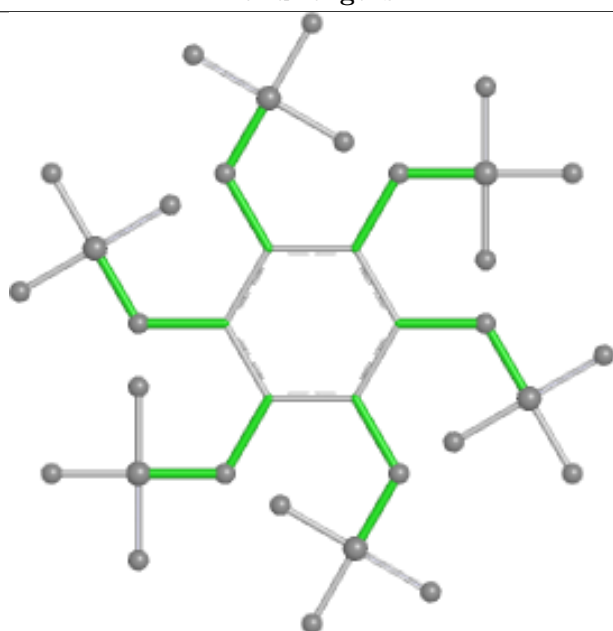
Ligand IHP E 301



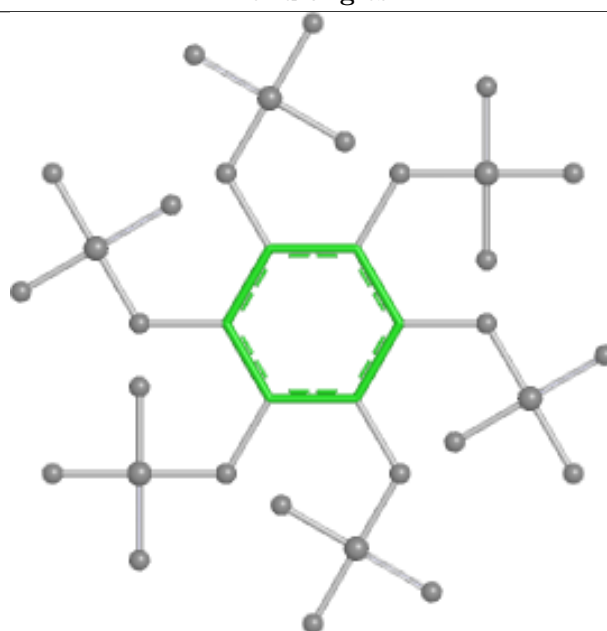
Bond lengths



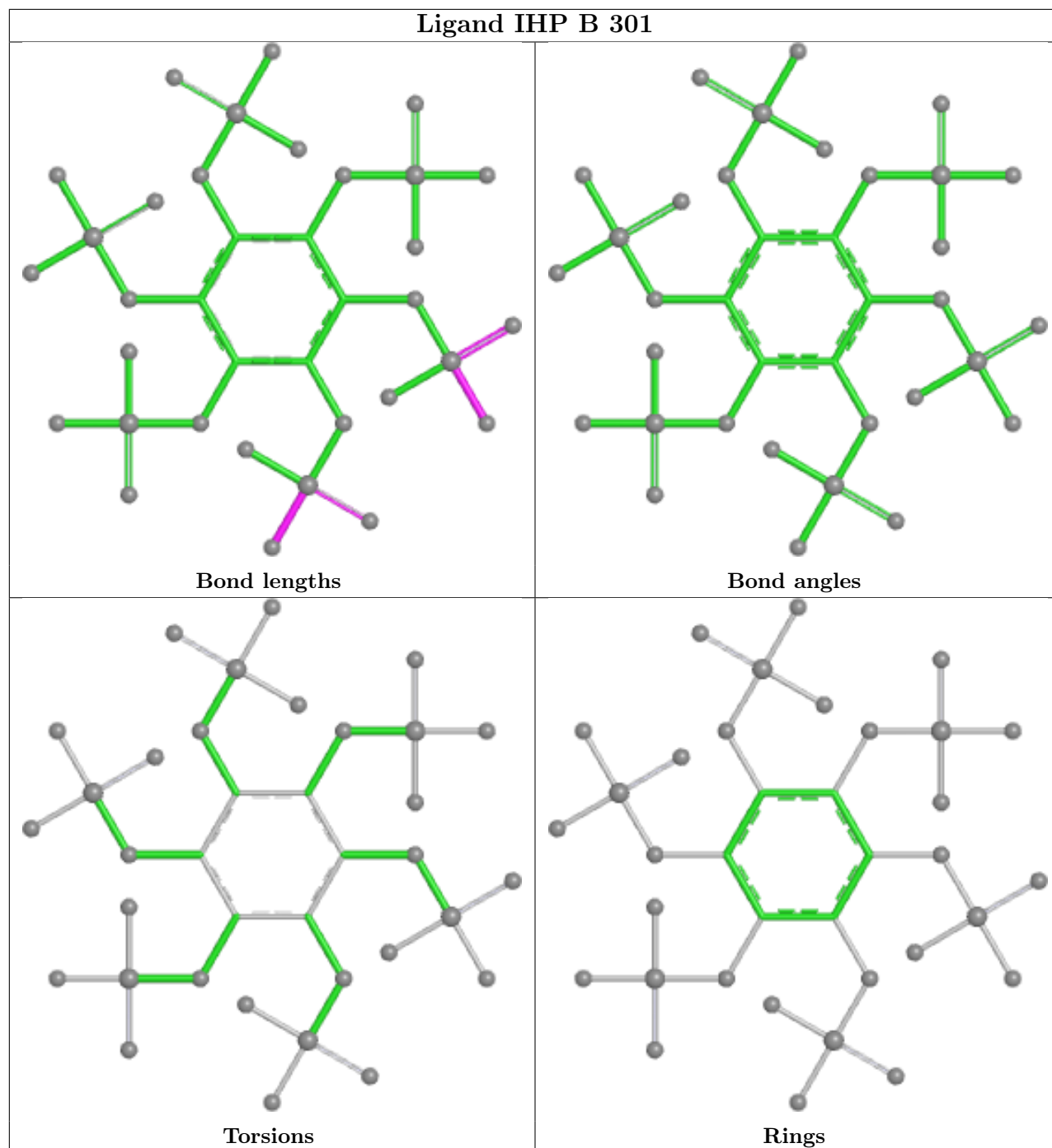
Bond angles



Torsions



Rings



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	209/231 (90%)	-0.01	3 (1%) 73 64	33, 71, 117, 129	1 (0%)
1	B	201/231 (87%)	0.22	11 (5%) 30 23	33, 82, 138, 166	1 (0%)
1	C	207/231 (89%)	0.06	5 (2%) 59 49	37, 83, 129, 146	2 (0%)
1	D	209/231 (90%)	0.25	12 (5%) 29 22	31, 79, 123, 139	3 (1%)
1	E	213/231 (92%)	0.07	7 (3%) 49 39	31, 73, 129, 152	1 (0%)
1	F	212/231 (91%)	0.06	7 (3%) 49 39	31, 74, 130, 160	1 (0%)
1	G	201/231 (87%)	0.19	7 (3%) 47 37	51, 82, 130, 143	0
1	H	209/231 (90%)	0.04	4 (1%) 66 57	50, 80, 138, 156	0
1	I	209/231 (90%)	0.32	12 (5%) 29 22	53, 87, 137, 153	0
1	J	208/231 (90%)	0.26	15 (7%) 21 15	52, 89, 139, 162	0
1	K	209/231 (90%)	0.22	10 (4%) 35 27	37, 81, 111, 131	1 (0%)
1	L	206/231 (89%)	0.06	4 (1%) 66 57	35, 74, 161, 175	1 (0%)
2	M	14/15 (93%)	0.30	1 (7%) 22 16	62, 85, 107, 115	0
2	N	13/15 (86%)	0.35	0 100 100	59, 78, 97, 106	0
2	O	14/15 (93%)	0.45	0 100 100	62, 92, 117, 118	0
2	P	13/15 (86%)	0.35	0 100 100	66, 84, 112, 115	0
2	Q	13/15 (86%)	0.51	0 100 100	65, 91, 109, 127	0
2	R	14/15 (93%)	0.34	0 100 100	57, 84, 100, 117	0
2	S	13/15 (86%)	1.05	1 (7%) 19 14	75, 104, 144, 146	0
2	T	14/15 (93%)	0.82	3 (21%) 2 2	62, 97, 133, 138	0
2	U	13/15 (86%)	0.88	0 100 100	71, 94, 113, 114	0
2	V	12/15 (80%)	0.32	0 100 100	74, 93, 103, 105	0
2	W	14/15 (93%)	1.03	3 (21%) 2 2	65, 101, 124, 134	0
2	X	13/15 (86%)	0.34	0 100 100	59, 81, 101, 114	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	2653/2952 (89%)	0.17	105 (3%) 42 33	31, 81, 133, 175	11 (0%)

The worst 5 of 105 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	183	ASN	5.5
1	I	90	PRO	5.3
1	D	21[A]	ASN	5.2
1	J	85	PRO	4.1
1	D	185	ALA	3.9

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

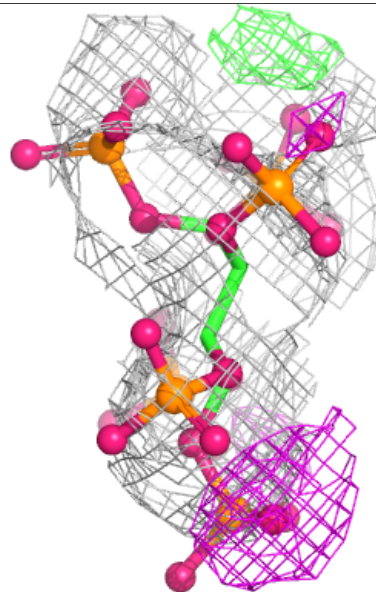
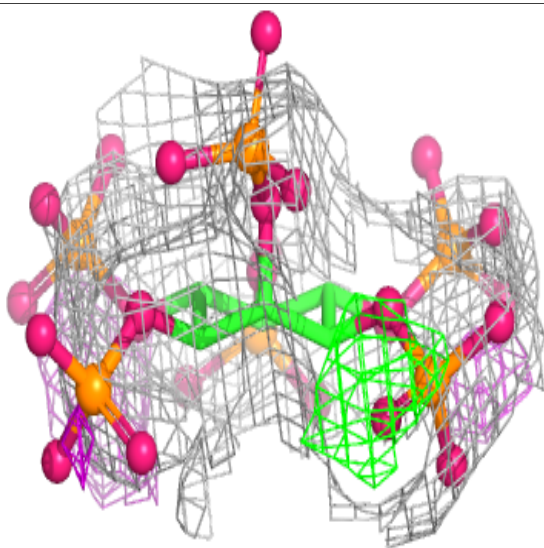
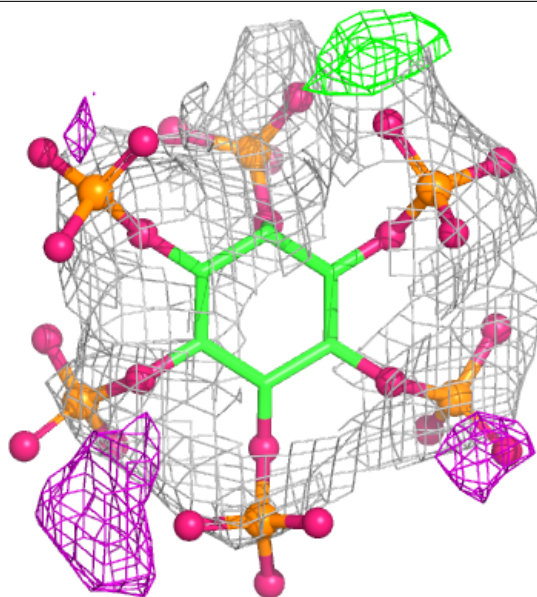
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	IHP	K	301	36/36	0.38	0.14	130,175,182,182	0
3	IHP	B	301	36/36	0.49	0.14	137,167,173,174	0
3	IHP	E	301	36/36	0.51	0.14	124,163,172,176	0
4	CL	E	302	1/1	0.51	0.36	263,263,263,263	0
3	IHP	G	301	36/36	0.57	0.12	123,164,168,175	0
4	CL	G	302	1/1	0.88	0.17	83,83,83,83	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.

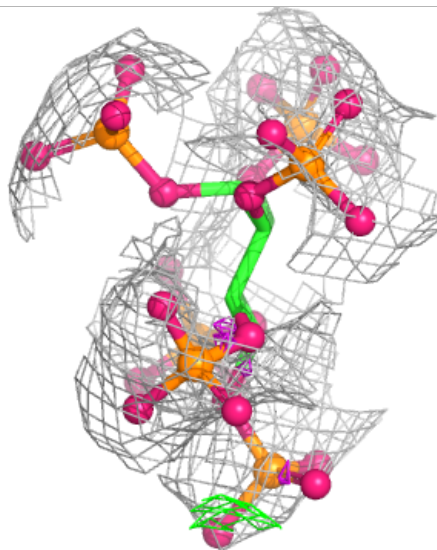
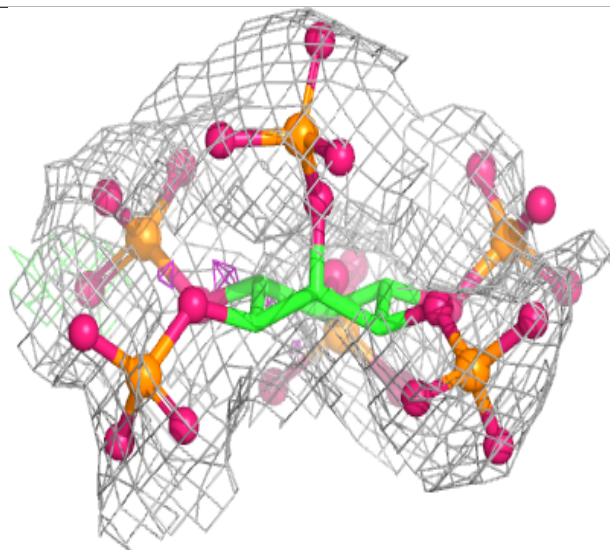
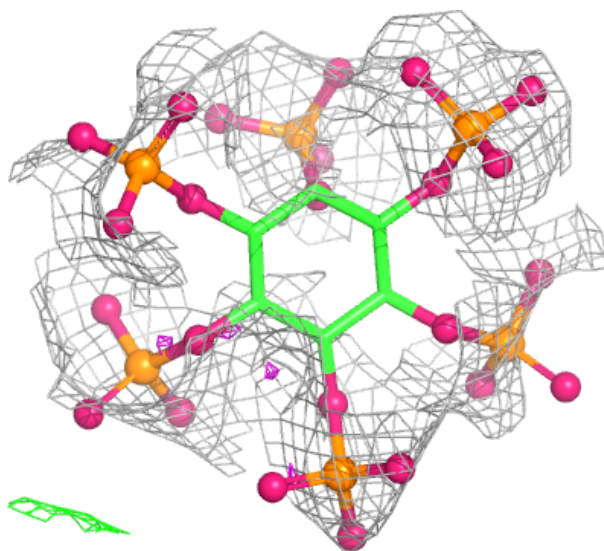
Electron density around IHP K 301:

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



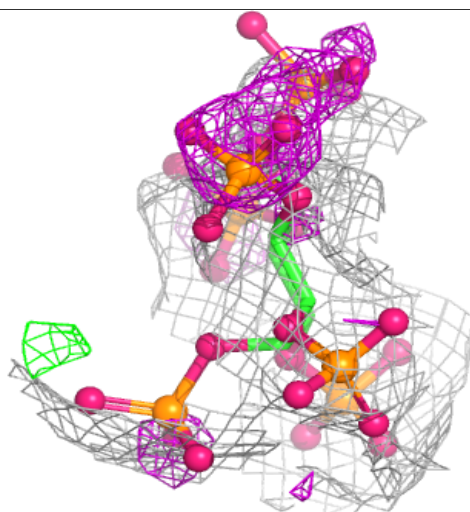
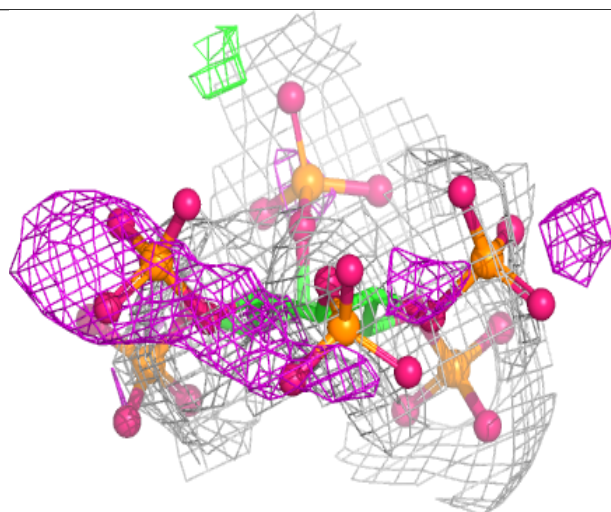
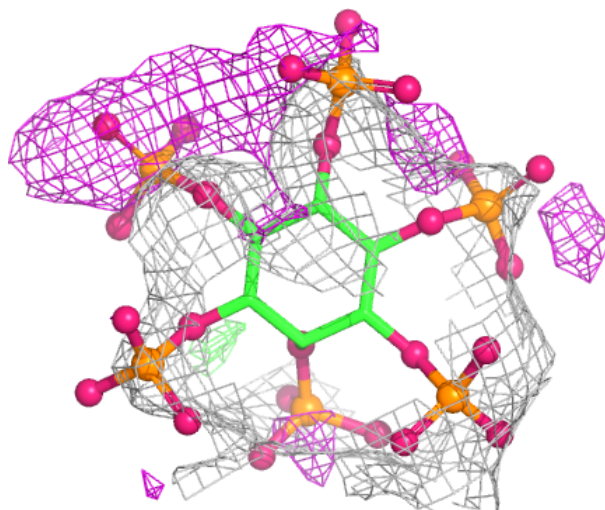
Electron density around IHP B 301:

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



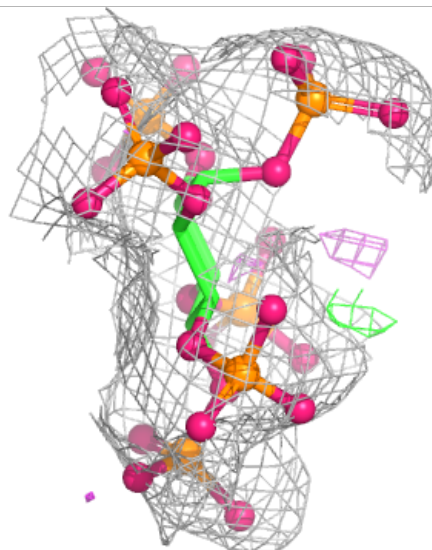
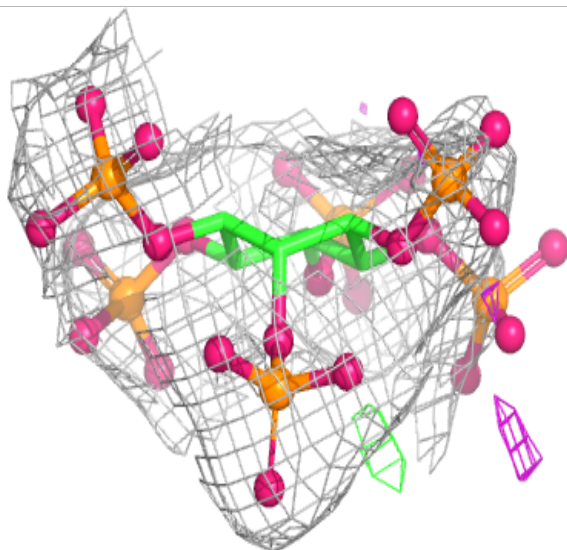
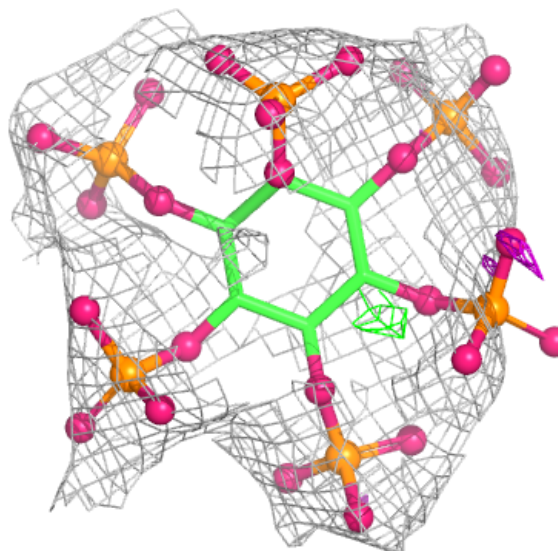
Electron density around IHP E 301:

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



Electron density around IHP G 301:

$2mF_o-DF_c$ (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.