



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 14, 2025 – 07:07 pm BST

PDB ID : 9QE4 / pdb\_00009qe4  
Title : VCB in complex with VHL-binding compound 114  
Authors : Braun, M.B.; Dierlamm, N.; Hartmann, M.D.  
Deposited on : 2025-03-07  
Resolution : 2.28 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 3.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.003 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.42

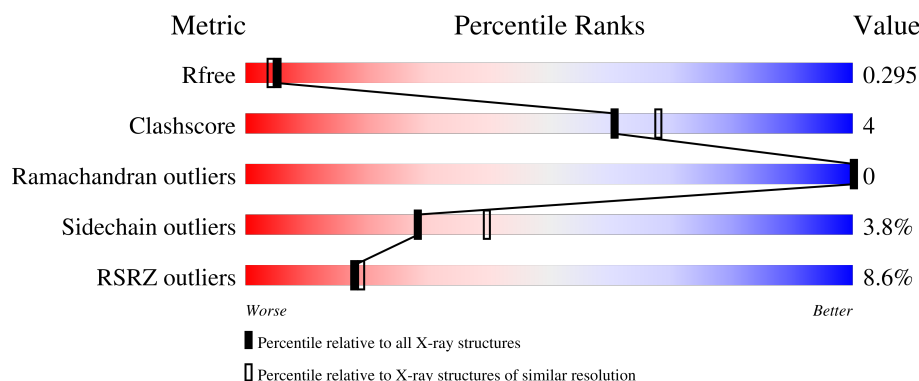
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.28 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))
$R_{free}$	164625	8487 (2.30-2.26)
Clashscore	180529	9437 (2.30-2.26)
Ramachandran outliers	177936	9341 (2.30-2.26)
Sidechain outliers	177891	9342 (2.30-2.26)
RSRZ outliers	164620	8487 (2.30-2.26)

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

Mol	Chain	Length	Quality of chain
1	A	129	<div> <div>3%</div> <div>71%</div> <div>10%</div> <div>19%</div> </div>
1	D	129	<div> <div>10%</div> <div>67%</div> <div>9%</div> <div>23%</div> </div>
1	G	129	<div> <div>7%</div> <div>64%</div> <div>15%</div> <div>20%</div> </div>
1	J	129	<div> <div>3%</div> <div>73%</div> <div>7%</div> <div>20%</div> </div>
2	B	97	<div> <div>3%</div> <div>78%</div> <div>11%</div> <div>10%</div> </div>

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Mol	Chain	Length	Quality of chain
2	E	97	
2	H	97	
2	K	97	
3	C	203	
3	F	203	
3	I	203	
3	L	203	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10665 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 Elongin-B.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	104	Total	As	C	N	O	S	0	0	0
			811	2	516	136	152	5			
1	D	99	Total	As	C	N	O	S	0	0	0
			756	2	485	124	140	5			
1	G	103	Total	As	C	N	O	S	0	0	0
			809	2	513	135	154	5			
1	J	103	Total	As	C	N	O	S	0	0	0
			809	2	514	136	152	5			

There are 100 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-24	MET	-	initiating methionine	UNP Q15370
A	-23	LYS	-	expression tag	UNP Q15370
A	-22	HIS	-	expression tag	UNP Q15370
A	-21	HIS	-	expression tag	UNP Q15370
A	-20	HIS	-	expression tag	UNP Q15370
A	-19	HIS	-	expression tag	UNP Q15370
A	-18	HIS	-	expression tag	UNP Q15370
A	-17	HIS	-	expression tag	UNP Q15370
A	-16	PRO	-	expression tag	UNP Q15370
A	-15	MET	-	expression tag	UNP Q15370
A	-14	SER	-	expression tag	UNP Q15370
A	-13	ASP	-	expression tag	UNP Q15370
A	-12	TYR	-	expression tag	UNP Q15370
A	-11	ASP	-	expression tag	UNP Q15370
A	-10	ILE	-	expression tag	UNP Q15370
A	-9	PRO	-	expression tag	UNP Q15370
A	-8	THR	-	expression tag	UNP Q15370
A	-7	THR	-	expression tag	UNP Q15370
A	-6	GLU	-	expression tag	UNP Q15370
A	-5	ASN	-	expression tag	UNP Q15370
A	-4	LEU	-	expression tag	UNP Q15370

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	TYR	-	expression tag	UNP Q15370
A	-2	PHE	-	expression tag	UNP Q15370
A	-1	GLN	-	expression tag	UNP Q15370
A	0	GLY	-	expression tag	UNP Q15370
D	-24	MET	-	initiating methionine	UNP Q15370
D	-23	LYS	-	expression tag	UNP Q15370
D	-22	HIS	-	expression tag	UNP Q15370
D	-21	HIS	-	expression tag	UNP Q15370
D	-20	HIS	-	expression tag	UNP Q15370
D	-19	HIS	-	expression tag	UNP Q15370
D	-18	HIS	-	expression tag	UNP Q15370
D	-17	HIS	-	expression tag	UNP Q15370
D	-16	PRO	-	expression tag	UNP Q15370
D	-15	MET	-	expression tag	UNP Q15370
D	-14	SER	-	expression tag	UNP Q15370
D	-13	ASP	-	expression tag	UNP Q15370
D	-12	TYR	-	expression tag	UNP Q15370
D	-11	ASP	-	expression tag	UNP Q15370
D	-10	ILE	-	expression tag	UNP Q15370
D	-9	PRO	-	expression tag	UNP Q15370
D	-8	THR	-	expression tag	UNP Q15370
D	-7	THR	-	expression tag	UNP Q15370
D	-6	GLU	-	expression tag	UNP Q15370
D	-5	ASN	-	expression tag	UNP Q15370
D	-4	LEU	-	expression tag	UNP Q15370
D	-3	TYR	-	expression tag	UNP Q15370
D	-2	PHE	-	expression tag	UNP Q15370
D	-1	GLN	-	expression tag	UNP Q15370
D	0	GLY	-	expression tag	UNP Q15370
G	-24	MET	-	initiating methionine	UNP Q15370
G	-23	LYS	-	expression tag	UNP Q15370
G	-22	HIS	-	expression tag	UNP Q15370
G	-21	HIS	-	expression tag	UNP Q15370
G	-20	HIS	-	expression tag	UNP Q15370
G	-19	HIS	-	expression tag	UNP Q15370
G	-18	HIS	-	expression tag	UNP Q15370
G	-17	HIS	-	expression tag	UNP Q15370
G	-16	PRO	-	expression tag	UNP Q15370
G	-15	MET	-	expression tag	UNP Q15370
G	-14	SER	-	expression tag	UNP Q15370
G	-13	ASP	-	expression tag	UNP Q15370
G	-12	TYR	-	expression tag	UNP Q15370

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-11	ASP	-	expression tag	UNP Q15370
G	-10	ILE	-	expression tag	UNP Q15370
G	-9	PRO	-	expression tag	UNP Q15370
G	-8	THR	-	expression tag	UNP Q15370
G	-7	THR	-	expression tag	UNP Q15370
G	-6	GLU	-	expression tag	UNP Q15370
G	-5	ASN	-	expression tag	UNP Q15370
G	-4	LEU	-	expression tag	UNP Q15370
G	-3	TYR	-	expression tag	UNP Q15370
G	-2	PHE	-	expression tag	UNP Q15370
G	-1	GLN	-	expression tag	UNP Q15370
G	0	GLY	-	expression tag	UNP Q15370
J	-24	MET	-	initiating methionine	UNP Q15370
J	-23	LYS	-	expression tag	UNP Q15370
J	-22	HIS	-	expression tag	UNP Q15370
J	-21	HIS	-	expression tag	UNP Q15370
J	-20	HIS	-	expression tag	UNP Q15370
J	-19	HIS	-	expression tag	UNP Q15370
J	-18	HIS	-	expression tag	UNP Q15370
J	-17	HIS	-	expression tag	UNP Q15370
J	-16	PRO	-	expression tag	UNP Q15370
J	-15	MET	-	expression tag	UNP Q15370
J	-14	SER	-	expression tag	UNP Q15370
J	-13	ASP	-	expression tag	UNP Q15370
J	-12	TYR	-	expression tag	UNP Q15370
J	-11	ASP	-	expression tag	UNP Q15370
J	-10	ILE	-	expression tag	UNP Q15370
J	-9	PRO	-	expression tag	UNP Q15370
J	-8	THR	-	expression tag	UNP Q15370
J	-7	THR	-	expression tag	UNP Q15370
J	-6	GLU	-	expression tag	UNP Q15370
J	-5	ASN	-	expression tag	UNP Q15370
J	-4	LEU	-	expression tag	UNP Q15370
J	-3	TYR	-	expression tag	UNP Q15370
J	-2	PHE	-	expression tag	UNP Q15370
J	-1	GLN	-	expression tag	UNP Q15370
J	0	GLY	-	expression tag	UNP Q15370

- Molecule 2 is a protein called Elongin-C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	87	Total	C	N	O	S	0	0	0
			694	448	111	128	7			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	89	Total	C	N	O	S	0	0	0
			701	452	112	130	7			
2	H	88	Total	C	N	O	S	0	0	0
			688	445	111	127	5			
2	K	88	Total	C	N	O	S	0	0	0
			694	449	112	126	7			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	16	MET	-	initiating methionine	UNP Q15369
E	16	MET	-	initiating methionine	UNP Q15369
H	16	MET	-	initiating methionine	UNP Q15369
K	16	MET	-	initiating methionine	UNP Q15369

- Molecule 3 is a protein called von Hippel-Lindau disease tumor suppressor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	142	Total	As	C	N	O	S	0	0
			1124	1	716	203	202	2		
3	F	142	Total	As	C	N	O	S	0	0
			1129	1	722	197	207	2		
3	I	143	Total	As	C	N	O	S	0	0
			1156	1	737	208	208	2		
3	L	143	Total	As	C	N	O	S	0	0
			1146	1	731	206	206	2		

There are 172 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	11	MET	-	initiating methionine	UNP P40337
C	12	ALA	-	expression tag	UNP P40337
C	13	SER	-	expression tag	UNP P40337
C	14	ALA	-	expression tag	UNP P40337
C	15	TRP	-	expression tag	UNP P40337
C	16	SER	-	expression tag	UNP P40337
C	17	HIS	-	expression tag	UNP P40337
C	18	PRO	-	expression tag	UNP P40337
C	19	GLN	-	expression tag	UNP P40337
C	20	PHE	-	expression tag	UNP P40337
C	21	GLU	-	expression tag	UNP P40337
C	22	LYS	-	expression tag	UNP P40337

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Chain	Residue	Modelled	Actual	Comment	Reference
C	23	GLY	-	expression tag	UNP P40337
C	24	GLY	-	expression tag	UNP P40337
C	25	GLY	-	expression tag	UNP P40337
C	26	SER	-	expression tag	UNP P40337
C	27	GLY	-	expression tag	UNP P40337
C	28	GLY	-	expression tag	UNP P40337
C	29	GLY	-	expression tag	UNP P40337
C	30	SER	-	expression tag	UNP P40337
C	31	GLY	-	expression tag	UNP P40337
C	32	GLY	-	expression tag	UNP P40337
C	33	SER	-	expression tag	UNP P40337
C	34	ALA	-	expression tag	UNP P40337
C	35	TRP	-	expression tag	UNP P40337
C	36	SER	-	expression tag	UNP P40337
C	37	HIS	-	expression tag	UNP P40337
C	38	PRO	-	expression tag	UNP P40337
C	39	GLN	-	expression tag	UNP P40337
C	40	PHE	-	expression tag	UNP P40337
C	41	GLU	-	expression tag	UNP P40337
C	42	LYS	-	expression tag	UNP P40337
C	43	SER	-	expression tag	UNP P40337
C	44	GLY	-	expression tag	UNP P40337
C	45	GLU	-	expression tag	UNP P40337
C	46	ASN	-	expression tag	UNP P40337
C	47	LEU	-	expression tag	UNP P40337
C	48	TYR	-	expression tag	UNP P40337
C	49	PHE	-	expression tag	UNP P40337
C	50	GLN	-	expression tag	UNP P40337
C	51	GLY	-	expression tag	UNP P40337
C	52	SER	-	expression tag	UNP P40337
C	53	HIS	-	expression tag	UNP P40337
F	11	MET	-	initiating methionine	UNP P40337
F	12	ALA	-	expression tag	UNP P40337
F	13	SER	-	expression tag	UNP P40337
F	14	ALA	-	expression tag	UNP P40337
F	15	TRP	-	expression tag	UNP P40337
F	16	SER	-	expression tag	UNP P40337
F	17	HIS	-	expression tag	UNP P40337
F	18	PRO	-	expression tag	UNP P40337
F	19	GLN	-	expression tag	UNP P40337
F	20	PHE	-	expression tag	UNP P40337
F	21	GLU	-	expression tag	UNP P40337

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Chain	Residue	Modelled	Actual	Comment	Reference
F	22	LYS	-	expression tag	UNP P40337
F	23	GLY	-	expression tag	UNP P40337
F	24	GLY	-	expression tag	UNP P40337
F	25	GLY	-	expression tag	UNP P40337
F	26	SER	-	expression tag	UNP P40337
F	27	GLY	-	expression tag	UNP P40337
F	28	GLY	-	expression tag	UNP P40337
F	29	GLY	-	expression tag	UNP P40337
F	30	SER	-	expression tag	UNP P40337
F	31	GLY	-	expression tag	UNP P40337
F	32	GLY	-	expression tag	UNP P40337
F	33	SER	-	expression tag	UNP P40337
F	34	ALA	-	expression tag	UNP P40337
F	35	TRP	-	expression tag	UNP P40337
F	36	SER	-	expression tag	UNP P40337
F	37	HIS	-	expression tag	UNP P40337
F	38	PRO	-	expression tag	UNP P40337
F	39	GLN	-	expression tag	UNP P40337
F	40	PHE	-	expression tag	UNP P40337
F	41	GLU	-	expression tag	UNP P40337
F	42	LYS	-	expression tag	UNP P40337
F	43	SER	-	expression tag	UNP P40337
F	44	GLY	-	expression tag	UNP P40337
F	45	GLU	-	expression tag	UNP P40337
F	46	ASN	-	expression tag	UNP P40337
F	47	LEU	-	expression tag	UNP P40337
F	48	TYR	-	expression tag	UNP P40337
F	49	PHE	-	expression tag	UNP P40337
F	50	GLN	-	expression tag	UNP P40337
F	51	GLY	-	expression tag	UNP P40337
F	52	SER	-	expression tag	UNP P40337
F	53	HIS	-	expression tag	UNP P40337
I	11	MET	-	initiating methionine	UNP P40337
I	12	ALA	-	expression tag	UNP P40337
I	13	SER	-	expression tag	UNP P40337
I	14	ALA	-	expression tag	UNP P40337
I	15	TRP	-	expression tag	UNP P40337
I	16	SER	-	expression tag	UNP P40337
I	17	HIS	-	expression tag	UNP P40337
I	18	PRO	-	expression tag	UNP P40337
I	19	GLN	-	expression tag	UNP P40337
I	20	PHE	-	expression tag	UNP P40337

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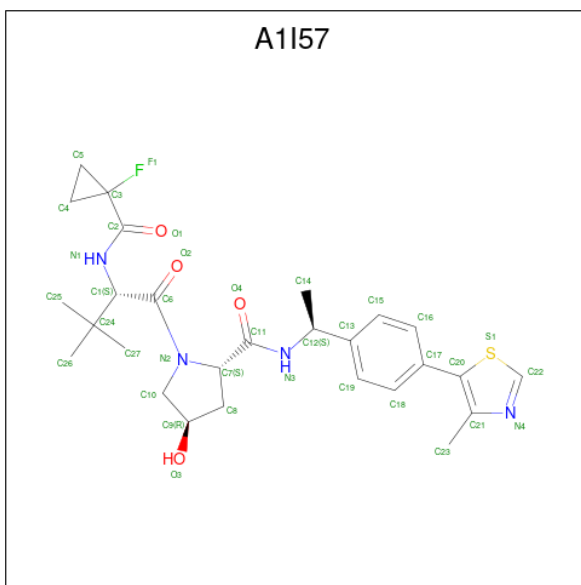
Chain	Residue	Modelled	Actual	Comment	Reference
I	21	GLU	-	expression tag	UNP P40337
I	22	LYS	-	expression tag	UNP P40337
I	23	GLY	-	expression tag	UNP P40337
I	24	GLY	-	expression tag	UNP P40337
I	25	GLY	-	expression tag	UNP P40337
I	26	SER	-	expression tag	UNP P40337
I	27	GLY	-	expression tag	UNP P40337
I	28	GLY	-	expression tag	UNP P40337
I	29	GLY	-	expression tag	UNP P40337
I	30	SER	-	expression tag	UNP P40337
I	31	GLY	-	expression tag	UNP P40337
I	32	GLY	-	expression tag	UNP P40337
I	33	SER	-	expression tag	UNP P40337
I	34	ALA	-	expression tag	UNP P40337
I	35	TRP	-	expression tag	UNP P40337
I	36	SER	-	expression tag	UNP P40337
I	37	HIS	-	expression tag	UNP P40337
I	38	PRO	-	expression tag	UNP P40337
I	39	GLN	-	expression tag	UNP P40337
I	40	PHE	-	expression tag	UNP P40337
I	41	GLU	-	expression tag	UNP P40337
I	42	LYS	-	expression tag	UNP P40337
I	43	SER	-	expression tag	UNP P40337
I	44	GLY	-	expression tag	UNP P40337
I	45	GLU	-	expression tag	UNP P40337
I	46	ASN	-	expression tag	UNP P40337
I	47	LEU	-	expression tag	UNP P40337
I	48	TYR	-	expression tag	UNP P40337
I	49	PHE	-	expression tag	UNP P40337
I	50	GLN	-	expression tag	UNP P40337
I	51	GLY	-	expression tag	UNP P40337
I	52	SER	-	expression tag	UNP P40337
I	53	HIS	-	expression tag	UNP P40337
L	11	MET	-	initiating methionine	UNP P40337
L	12	ALA	-	expression tag	UNP P40337
L	13	SER	-	expression tag	UNP P40337
L	14	ALA	-	expression tag	UNP P40337
L	15	TRP	-	expression tag	UNP P40337
L	16	SER	-	expression tag	UNP P40337
L	17	HIS	-	expression tag	UNP P40337
L	18	PRO	-	expression tag	UNP P40337
L	19	GLN	-	expression tag	UNP P40337

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Chain	Residue	Modelled	Actual	Comment	Reference
L	20	PHE	-	expression tag	UNP P40337
L	21	GLU	-	expression tag	UNP P40337
L	22	LYS	-	expression tag	UNP P40337
L	23	GLY	-	expression tag	UNP P40337
L	24	GLY	-	expression tag	UNP P40337
L	25	GLY	-	expression tag	UNP P40337
L	26	SER	-	expression tag	UNP P40337
L	27	GLY	-	expression tag	UNP P40337
L	28	GLY	-	expression tag	UNP P40337
L	29	GLY	-	expression tag	UNP P40337
L	30	SER	-	expression tag	UNP P40337
L	31	GLY	-	expression tag	UNP P40337
L	32	GLY	-	expression tag	UNP P40337
L	33	SER	-	expression tag	UNP P40337
L	34	ALA	-	expression tag	UNP P40337
L	35	TRP	-	expression tag	UNP P40337
L	36	SER	-	expression tag	UNP P40337
L	37	HIS	-	expression tag	UNP P40337
L	38	PRO	-	expression tag	UNP P40337
L	39	GLN	-	expression tag	UNP P40337
L	40	PHE	-	expression tag	UNP P40337
L	41	GLU	-	expression tag	UNP P40337
L	42	LYS	-	expression tag	UNP P40337
L	43	SER	-	expression tag	UNP P40337
L	44	GLY	-	expression tag	UNP P40337
L	45	GLU	-	expression tag	UNP P40337
L	46	ASN	-	expression tag	UNP P40337
L	47	LEU	-	expression tag	UNP P40337
L	48	TYR	-	expression tag	UNP P40337
L	49	PHE	-	expression tag	UNP P40337
L	50	GLN	-	expression tag	UNP P40337
L	51	GLY	-	expression tag	UNP P40337
L	52	SER	-	expression tag	UNP P40337
L	53	HIS	-	expression tag	UNP P40337

- Molecule 4 is (2 {S},4 {R})-1-[(2 {S})-2-[(1-fluoranylcyclopropyl)carbonylamino]-3,3-dimethyl-butanoyl]- {N}-[(1 {S})-1-[4-(4-methyl-1,3-thiazol-5-yl)phenyl]ethyl]-4-oxidanyl-pyrolidine-2-carboxamide (CCD ID: A1I57) (formula: C<sub>27</sub>H<sub>35</sub>FN<sub>4</sub>O<sub>4</sub>S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	C	1	Total 37	C 27	F 1	N 4	O 4	S 1	0	0
4	F	1	Total 37	C 27	F 1	N 4	O 4	S 1	0	0
4	I	1	Total 37	C 27	F 1	N 4	O 4	S 1	0	0
4	L	1	Total 37	C 27	F 1	N 4	O 4	S 1	0	0

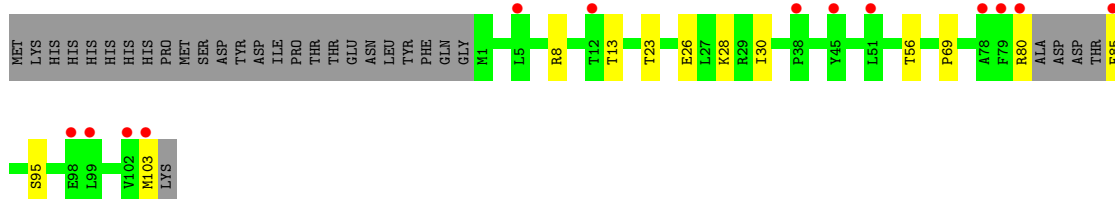
### 3 Residue-property plots [i](#)

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.

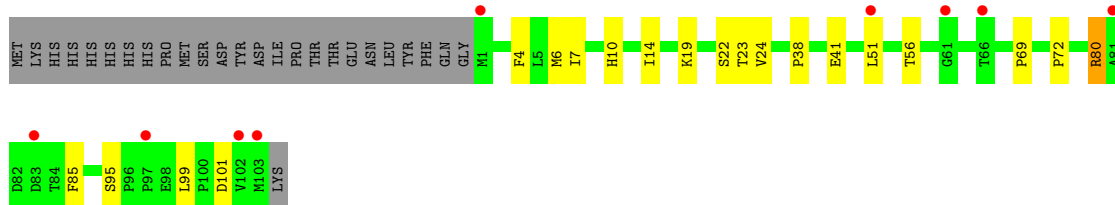
- Molecule 1: Elongin-B



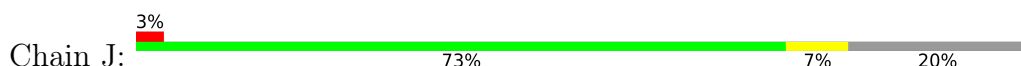
- Molecule 1: Elongin-B



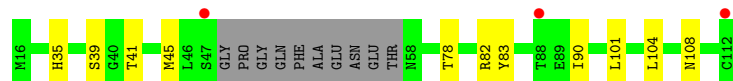
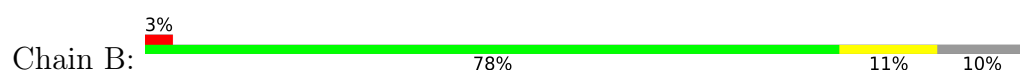
- Molecule 1: Elongin-B



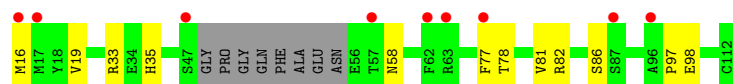
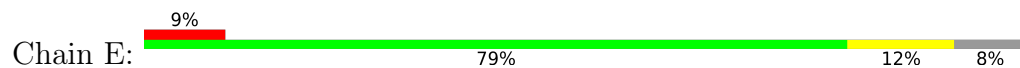
- Molecule 1: Elongin-B



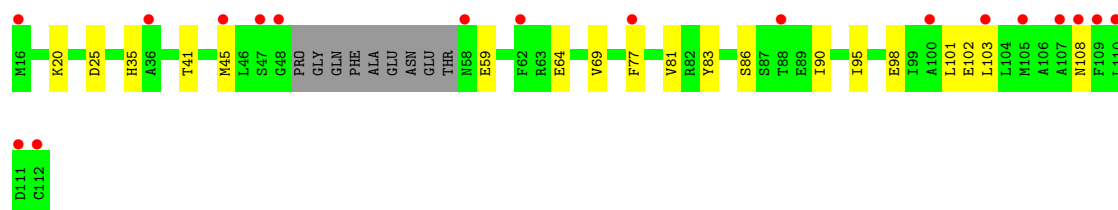
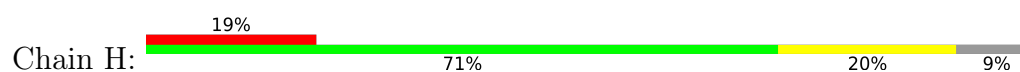
- Molecule 2: Elongin-C



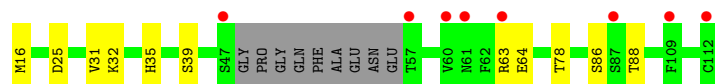
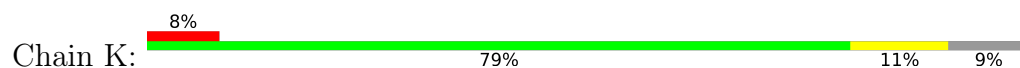
- Molecule 2: Elongin-C



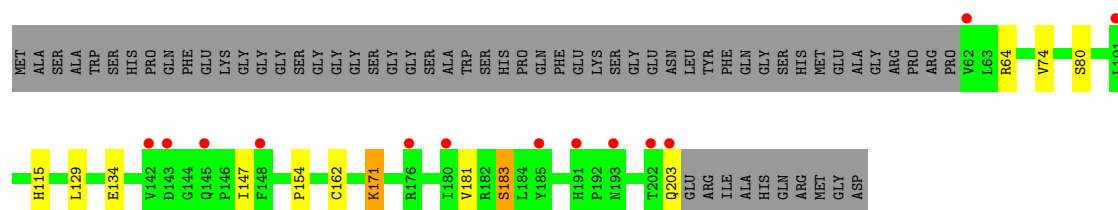
- Molecule 2: Elongin-C



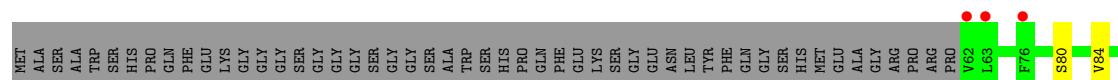
- Molecule 2: Elongin-C

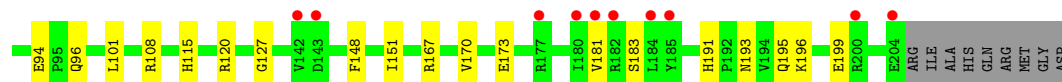


- Molecule 3: von Hippel-Lindau disease tumor suppressor



- Molecule 3: von Hippel-Lindau disease tumor suppressor





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	94.09Å 94.09Å 365.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.21 – 2.28 49.21 – 2.28	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.21-2.28) 99.9 (49.21-2.28)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.27 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.247 , 0.301 0.244 , 0.295	Depositor DCC
$R_{free}$ test set	1593 reflections (2.10%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	55.8	Xtriage
Anisotropy	0.471	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 37.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	10665	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 31.22 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.1476e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

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



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CAS, A1I57

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	0.25	0/807	0.53	0/1089
1	D	0.24	0/751	0.50	0/1014
1	G	0.24	0/805	0.53	0/1087
1	J	0.25	0/805	0.52	0/1086
2	B	0.24	0/708	0.42	0/954
2	E	0.24	0/715	0.42	0/965
2	H	0.24	0/702	0.42	0/947
2	K	0.26	0/708	0.45	0/955
3	C	0.24	0/1143	0.51	0/1563
3	F	0.24	0/1149	0.49	0/1573
3	I	0.24	0/1176	0.50	0/1605
3	L	0.24	0/1166	0.50	0/1594
All	All	0.24	0/10635	0.49	0/14432

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 [i](#)

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	811	0	797	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	756	0	730	6	0
1	G	809	0	792	10	0
1	J	809	0	800	6	0
2	B	694	0	694	5	1
2	E	701	0	689	8	0
2	H	688	0	682	11	0
2	K	694	0	689	4	0
3	C	1124	0	1090	7	0
3	F	1129	0	1090	10	0
3	I	1156	0	1136	10	0
3	L	1146	0	1118	12	1
4	C	37	0	0	1	0
4	F	37	0	0	1	0
4	I	37	0	0	1	0
4	L	37	0	0	1	0
All	All	10665	0	10307	86	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 86 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)
3:L:115:HIS:ND1	4:L:301:A1I57:O3	2.22	0.72
1:J:1:MET:N	1:J:1:MET:SD	2.63	0.71
3:F:193:ASN:OD1	3:F:196:LYS:N	2.24	0.69
3:C:115:HIS:ND1	4:C:301:A1I57:O3	2.25	0.68
3:L:73:GLN:NE2	3:L:108:ARG:HE	1.92	0.68

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:108:ASN:O	3:L:108:ARG:NH1[1_655]	2.12	0.08

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	100/129 (78%)	96 (96%)	4 (4%)	0	100	100
1	D	93/129 (72%)	90 (97%)	3 (3%)	0	100	100
1	G	99/129 (77%)	95 (96%)	4 (4%)	0	100	100
1	J	99/129 (77%)	94 (95%)	5 (5%)	0	100	100
2	B	83/97 (86%)	82 (99%)	1 (1%)	0	100	100
2	E	85/97 (88%)	83 (98%)	2 (2%)	0	100	100
2	H	84/97 (87%)	83 (99%)	1 (1%)	0	100	100
2	K	84/97 (87%)	83 (99%)	1 (1%)	0	100	100
3	C	139/203 (68%)	133 (96%)	6 (4%)	0	100	100
3	F	139/203 (68%)	134 (96%)	5 (4%)	0	100	100
3	I	140/203 (69%)	135 (96%)	5 (4%)	0	100	100
3	L	140/203 (69%)	132 (94%)	8 (6%)	0	100	100
All	All	1285/1716 (75%)	1240 (96%)	45 (4%)	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	85/114 (75%)	83 (98%)	2 (2%)	44	59
1	D	77/114 (68%)	75 (97%)	2 (3%)	41	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	86/114 (75%)	83 (96%)	3 (4%)	31	43
1	J	86/114 (75%)	86 (100%)	0	100	100
2	B	78/86 (91%)	75 (96%)	3 (4%)	28	40
2	E	77/86 (90%)	74 (96%)	3 (4%)	27	39
2	H	75/86 (87%)	73 (97%)	2 (3%)	40	54
2	K	76/86 (88%)	70 (92%)	6 (8%)	10	12
3	C	122/176 (69%)	116 (95%)	6 (5%)	21	29
3	F	124/176 (70%)	118 (95%)	6 (5%)	21	29
3	I	128/176 (73%)	122 (95%)	6 (5%)	22	30
3	L	126/176 (72%)	122 (97%)	4 (3%)	34	47
All	All	1140/1504 (76%)	1097 (96%)	43 (4%)	28	40

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	I	80	SER
2	K	35	HIS
3	I	107	ARG
3	I	183	SER
2	K	63	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
3	L	73	GLN
3	L	96	GLN
3	L	174	ASN
3	I	96	GLN
3	F	174	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

12 non-standard protein/DNA/RNA residues 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
1	CAS	J	89	1	5,8,9	1.15	0	1,9,11	1.39	0
1	CAS	G	89	1	5,8,9	1.14	0	1,9,11	1.42	0
3	CAS	L	77	3	5,8,9	1.07	0	1,9,11	0.77	0
1	CAS	J	60	1	5,8,9	1.06	0	1,9,11	0.71	0
1	CAS	A	60	1	5,8,9	1.12	0	1,9,11	1.61	0
3	CAS	I	77	3	5,8,9	1.11	0	1,9,11	0.62	0
3	CAS	F	77	3	5,8,9	1.10	0	1,9,11	0.95	0
1	CAS	D	60	1	5,8,9	1.07	0	1,9,11	1.80	0
3	CAS	C	77	3	5,8,9	1.11	0	1,9,11	1.20	0
1	CAS	D	89	1	5,8,9	1.15	0	1,9,11	1.41	0
1	CAS	G	60	1	5,8,9	1.11	0	1,9,11	1.03	0
1	CAS	A	89	1	5,8,9	1.11	0	1,9,11	1.20	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
1	CAS	J	89	1	-	0/0/7/9	-
1	CAS	G	89	1	-	0/0/7/9	-
3	CAS	L	77	3	-	0/0/7/9	-
1	CAS	J	60	1	-	0/0/7/9	-
1	CAS	A	60	1	-	0/0/7/9	-
3	CAS	I	77	3	-	0/0/7/9	-
3	CAS	F	77	3	-	0/0/7/9	-
1	CAS	D	60	1	-	0/0/7/9	-
3	CAS	C	77	3	-	0/0/7/9	-
1	CAS	D	89	1	-	0/0/7/9	-
1	CAS	G	60	1	-	0/0/7/9	-
1	CAS	A	89	1	-	0/0/7/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	60	CAS	1	0
1	A	89	CAS	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

4 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	A1I57	I	301	-	33,40,40	3.62	20 (60%)	45,61,61	2.36	12 (26%)
4	A1I57	L	301	-	33,40,40	3.61	20 (60%)	45,61,61	2.35	14 (31%)
4	A1I57	F	301	-	33,40,40	3.62	20 (60%)	45,61,61	2.37	13 (28%)
4	A1I57	C	301	-	33,40,40	3.59	20 (60%)	45,61,61	2.38	13 (28%)

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	A1I57	I	301	-	-	3/38/56/56	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	A1I57	L	301	-	-	5/38/56/56	0/4/4/4
4	A1I57	F	301	-	-	4/38/56/56	0/4/4/4
4	A1I57	C	301	-	-	2/38/56/56	0/4/4/4

The worst 5 of 80 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	301	A1I57	C17-C20	10.08	1.58	1.48
4	C	301	A1I57	C17-C20	10.05	1.58	1.48
4	L	301	A1I57	C17-C20	9.89	1.57	1.48
4	I	301	A1I57	C17-C20	9.65	1.57	1.48
4	I	301	A1I57	C1-C6	7.85	1.65	1.53

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	301	A1I57	C1-C6-N2	8.79	129.09	118.52
4	I	301	A1I57	C1-C6-N2	8.70	128.97	118.52
4	F	301	A1I57	C1-C6-N2	8.64	128.90	118.52
4	L	301	A1I57	C1-C6-N2	8.19	128.36	118.52
4	F	301	A1I57	C9-C10-N2	6.01	109.46	103.08

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

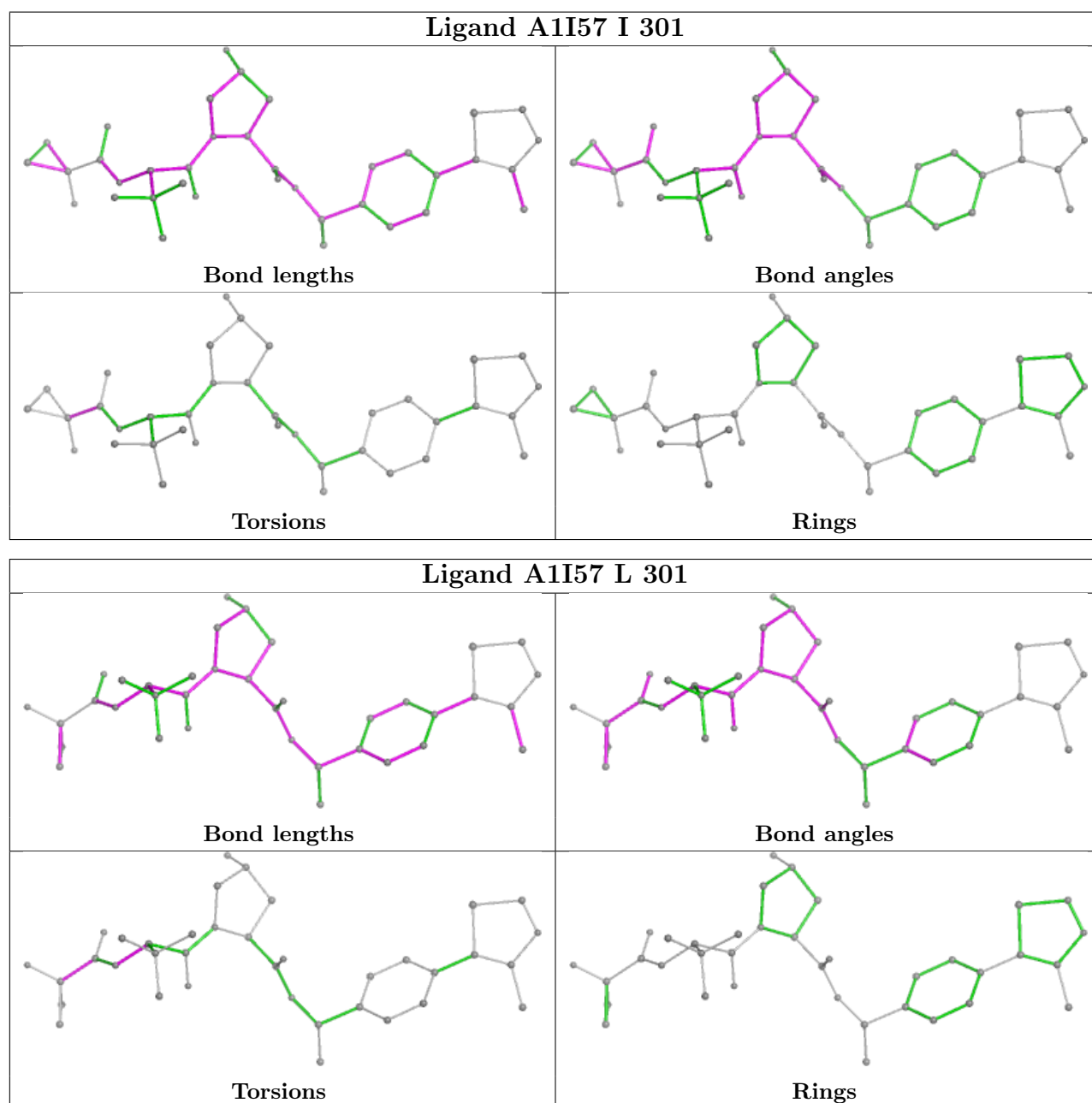
Mol	Chain	Res	Type	Atoms
4	C	301	A1I57	N1-C2-C3-C5
4	C	301	A1I57	O1-C2-C3-C5
4	F	301	A1I57	N1-C2-C3-C4
4	F	301	A1I57	N1-C2-C3-C5
4	F	301	A1I57	O1-C2-C3-C4

There are no ring outliers.

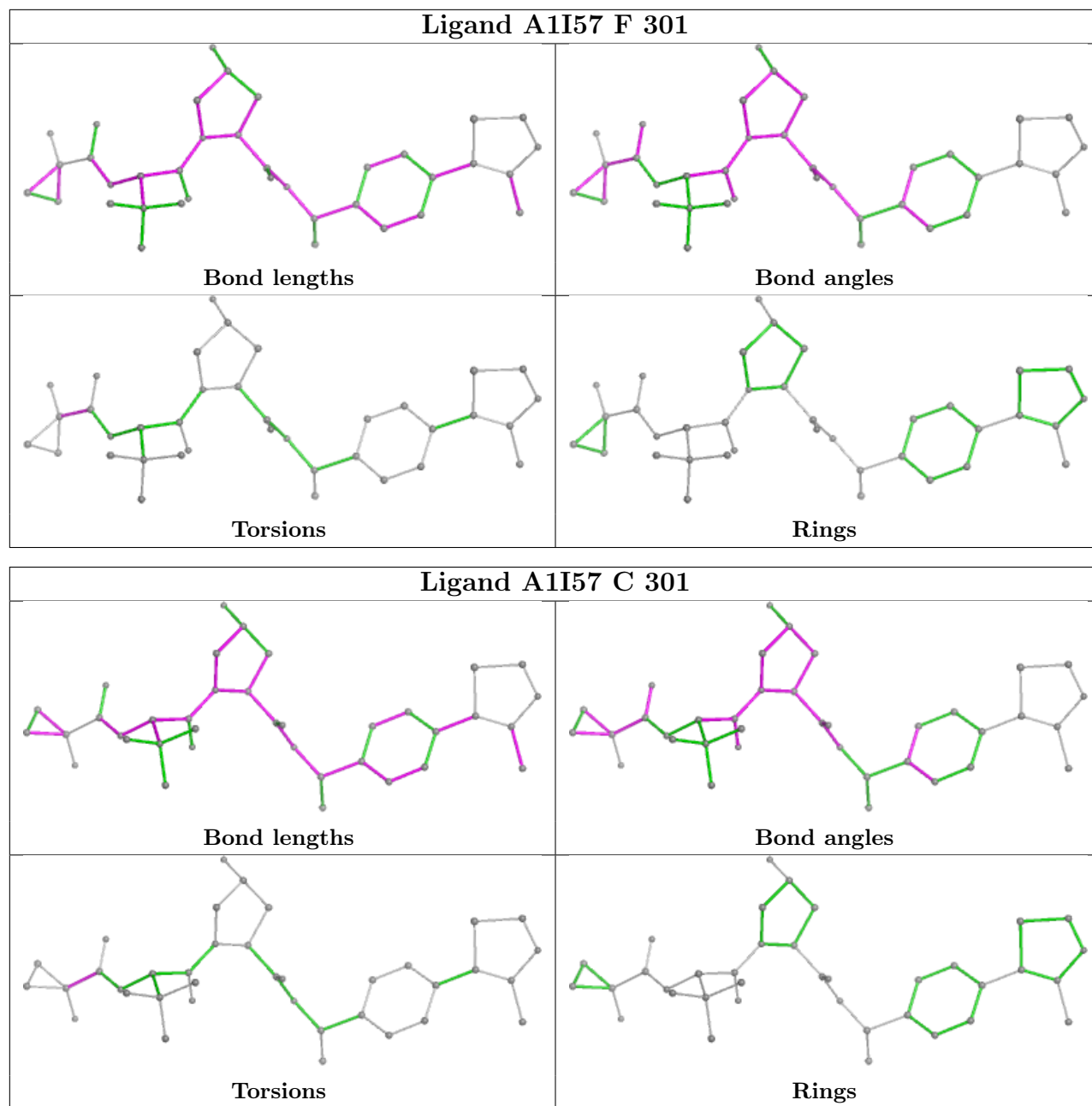
4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	I	301	A1I57	1	0
4	L	301	A1I57	1	0
4	F	301	A1I57	1	0
4	C	301	A1I57	1	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	102/129 (79%)	0.46	4 (3%) 44 45	40, 54, 86, 103	0
1	D	97/129 (75%)	1.03	13 (13%) 8 9	48, 73, 92, 98	0
1	G	101/129 (78%)	0.82	9 (8%) 17 18	45, 64, 83, 93	0
1	J	101/129 (78%)	0.34	4 (3%) 43 44	39, 51, 74, 85	0
2	B	87/97 (89%)	0.51	3 (3%) 48 50	42, 56, 80, 93	0
2	E	89/97 (91%)	0.82	9 (10%) 14 15	51, 66, 90, 95	0
2	H	88/97 (90%)	1.16	18 (20%) 3 4	48, 65, 86, 100	0
2	K	88/97 (90%)	0.62	8 (9%) 16 17	41, 54, 79, 100	0
3	C	141/203 (69%)	0.84	13 (9%) 16 17	44, 61, 90, 107	0
3	F	141/203 (69%)	0.75	11 (7%) 20 21	47, 62, 89, 104	0
3	I	142/203 (69%)	0.76	10 (7%) 24 25	43, 59, 89, 97	0
3	L	142/203 (69%)	0.59	12 (8%) 18 19	37, 53, 86, 100	0
All	All	1319/1716 (76%)	0.72	114 (8%) 18 19	37, 60, 89, 107	0

The worst 5 of 114 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	203	GLN	5.7
3	L	204	GLU	4.7
2	H	109	PHE	4.5
1	G	61	GLY	4.2
2	H	111	ASP	3.9

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
1	CAS	D	89	9/10	0.69	0.17	75,87,117,145	0
1	CAS	D	60	9/10	0.78	0.20	63,65,92,139	3
1	CAS	A	60	9/10	0.80	0.23	44,51,72,125	3
1	CAS	J	60	9/10	0.81	0.26	51,60,84,133	3
1	CAS	G	60	9/10	0.82	0.23	61,68,83,114	3
1	CAS	A	89	9/10	0.84	0.15	53,59,83,100	3
3	CAS	C	77	9/10	0.85	0.19	45,55,88,90	3
1	CAS	G	89	9/10	0.89	0.12	50,59,100,123	0
3	CAS	F	77	9/10	0.89	0.14	52,64,77,80	3
1	CAS	J	89	9/10	0.92	0.12	40,55,68,83	3
3	CAS	I	77	9/10	0.94	0.12	40,51,74,82	3
3	CAS	L	77	9/10	0.96	0.10	35,48,70,71	0

### 6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

### 6.4 Ligands ⓘ

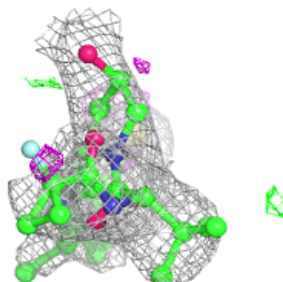
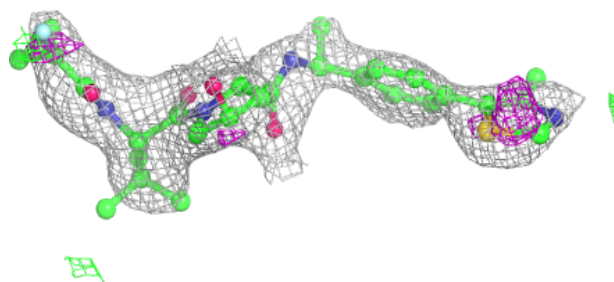
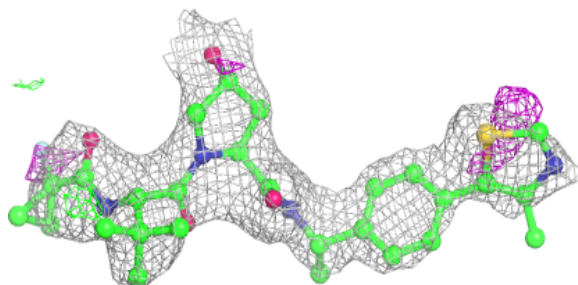
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	A1I57	F	301	37/37	0.85	0.14	54,67,86,93	0
4	A1I57	C	301	37/37	0.87	0.14	43,64,79,81	0
4	A1I57	I	301	37/37	0.88	0.14	48,66,81,84	0
4	A1I57	L	301	37/37	0.90	0.13	48,60,75,81	0

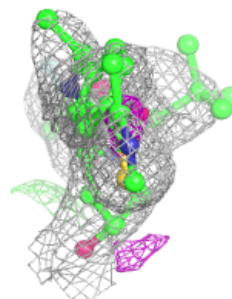
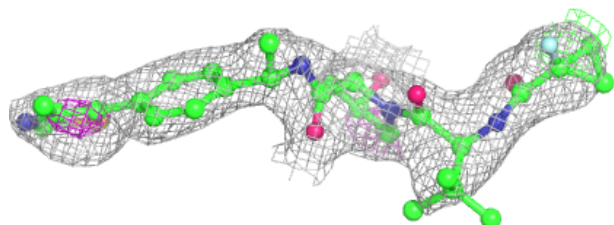
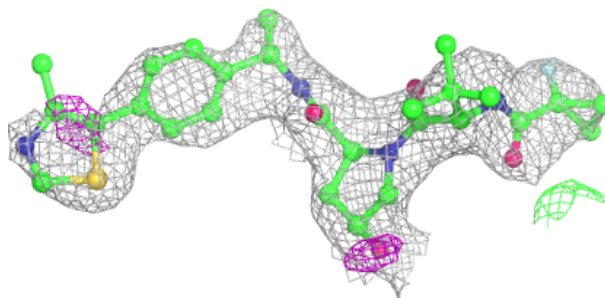
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around A1I57 F 301:**

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

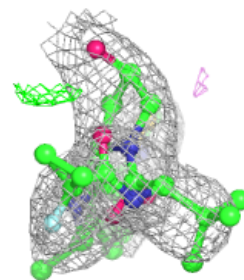
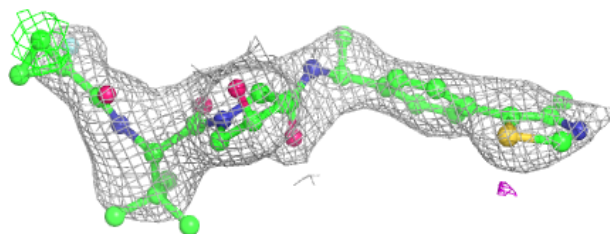
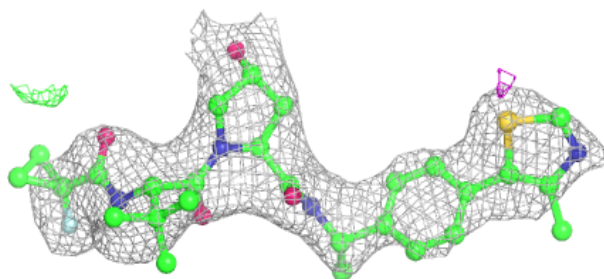
**Electron density around A1I57 C 301:**

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

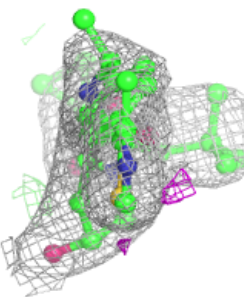
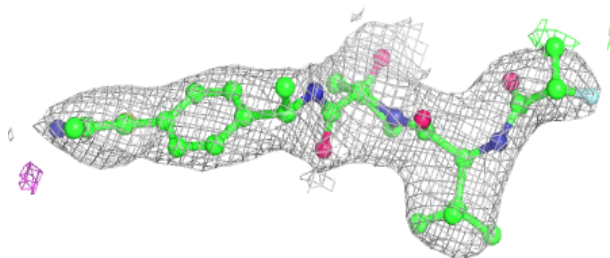
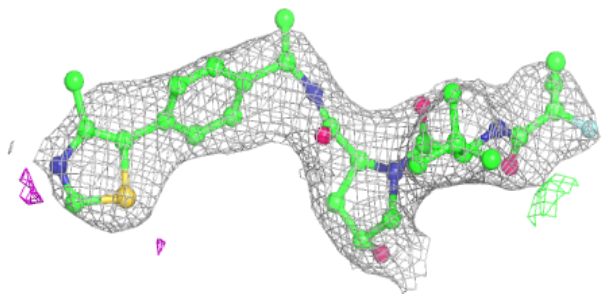


**Electron density around A1I57 I 301:**

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

**Electron density around A1I57 L 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.