



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 01:12 PM UTC

PDB ID : 3OGK / pdb_00003ogk
Title : Structure of COI1-ASK1 in complex with coronatine and an incomplete JAZ1 degnon
Authors : Sheard, L.B.; Tan, X.; Mao, H.; Withers, J.; Ben-Nissan, G.; Hinds, T.R.; Hsu, F.; Sharon, M.; Browse, J.; He, S.Y.; Rizo, J.; Howe, G.A.; Zheng, N.
Deposited on : 2010-08-16
Resolution : 2.80 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

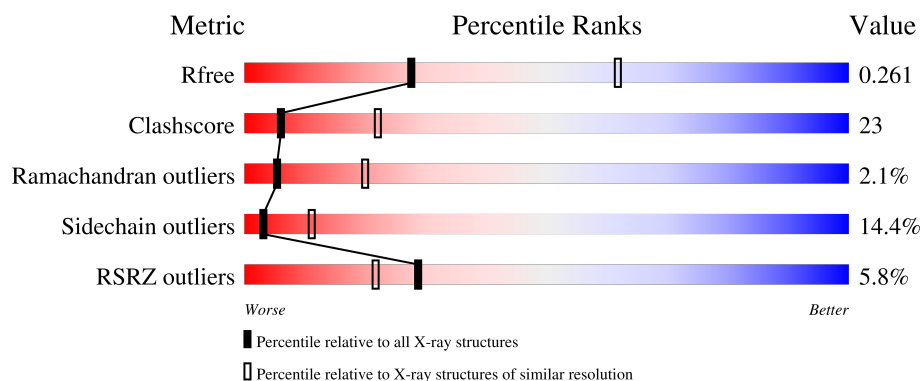
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	160	8% 54% 29% 8% 9%
1	C	160	8% 52% 29% 9% 9%
1	E	160	18% 56% 28% 7% 9%
1	G	160	6% 54% 29% 8% 9%

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Mol	Chain	Length	Quality of chain
1	I	160	
1	K	160	
1	M	160	
1	O	160	
2	B	592	
2	D	592	
2	F	592	
2	H	592	
2	J	592	
2	L	592	
2	N	592	
2	P	592	
3	Q	22	
3	R	22	
3	S	22	
3	U	22	
3	V	22	
3	W	22	
3	X	22	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	OGK	B	1100	X	-	-	-
4	OGK	D	1100	X	-	-	-
4	OGK	H	1100	X	-	-	-
4	OGK	L	1100	X	-	X	-
5	PO4	B	1101	-	X	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	PO4	B	1102	-	X	-	-
5	PO4	B	1103	-	X	X	-
5	PO4	B	1104	-	X	-	-
5	PO4	D	1101	-	X	-	-
5	PO4	D	1102	-	X	-	-
5	PO4	D	1103	-	X	X	-
5	PO4	D	1104	-	X	-	-
5	PO4	F	1101	-	X	-	-
5	PO4	F	1102	-	X	-	-
5	PO4	F	1103	-	X	-	-
5	PO4	F	1104	-	X	-	-
5	PO4	H	1101	-	X	X	-
5	PO4	H	1102	-	X	-	-
5	PO4	H	1103	-	X	X	-
5	PO4	H	1104	-	X	-	-
5	PO4	J	1101	-	X	-	-
5	PO4	J	1102	-	X	-	-
5	PO4	J	1103	-	X	X	-
5	PO4	J	1104	-	X	-	-
5	PO4	L	1101	-	X	-	-
5	PO4	L	1102	-	X	-	-
5	PO4	L	1103	-	X	-	-
5	PO4	L	1104	-	X	-	-
5	PO4	N	1101	-	X	-	-
5	PO4	N	1102	-	X	-	-
5	PO4	N	1103	-	X	X	-
5	PO4	N	1104	-	X	-	-
5	PO4	P	1101	-	X	-	-
5	PO4	P	1102	-	X	-	-
5	PO4	P	1103	-	X	X	-
5	PO4	P	1104	-	X	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 46526 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 SKP1-like protein 1A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	145	Total	C	N	O	S	0	0	0
			1152	723	186	237	6			
1	C	145	Total	C	N	O	S	0	0	0
			1152	723	186	237	6			
1	E	145	Total	C	N	O	S	0	0	0
			1152	723	186	237	6			
1	G	145	Total	C	N	O	S	0	0	0
			1152	723	186	237	6			
1	I	145	Total	C	N	O	S	0	0	0
			1152	723	186	237	6			
1	K	145	Total	C	N	O	S	0	0	0
			1152	723	186	237	6			
1	M	145	Total	C	N	O	S	0	0	0
			1152	723	186	237	6			
1	O	145	Total	C	N	O	S	0	0	0
			1152	723	186	237	6			

- Molecule 2 is a protein called Coronatine-insensitive protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	566	Total	C	N	O	S	0	0	0
			4521	2862	785	838	36			
2	D	566	Total	C	N	O	S	0	0	0
			4521	2862	785	838	36			
2	F	566	Total	C	N	O	S	0	0	0
			4521	2862	785	838	36			
2	H	562	Total	C	N	O	S	0	0	0
			4486	2840	779	831	36			
2	J	566	Total	C	N	O	S	0	0	0
			4521	2862	785	838	36			
2	L	566	Total	C	N	O	S	0	0	0
			4521	2862	785	838	36			

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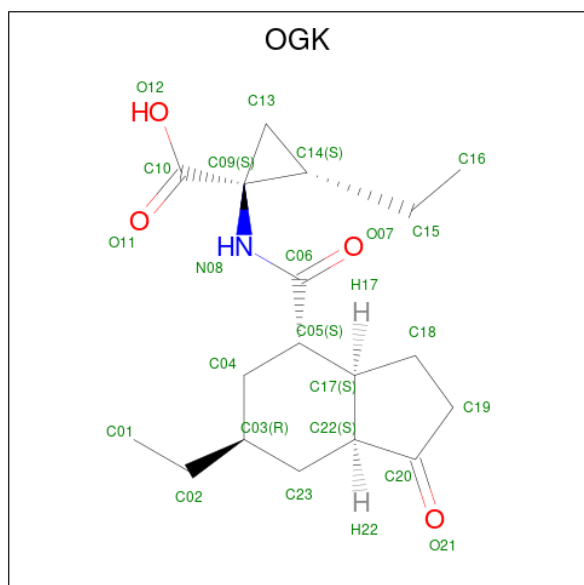
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	N	566	Total	C	N	O	S	0	0	0
			4521	2862	785	838	36			
2	P	566	Total	C	N	O	S	0	0	0
			4521	2862	785	838	36			

- Molecule 3 is a protein called JAZ1 incomplete degron peptide.

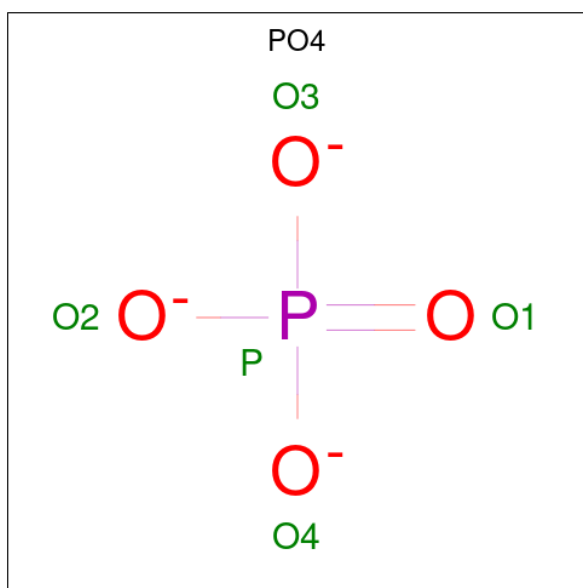
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	Q	13	Total	C	N	O	0	0	0
			119	74	29	16			
3	R	13	Total	C	N	O	0	0	0
			119	74	29	16			
3	S	13	Total	C	N	O	0	0	0
			119	74	29	16			
3	U	13	Total	C	N	O	0	0	0
			119	74	29	16			
3	V	13	Total	C	N	O	0	0	0
			119	74	29	16			
3	W	13	Total	C	N	O	0	0	0
			119	74	29	16			
3	X	13	Total	C	N	O	0	0	0
			119	74	29	16			

- Molecule 4 is (1S,2S)-2-ethyl-1-({[(3aS,4S,6R,7aS)-6-ethyl-1-oxooctahydro-1H-inden-4-yl]carbonyl}amino)cyclopropanecarboxylic acid (CCD ID: OGK) (formula: C₁₈H₂₇NO₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			23	18	1	4		
4	D	1	Total	C	N	O	0	0
			23	18	1	4		
4	F	1	Total	C	N	O	0	0
			23	18	1	4		
4	H	1	Total	C	N	O	0	0
			23	18	1	4		
4	J	1	Total	C	N	O	0	0
			23	18	1	4		
4	L	1	Total	C	N	O	0	0
			23	18	1	4		
4	N	1	Total	C	N	O	0	0
			23	18	1	4		
4	P	1	Total	C	N	O	0	0
			23	18	1	4		

- Molecule 5 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	O	P	0	0
			5	4	1		
5	B	1	Total	O	P	0	0
			5	4	1		
5	B	1	Total	O	P	0	0
			5	4	1		
5	B	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	O	P	0	0
			5	4	1		
5	D	1	Total	O	P	0	0
			5	4	1		
5	D	1	Total	O	P	0	0
			5	4	1		
5	D	1	Total	O	P	0	0
			5	4	1		
5	F	1	Total	O	P	0	0
			5	4	1		
5	F	1	Total	O	P	0	0
			5	4	1		
5	F	1	Total	O	P	0	0
			5	4	1		
5	F	1	Total	O	P	0	0
			5	4	1		
5	H	1	Total	O	P	0	0
			5	4	1		
5	H	1	Total	O	P	0	0
			5	4	1		
5	H	1	Total	O	P	0	0
			5	4	1		
5	H	1	Total	O	P	0	0
			5	4	1		
5	J	1	Total	O	P	0	0
			5	4	1		
5	J	1	Total	O	P	0	0
			5	4	1		
5	J	1	Total	O	P	0	0
			5	4	1		
5	J	1	Total	O	P	0	0
			5	4	1		
5	L	1	Total	O	P	0	0
			5	4	1		
5	L	1	Total	O	P	0	0
			5	4	1		
5	L	1	Total	O	P	0	0
			5	4	1		
5	L	1	Total	O	P	0	0
			5	4	1		
5	N	1	Total	O	P	0	0
			5	4	1		

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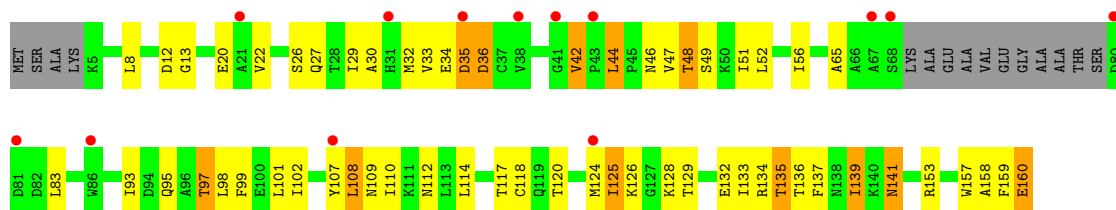
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	N	1	Total	O	P	0	0
			5	4	1		
5	N	1	Total	O	P	0	0
			5	4	1		
5	N	1	Total	O	P	0	0
			5	4	1		
5	P	1	Total	O	P	0	0
			5	4	1		
5	P	1	Total	O	P	0	0
			5	4	1		
5	P	1	Total	O	P	0	0
			5	4	1		
5	P	1	Total	O	P	0	0
			5	4	1		

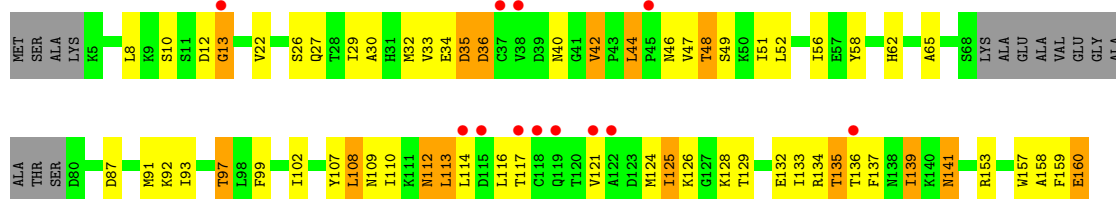
3 Residue-property plots [i](#)

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.

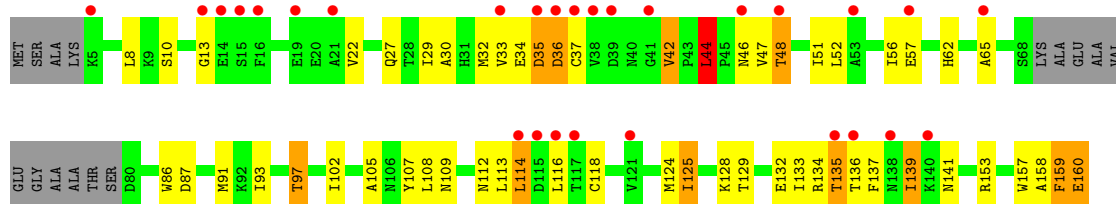
- Molecule 1: SKP1-like protein 1A



- Molecule 1: SKP1-like protein 1A

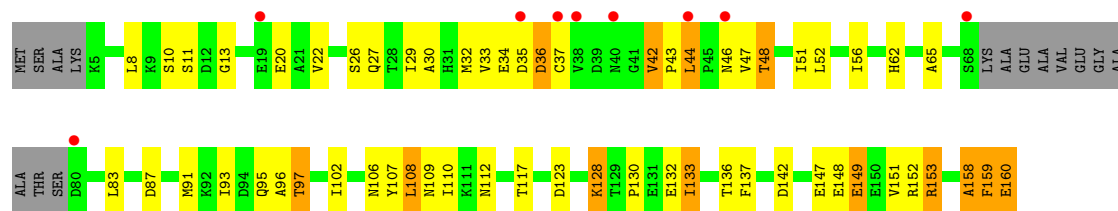


- Molecule 1: SKP1-like protein 1A

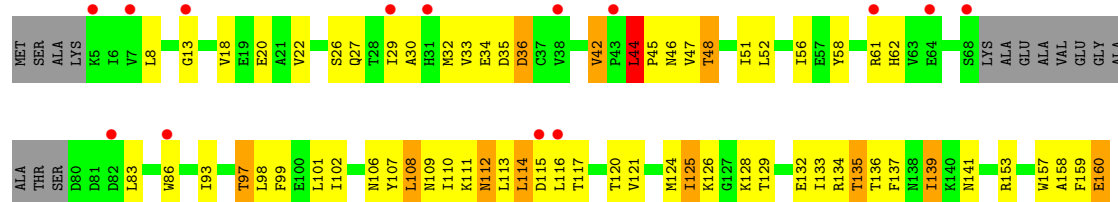


- Molecule 1: SKP1-like protein 1A

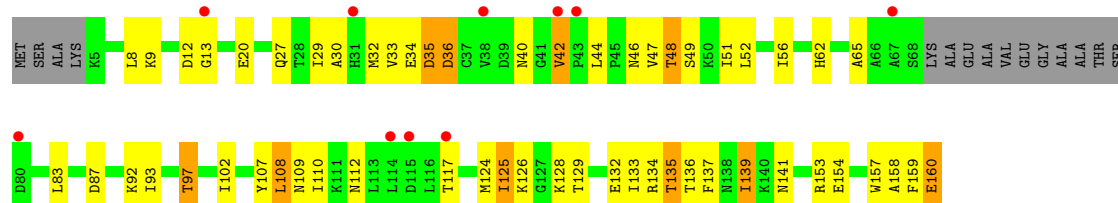




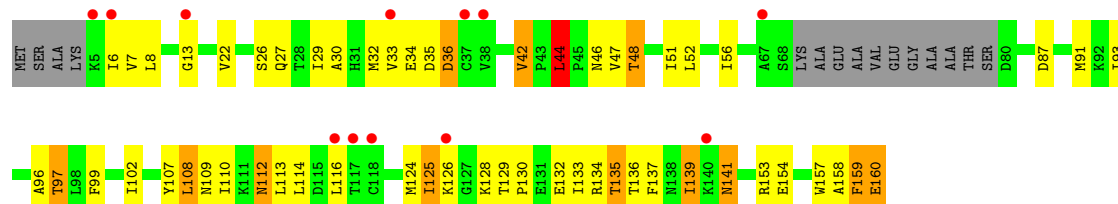
• Molecule 1: SKP1-like protein 1A



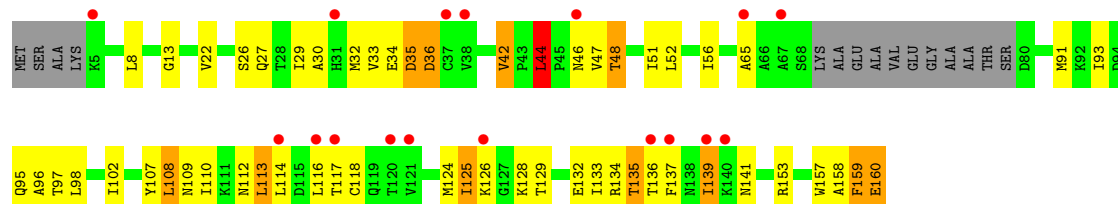
• Molecule 1: SKP1-like protein 1A



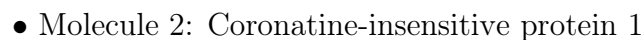
• Molecule 1: SKP1-like protein 1A

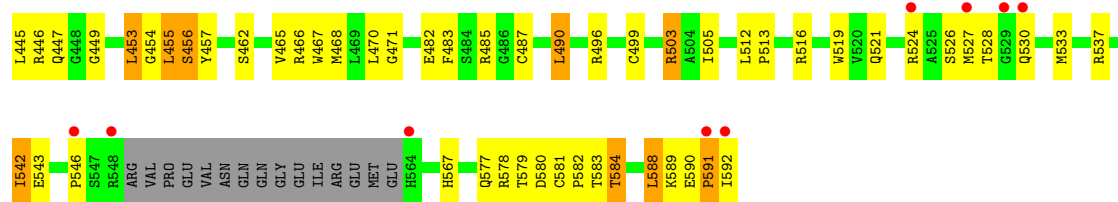


• Molecule 1: SKP1-like protein 1A

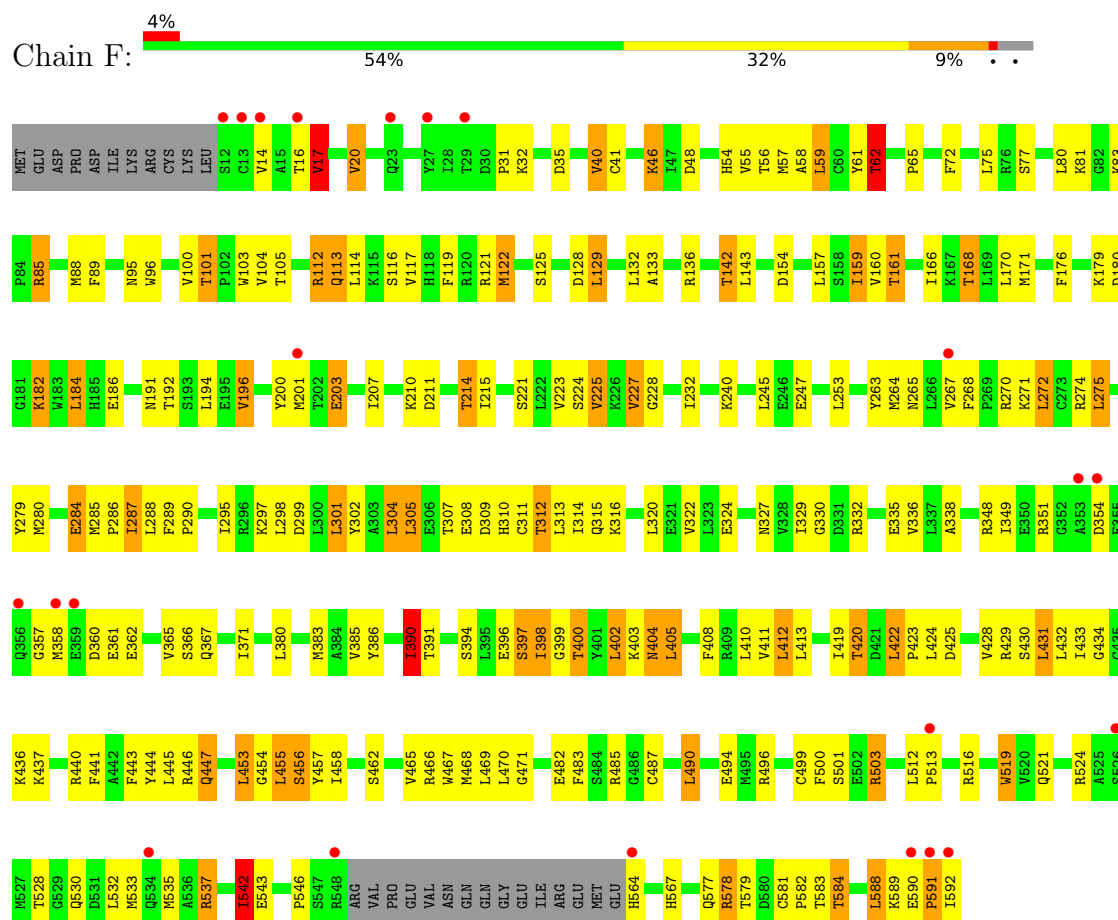


Chain B: 5% 57% 29% 8% ...



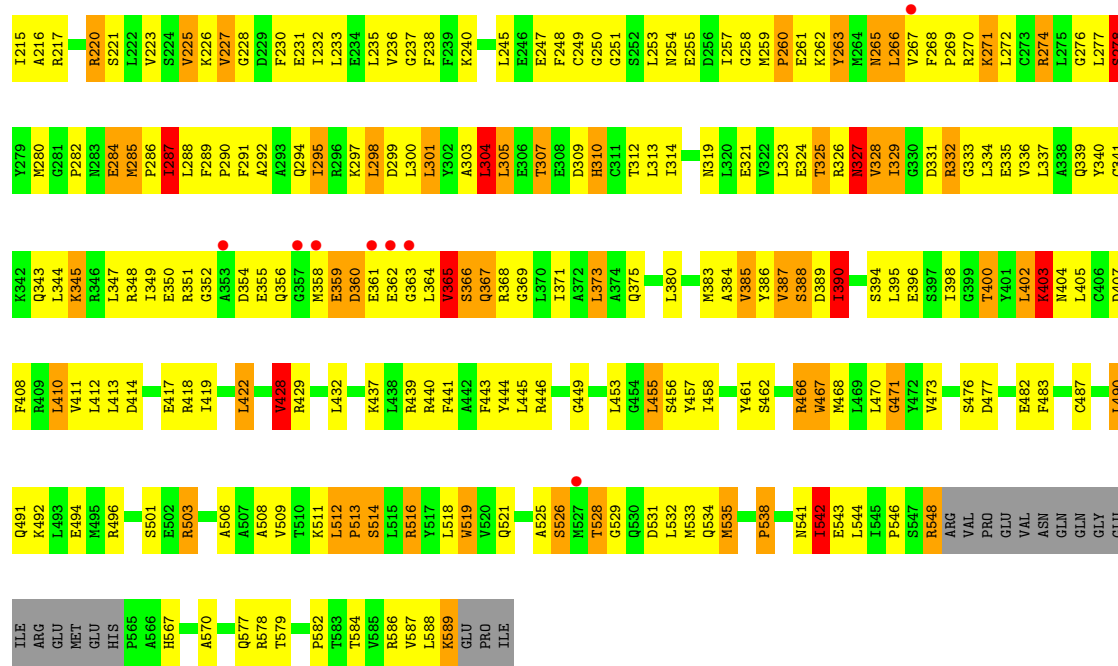


• Molecule 2: Coronatine-insensitive protein 1

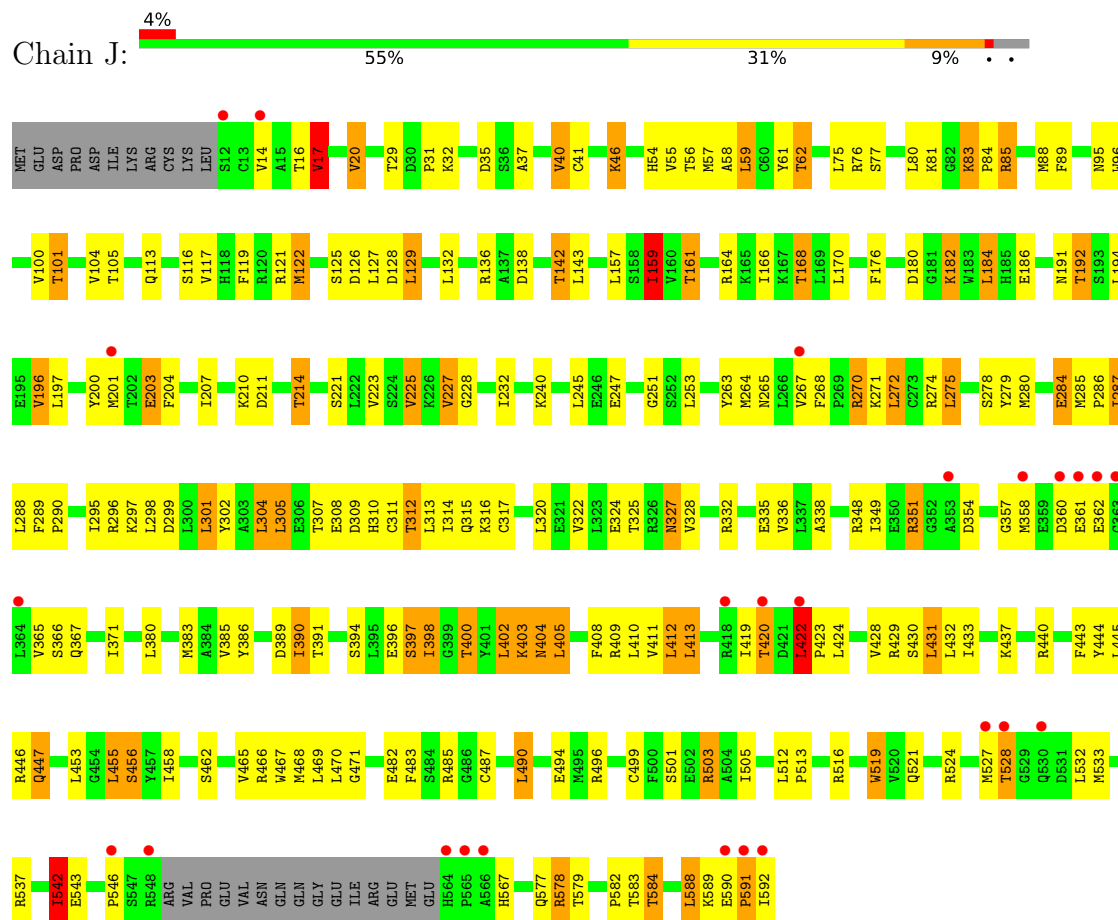


• Molecule 2: Coronatine-insensitive protein 1

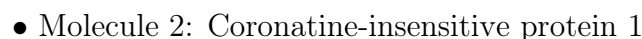


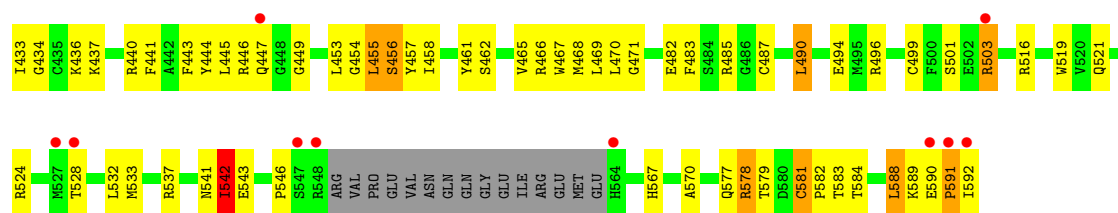


• Molecule 2: Coronatine-insensitive protein 1

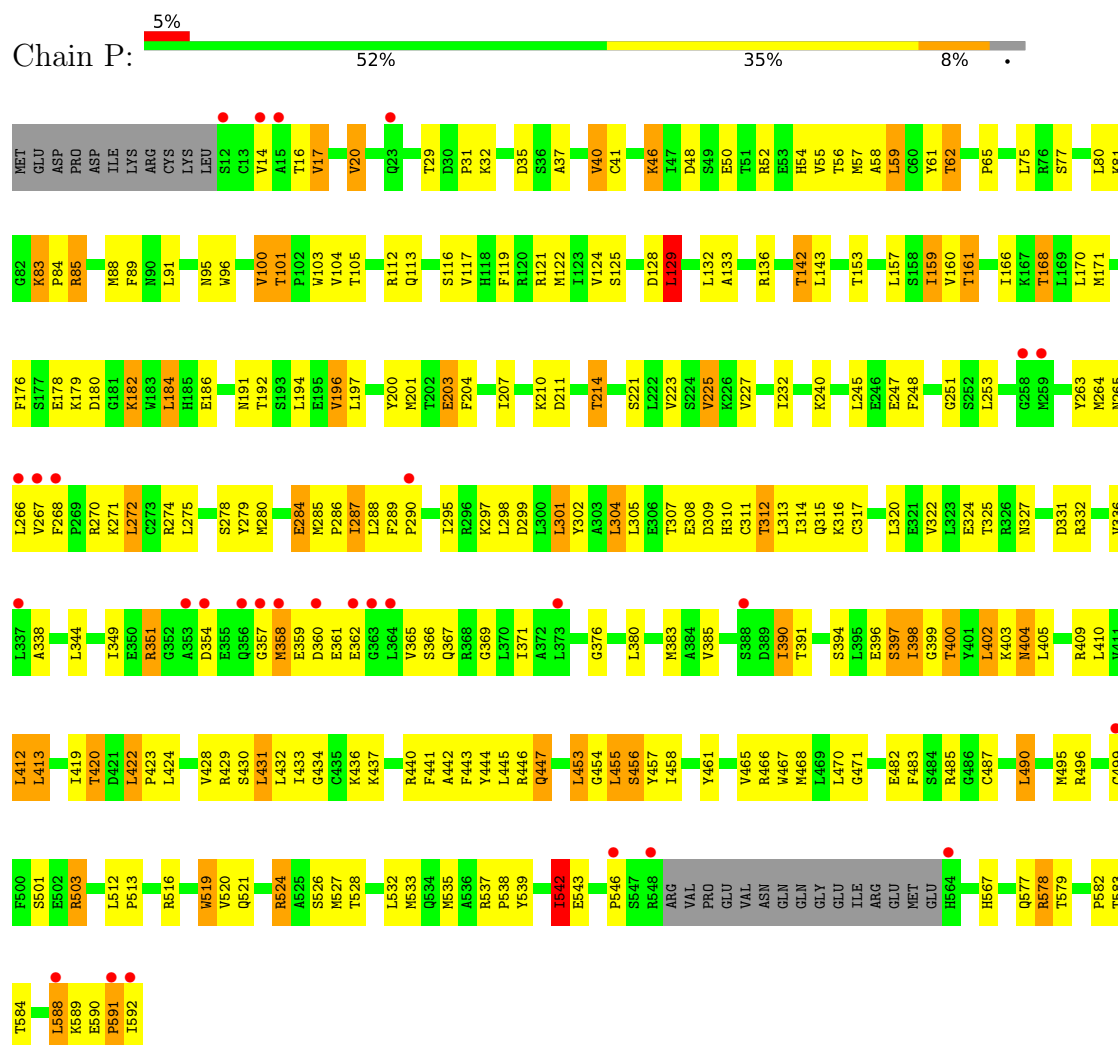


• Molecule 2: Coronatine-insensitive protein 1

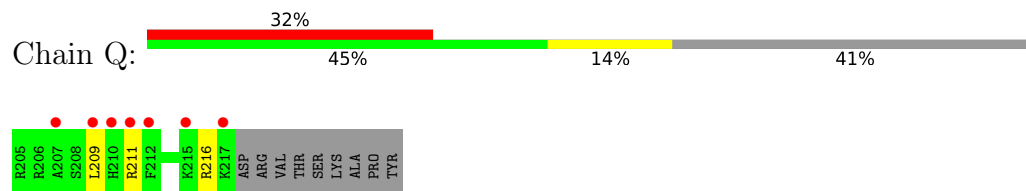




• Molecule 2: Coronatine-insensitive protein 1

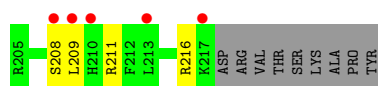


• Molecule 3: JAZ1 incomplete degron peptide

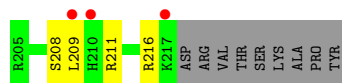


• Molecule 3: JAZ1 incomplete degron peptide

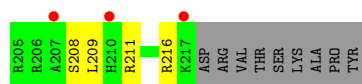




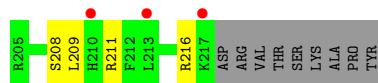
- Molecule 3: JAZ1 incomplete degron peptide



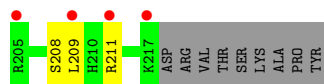
- Molecule 3: JAZ1 incomplete degron peptide



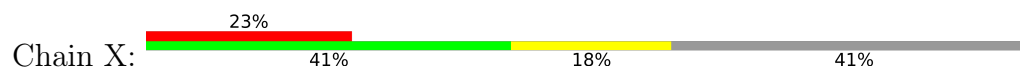
- Molecule 3: JAZ1 incomplete degron peptide



- Molecule 3: JAZ1 incomplete degron peptide



- Molecule 3: JAZ1 incomplete degron peptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	121.85Å 221.46Å 148.47Å 90.00° 104.49° 90.00°	Depositor
Resolution (Å)	49.63 – 2.80 49.63 – 2.80	Depositor EDS
% Data completeness (in resolution range)	93.7 (49.63-2.80) 93.7 (49.63-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 2.81Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.225 , 0.268 0.219 , 0.261	Depositor DCC
R_{free} test set	9332 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	46.6	Xtriage
Anisotropy	0.188	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 45.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	46526	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.31% 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: PO4, OGK

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	0.70	0/1168	0.91	1/1579 (0.1%)
1	C	0.81	3/1168 (0.3%)	0.96	5/1579 (0.3%)
1	E	0.85	2/1168 (0.2%)	1.01	7/1579 (0.4%)
1	G	0.81	0/1168	1.00	7/1579 (0.4%)
1	I	0.65	0/1168	0.94	3/1579 (0.2%)
1	K	0.65	0/1168	0.93	1/1579 (0.1%)
1	M	0.65	0/1168	0.93	3/1579 (0.2%)
1	O	0.72	0/1168	0.96	5/1579 (0.3%)
2	B	0.92	1/4603 (0.0%)	1.08	12/6212 (0.2%)
2	D	0.88	0/4603	1.07	15/6212 (0.2%)
2	F	0.80	1/4603 (0.0%)	1.08	14/6212 (0.2%)
2	H	0.94	2/4566 (0.0%)	1.31	39/6161 (0.6%)
2	J	0.79	1/4603 (0.0%)	1.09	16/6212 (0.3%)
2	L	0.75	1/4603 (0.0%)	1.05	13/6212 (0.2%)
2	N	0.81	1/4603 (0.0%)	1.10	17/6212 (0.3%)
2	P	0.77	1/4603 (0.0%)	1.07	7/6212 (0.1%)
3	Q	0.50	0/120	0.79	0/155
3	R	0.55	0/120	0.78	0/155
3	S	0.55	0/120	0.81	0/155
3	U	0.51	0/120	0.75	0/155
3	V	0.54	0/120	0.79	0/155
3	W	0.53	0/120	0.77	0/155
3	X	0.54	0/120	0.73	0/155
All	All	0.81	13/46971 (0.0%)	1.08	165/63362 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	H	0	1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	113	LEU	C-N	9.53	1.45	1.33
1	C	114	LEU	N-CA	8.69	1.57	1.46
1	E	113	LEU	C-N	-7.15	1.23	1.33
1	C	113	LEU	CA-C	6.81	1.62	1.52
2	F	542	ILE	CA-CB	6.63	1.62	1.54

The worst 5 of 165 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	449	GLY	N-CA-C	11.33	128.34	113.27
2	H	366	SER	N-CA-C	-9.66	96.23	110.23
2	H	458	ILE	CB-CA-C	-8.73	100.80	111.97
2	H	512	LEU	CA-C-N	8.57	130.55	119.84
2	H	512	LEU	C-N-CA	8.57	130.55	119.84

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	365	VAL	Peptide

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	1152	0	1122	46	0
1	C	1152	0	1122	60	0
1	E	1152	0	1122	48	0
1	G	1152	0	1122	57	0
1	I	1152	0	1122	58	2
1	K	1152	0	1122	53	0
1	M	1152	0	1122	67	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	O	1152	0	1122	51	0
2	B	4521	0	4564	182	0
2	D	4521	0	4564	215	2
2	F	4521	0	4564	204	0
2	H	4486	0	4534	373	0
2	J	4521	0	4564	202	0
2	L	4521	0	4564	204	0
2	N	4521	0	4564	230	0
2	P	4521	0	4564	205	0
3	Q	119	0	131	2	0
3	R	119	0	131	3	0
3	S	119	0	131	3	0
3	U	119	0	131	3	0
3	V	119	0	131	4	0
3	W	119	0	131	2	0
3	X	119	0	131	3	0
4	B	23	0	26	6	0
4	D	23	0	26	2	0
4	F	23	0	27	8	0
4	H	23	0	26	8	0
4	J	23	0	27	7	0
4	L	23	0	27	11	0
4	N	23	0	27	7	0
4	P	23	0	27	7	0
5	B	20	0	0	3	0
5	D	20	0	0	3	0
5	F	20	0	0	2	0
5	H	20	0	0	6	0
5	J	20	0	0	2	0
5	L	20	0	0	1	0
5	N	20	0	0	3	0
5	P	20	0	0	3	0
All	All	46526	0	46588	2115	2

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 23.

The worst 5 of 2115 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:168:THR:HB	2:H:196:VAL:HG13	1.34	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:305:LEU:HD23	2:H:305:LEU:H	1.24	1.01
1:M:102:ILE:HG21	2:N:20:VAL:HG22	1.43	1.00
2:H:364:LEU:HB3	2:H:365:VAL:HG22	1.41	1.00
2:B:444:TYR:HA	2:B:471:GLY:HA3	1.47	0.97

All (2) 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:D:429:ARG:NH2	1:I:61:ARG:NH1[2_555]	2.03	0.17
2:D:429:ARG:NH1	1:I:86:TRP:CE3[2_555]	2.06	0.14

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	141/160 (88%)	115 (82%)	21 (15%)	5 (4%)	3	10
1	C	141/160 (88%)	115 (82%)	21 (15%)	5 (4%)	3	10
1	E	141/160 (88%)	117 (83%)	21 (15%)	3 (2%)	5	20
1	G	141/160 (88%)	119 (84%)	18 (13%)	4 (3%)	4	14
1	I	141/160 (88%)	116 (82%)	21 (15%)	4 (3%)	4	14
1	K	141/160 (88%)	118 (84%)	19 (14%)	4 (3%)	4	14
1	M	141/160 (88%)	114 (81%)	22 (16%)	5 (4%)	3	10
1	O	141/160 (88%)	114 (81%)	23 (16%)	4 (3%)	4	14
2	B	562/592 (95%)	509 (91%)	44 (8%)	9 (2%)	7	27
2	D	562/592 (95%)	508 (90%)	44 (8%)	10 (2%)	6	23
2	F	562/592 (95%)	509 (91%)	44 (8%)	9 (2%)	7	27
2	H	558/592 (94%)	475 (85%)	63 (11%)	20 (4%)	2	10

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	J	562/592 (95%)	508 (90%)	44 (8%)	10 (2%)	6	23
2	L	562/592 (95%)	508 (90%)	46 (8%)	8 (1%)	9	30
2	N	562/592 (95%)	505 (90%)	49 (9%)	8 (1%)	9	30
2	P	562/592 (95%)	503 (90%)	49 (9%)	10 (2%)	6	23
3	Q	11/22 (50%)	10 (91%)	1 (9%)	0	100	100
3	R	11/22 (50%)	10 (91%)	1 (9%)	0	100	100
3	S	11/22 (50%)	9 (82%)	2 (18%)	0	100	100
3	U	11/22 (50%)	10 (91%)	1 (9%)	0	100	100
3	V	11/22 (50%)	10 (91%)	1 (9%)	0	100	100
3	W	11/22 (50%)	10 (91%)	1 (9%)	0	100	100
3	X	11/22 (50%)	10 (91%)	1 (9%)	0	100	100
All	All	5697/6170 (92%)	5022 (88%)	557 (10%)	118 (2%)	5	20

5 of 118 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	271	LYS
2	B	404	ASN
2	B	420	THR
2	D	271	LYS
2	D	420	THR

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	128/137 (93%)	116 (91%)	12 (9%)	8	27
1	C	128/137 (93%)	115 (90%)	13 (10%)	7	23
1	E	128/137 (93%)	115 (90%)	13 (10%)	7	23
1	G	128/137 (93%)	117 (91%)	11 (9%)	10	31
1	I	128/137 (93%)	117 (91%)	11 (9%)	10	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	128/137 (93%)	117 (91%)	11 (9%)	10	31
1	M	128/137 (93%)	117 (91%)	11 (9%)	10	31
1	O	128/137 (93%)	117 (91%)	11 (9%)	10	31
2	B	498/523 (95%)	420 (84%)	78 (16%)	2	9
2	D	498/523 (95%)	421 (84%)	77 (16%)	2	9
2	F	498/523 (95%)	418 (84%)	80 (16%)	2	8
2	H	494/523 (94%)	396 (80%)	98 (20%)	1	5
2	J	498/523 (95%)	422 (85%)	76 (15%)	3	10
2	L	498/523 (95%)	423 (85%)	75 (15%)	3	10
2	N	498/523 (95%)	425 (85%)	73 (15%)	3	10
2	P	498/523 (95%)	423 (85%)	75 (15%)	3	10
3	Q	12/20 (60%)	11 (92%)	1 (8%)	10	32
3	R	12/20 (60%)	11 (92%)	1 (8%)	10	32
3	S	12/20 (60%)	11 (92%)	1 (8%)	10	32
3	U	12/20 (60%)	11 (92%)	1 (8%)	10	32
3	V	12/20 (60%)	11 (92%)	1 (8%)	10	32
3	W	12/20 (60%)	11 (92%)	1 (8%)	10	32
3	X	12/20 (60%)	11 (92%)	1 (8%)	10	32
All	All	5088/5420 (94%)	4356 (86%)	732 (14%)	3	11

5 of 732 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	J	519	TRP
2	N	17	VAL
1	K	47	VAL
2	J	516	ARG
2	L	287	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 117 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	460	GLN
2	P	310	HIS
2	J	426	ASN

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Mol	Chain	Res	Type
2	P	191	ASN
2	N	343	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

40 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$
5	PO4	H	1101	-	4,4,4	4.42	4 (100%)	6,6,6	1.25	1 (16%)
5	PO4	D	1102	-	4,4,4	4.55	4 (100%)	6,6,6	0.60	0
5	PO4	L	1101	-	4,4,4	4.27	4 (100%)	6,6,6	1.58	1 (16%)
5	PO4	L	1103	-	4,4,4	4.52	4 (100%)	6,6,6	0.86	0
5	PO4	J	1103	-	4,4,4	4.19	4 (100%)	6,6,6	1.03	0
5	PO4	B	1103	-	4,4,4	4.25	3 (75%)	6,6,6	1.58	2 (33%)
5	PO4	J	1101	-	4,4,4	4.52	4 (100%)	6,6,6	0.83	0
5	PO4	N	1104	-	4,4,4	4.51	4 (100%)	6,6,6	0.87	0
5	PO4	D	1101	-	4,4,4	4.29	4 (100%)	6,6,6	1.21	1 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	PO4	N	1102	-	4,4,4	4.43	4 (100%)	6,6,6	0.54	0
5	PO4	D	1103	-	4,4,4	4.09	4 (100%)	6,6,6	0.99	0
5	PO4	L	1104	-	4,4,4	4.42	4 (100%)	6,6,6	0.61	0
5	PO4	P	1103	-	4,4,4	4.42	4 (100%)	6,6,6	1.10	0
5	PO4	F	1102	-	4,4,4	4.58	4 (100%)	6,6,6	0.60	0
5	PO4	N	1103	-	4,4,4	4.34	4 (100%)	6,6,6	1.04	0
4	OGK	L	1100	-	25,25,25	6.93	12 (48%)	31,38,38	3.02	16 (51%)
5	PO4	H	1104	-	4,4,4	4.38	3 (75%)	6,6,6	2.27	3 (50%)
4	OGK	J	1100	-	25,25,25	6.65	10 (40%)	31,38,38	2.73	14 (45%)
5	PO4	L	1102	-	4,4,4	4.47	4 (100%)	6,6,6	0.63	0
5	PO4	F	1101	-	4,4,4	4.38	4 (100%)	6,6,6	1.63	1 (16%)
5	PO4	H	1103	-	4,4,4	4.52	4 (100%)	6,6,6	0.54	0
5	PO4	N	1101	-	4,4,4	4.37	4 (100%)	6,6,6	1.26	1 (16%)
5	PO4	F	1103	-	4,4,4	4.33	4 (100%)	6,6,6	1.00	0
5	PO4	J	1104	-	4,4,4	4.29	4 (100%)	6,6,6	0.85	0
4	OGK	F	1100	-	25,25,25	6.91	10 (40%)	31,38,38	2.53	16 (51%)
5	PO4	P	1104	-	4,4,4	4.95	3 (75%)	6,6,6	1.37	1 (16%)
5	PO4	B	1104	-	4,4,4	4.17	4 (100%)	6,6,6	1.26	1 (16%)
4	OGK	B	1100	-	25,25,25	6.83	11 (44%)	31,38,38	2.78	12 (38%)
5	PO4	F	1104	-	4,4,4	4.61	4 (100%)	6,6,6	1.40	1 (16%)
5	PO4	P	1101	-	4,4,4	4.30	4 (100%)	6,6,6	0.88	0
4	OGK	H	1100	-	25,25,25	6.82	11 (44%)	31,38,38	2.54	15 (48%)
5	PO4	H	1102	-	4,4,4	4.75	4 (100%)	6,6,6	0.70	0
4	OGK	N	1100	-	25,25,25	6.87	11 (44%)	31,38,38	2.51	10 (32%)
5	PO4	B	1102	-	4,4,4	4.53	4 (100%)	6,6,6	0.48	0
5	PO4	D	1104	-	4,4,4	4.29	4 (100%)	6,6,6	1.43	1 (16%)
4	OGK	P	1100	-	25,25,25	7.01	11 (44%)	31,38,38	2.84	13 (41%)
4	OGK	D	1100	-	25,25,25	6.78	10 (40%)	31,38,38	3.12	13 (41%)
5	PO4	P	1102	-	4,4,4	4.52	4 (100%)	6,6,6	0.66	0
5	PO4	B	1101	-	4,4,4	4.32	4 (100%)	6,6,6	0.89	0
5	PO4	J	1102	-	4,4,4	4.59	4 (100%)	6,6,6	0.77	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	OGK	H	1100	-	1/1/9/10	9/19/52/52	0/3/3/3
4	OGK	F	1100	-	-	12/19/52/52	0/3/3/3
4	OGK	N	1100	-	-	7/19/52/52	0/3/3/3
4	OGK	P	1100	-	-	12/19/52/52	0/3/3/3
4	OGK	D	1100	-	1/1/9/10	7/19/52/52	0/3/3/3
4	OGK	L	1100	-	1/1/9/10	11/19/52/52	0/3/3/3
4	OGK	J	1100	-	-	5/19/52/52	0/3/3/3
4	OGK	B	1100	-	1/1/9/10	8/19/52/52	0/3/3/3

The worst 5 of 211 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1100	OGK	C13-C09	-22.91	1.27	1.51
4	P	1100	OGK	C13-C09	-22.58	1.27	1.51
4	L	1100	OGK	C13-C09	-22.33	1.28	1.51
4	F	1100	OGK	C13-C09	-22.09	1.28	1.51
4	H	1100	OGK	C13-C09	-22.01	1.28	1.51

The worst 5 of 123 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1100	OGK	C14-C09-C10	7.72	134.32	117.69
4	P	1100	OGK	C13-C09-N08	-7.40	108.01	117.77
4	B	1100	OGK	C04-C05-C17	7.22	123.99	110.06
4	D	1100	OGK	C13-C14-C09	-6.88	56.76	60.30
4	L	1100	OGK	C05-C04-C03	6.79	123.03	109.20

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	B	1100	OGK	C05
4	D	1100	OGK	C05
4	H	1100	OGK	C03
4	L	1100	OGK	C05

5 of 71 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1100	OGK	C01-C02-C03-C04
4	B	1100	OGK	C01-C02-C03-C23
4	B	1100	OGK	C17-C05-C06-O07

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Mol	Chain	Res	Type	Atoms
4	B	1100	OGK	C17-C05-C06-N08
4	B	1100	OGK	N08-C09-C10-O12

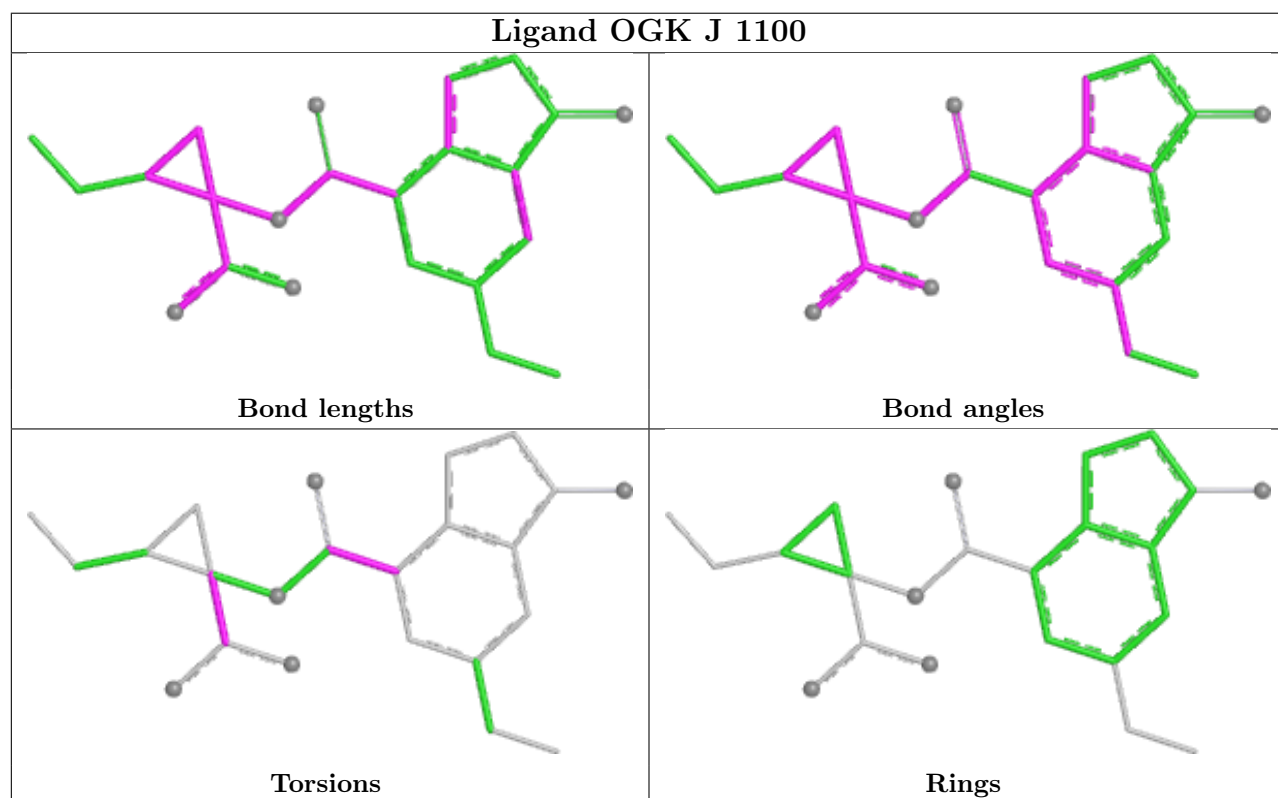
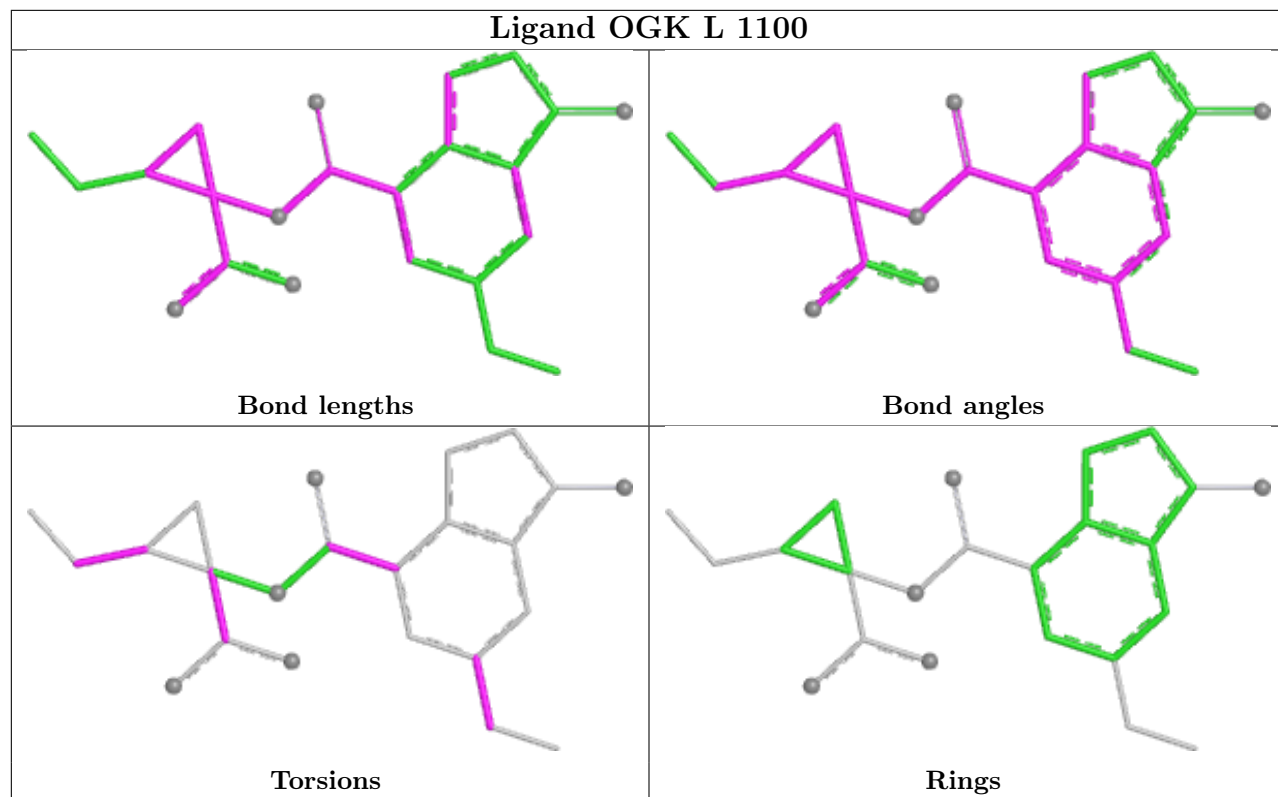
There are no ring outliers.

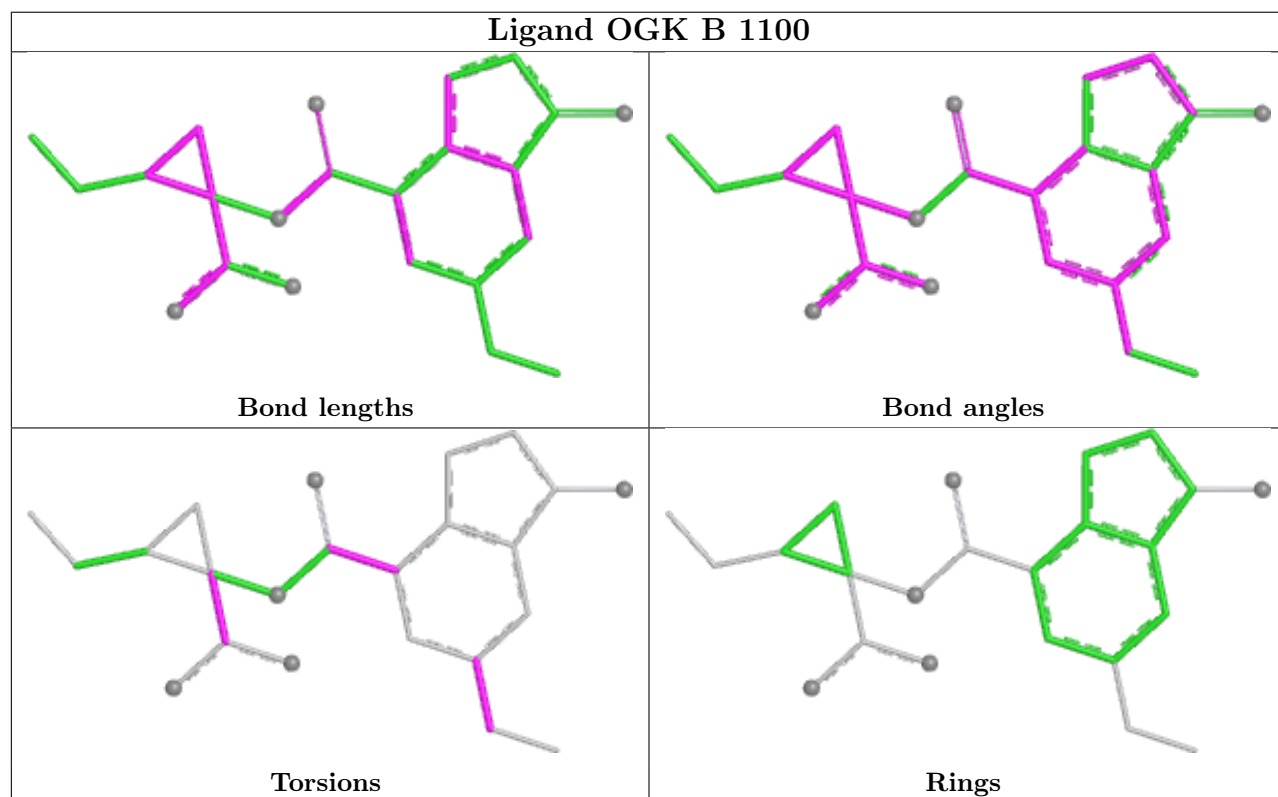
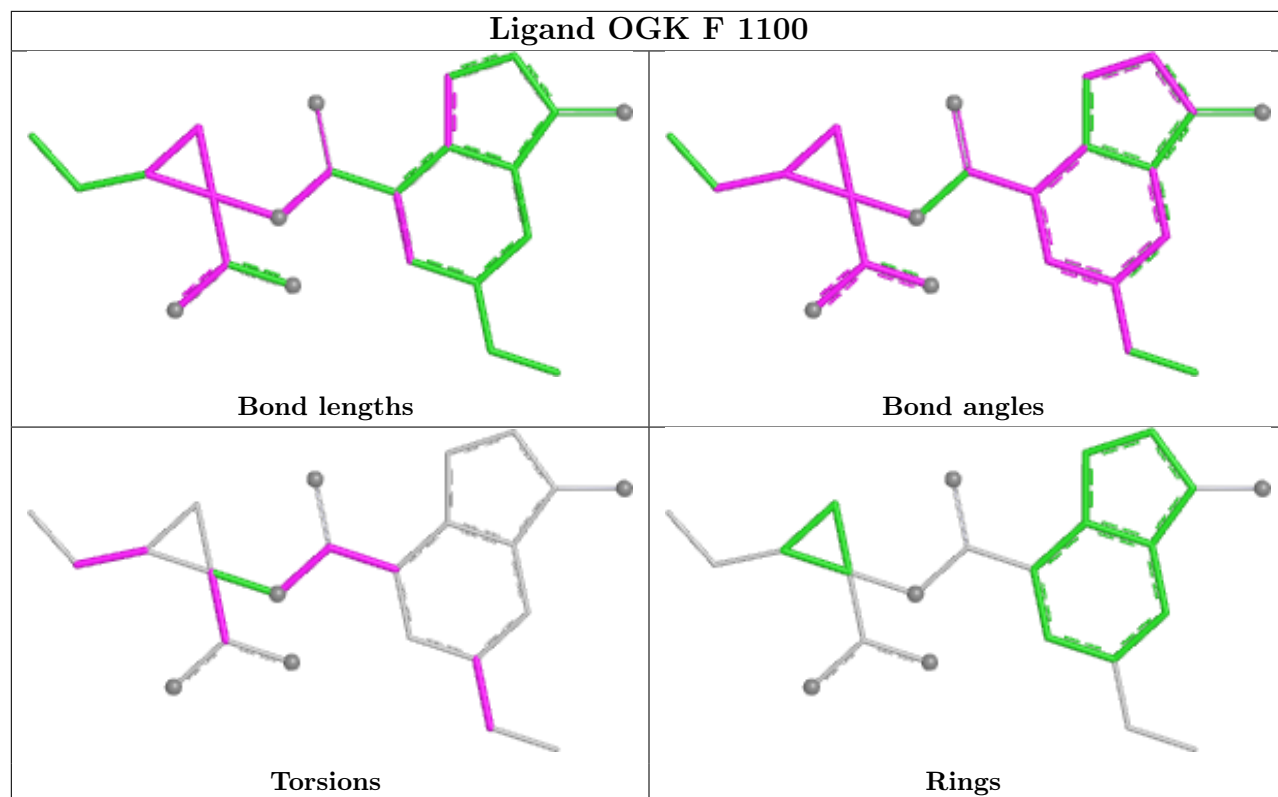
23 monomers are involved in 79 short contacts:

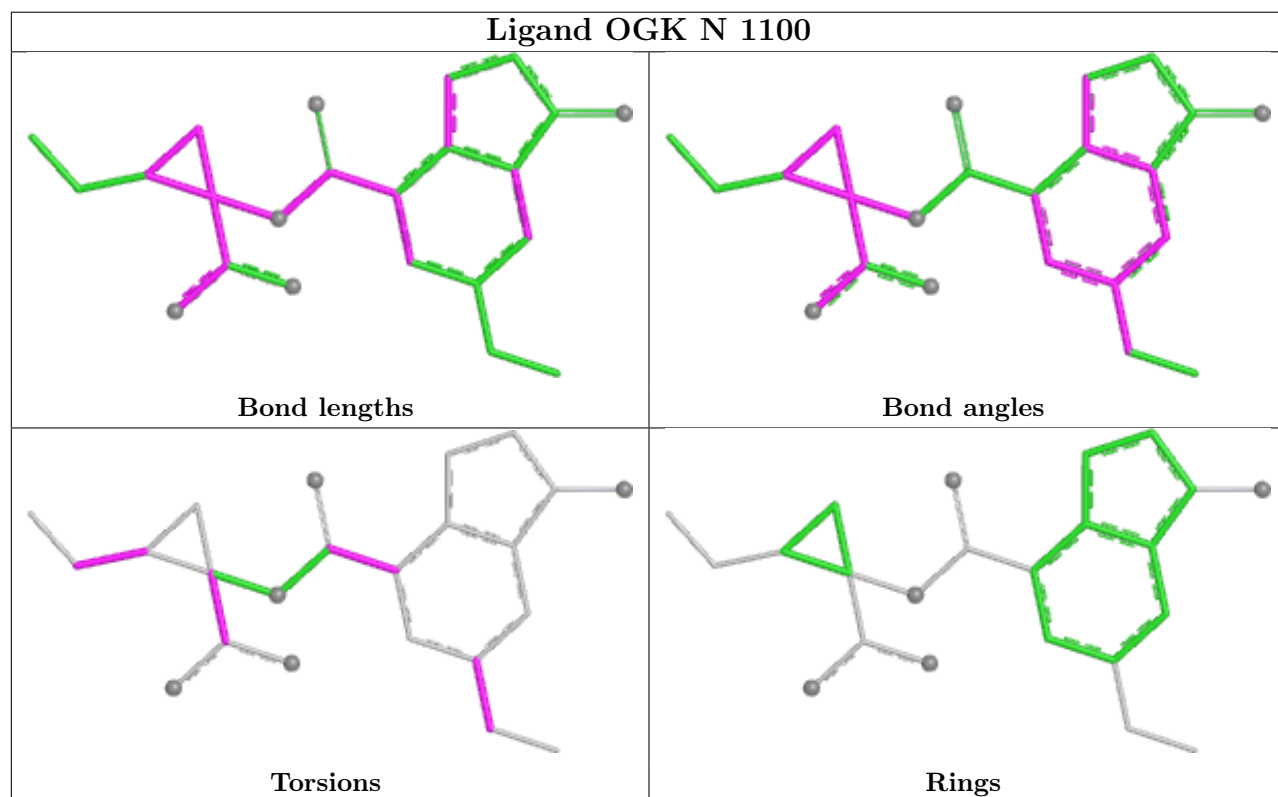
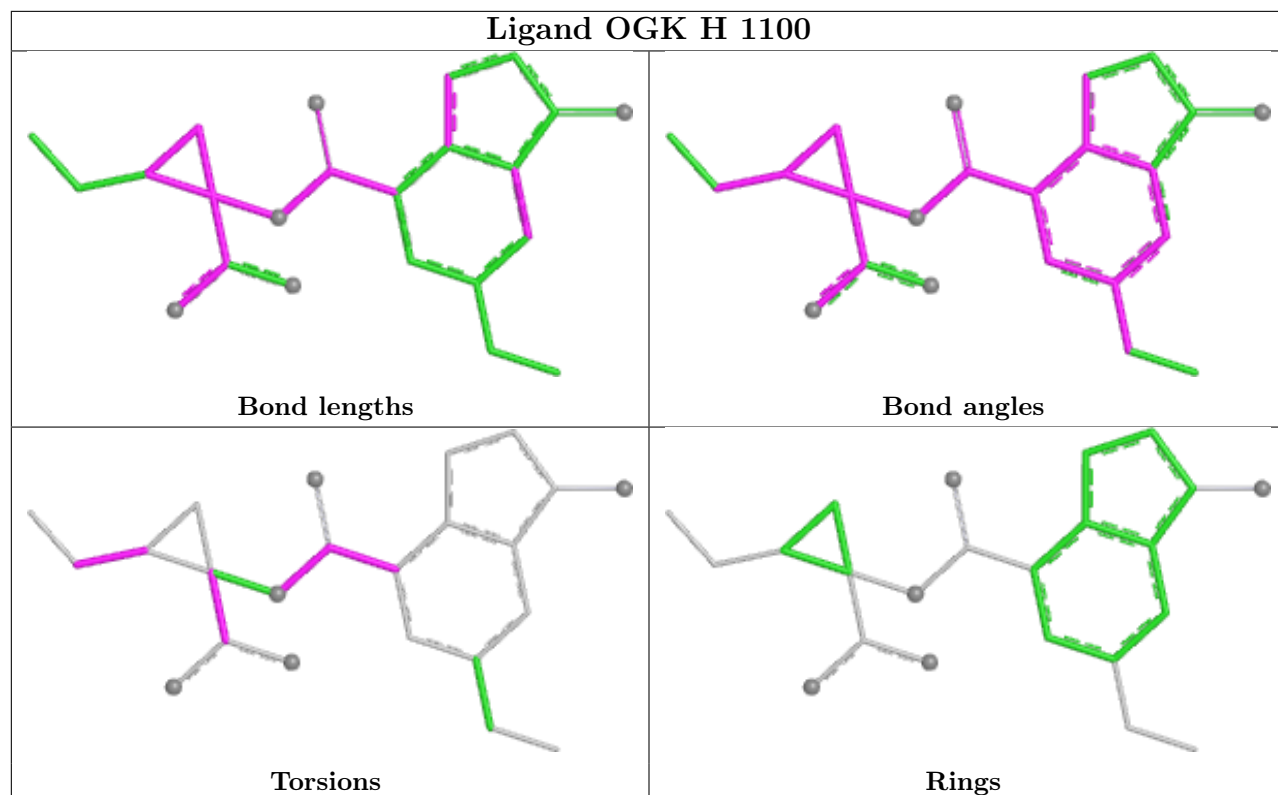
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	H	1101	PO4	2	0
5	L	1103	PO4	1	0
5	J	1103	PO4	2	0
5	B	1103	PO4	2	0
5	D	1101	PO4	1	0
5	D	1103	PO4	2	0
5	P	1103	PO4	2	0
5	N	1103	PO4	2	0
4	L	1100	OGK	11	0
5	H	1104	PO4	1	0
4	J	1100	OGK	7	0
5	F	1101	PO4	1	0
5	H	1103	PO4	4	0
5	N	1101	PO4	1	0
5	F	1103	PO4	1	0
4	F	1100	OGK	8	0
4	B	1100	OGK	6	0
5	P	1101	PO4	1	0
4	H	1100	OGK	8	0
4	N	1100	OGK	7	0
4	P	1100	OGK	7	0
4	D	1100	OGK	2	0
5	B	1101	PO4	1	0

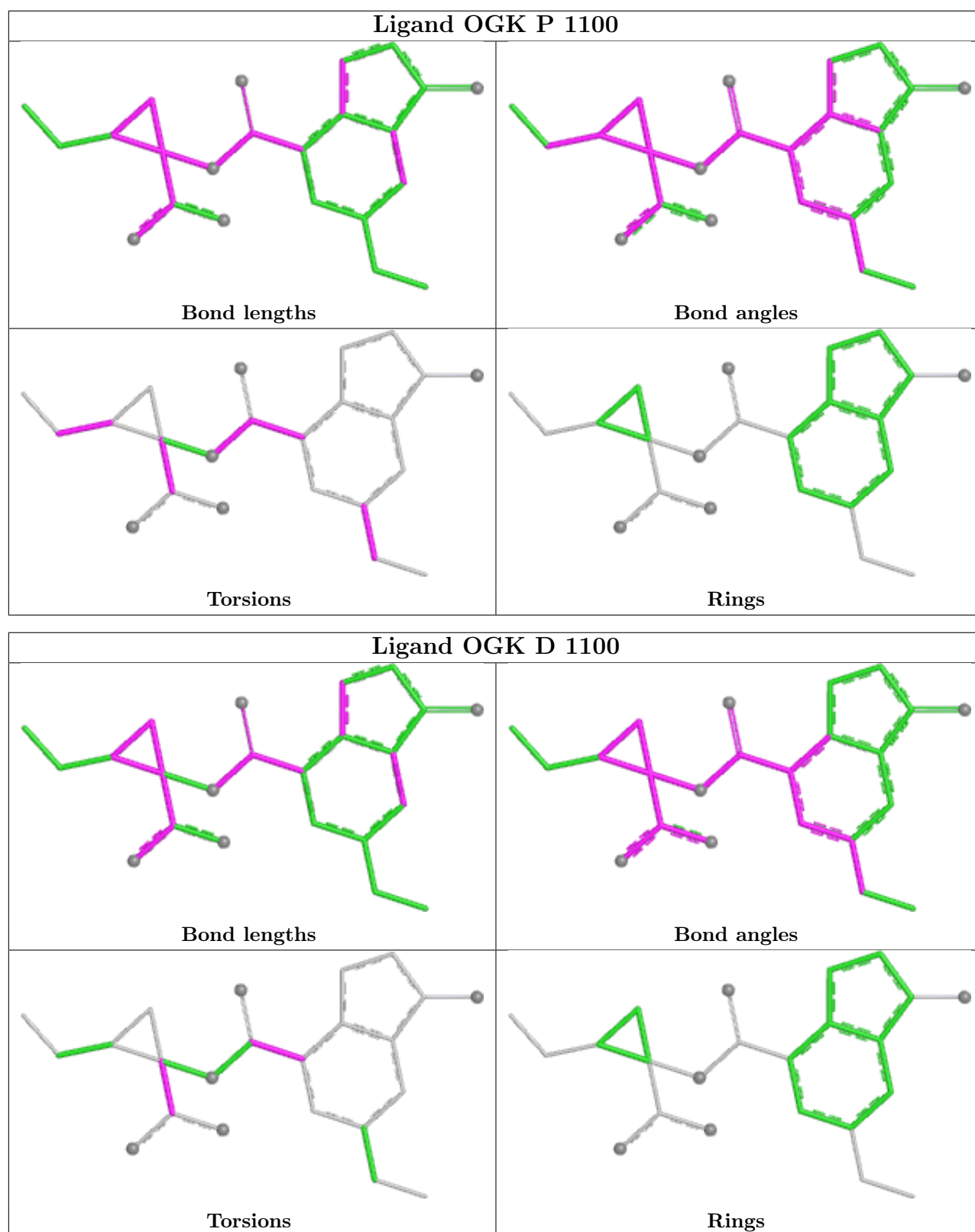
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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(Å²)	Q<0.9
1	A	145/160 (90%)	0.79	13 (8%)	15	11	27, 72, 133, 163	0
1	C	145/160 (90%)	0.88	12 (8%)	17	12	26, 75, 134, 163	0
1	E	145/160 (90%)	1.10	28 (19%)	3	2	28, 70, 133, 161	0
1	G	145/160 (90%)	0.39	9 (6%)	26	20	27, 66, 134, 161	0
1	I	145/160 (90%)	0.89	14 (9%)	13	10	29, 73, 134, 163	0
1	K	145/160 (90%)	0.60	10 (6%)	23	16	28, 75, 134, 165	0
1	M	145/160 (90%)	0.80	12 (8%)	17	12	32, 75, 133, 162	0
1	O	145/160 (90%)	0.95	17 (11%)	9	7	32, 76, 134, 164	0
2	B	566/592 (95%)	0.18	29 (5%)	33	25	21, 45, 107, 175	0
2	D	566/592 (95%)	0.16	31 (5%)	30	23	21, 46, 110, 176	0
2	F	566/592 (95%)	0.05	22 (3%)	43	34	20, 49, 111, 177	0
2	H	562/592 (94%)	-0.51	8 (1%)	73	64	19, 38, 91, 171	0
2	J	566/592 (95%)	0.05	25 (4%)	39	31	22, 49, 110, 177	0
2	L	566/592 (95%)	-0.03	18 (3%)	50	40	21, 50, 111, 176	0
2	N	566/592 (95%)	0.55	30 (5%)	32	24	24, 53, 112, 178	0
2	P	566/592 (95%)	0.44	29 (5%)	33	25	23, 54, 114, 176	0
3	Q	13/22 (59%)	2.11	7 (53%)	0	0	79, 102, 125, 126	0
3	R	13/22 (59%)	1.97	5 (38%)	1	0	86, 109, 128, 129	0
3	S	13/22 (59%)	1.51	3 (23%)	2	1	89, 108, 129, 131	0
3	U	13/22 (59%)	1.71	3 (23%)	2	1	87, 111, 128, 130	0
3	V	13/22 (59%)	1.50	3 (23%)	2	1	88, 111, 128, 128	0
3	W	13/22 (59%)	1.53	4 (30%)	1	1	88, 111, 128, 129	0
3	X	13/22 (59%)	1.89	5 (38%)	1	0	89, 110, 128, 129	0
All	All	5775/6170 (93%)	0.27	337 (5%)	29	22	19, 53, 119, 178	0

The worst 5 of 337 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	118	CYS	6.7
2	D	429	ARG	5.0
2	P	267	VAL	4.8
2	F	14	VAL	4.8
2	L	14	VAL	4.6

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($\text{\AA}^2$)	Q<0.9
5	PO4	P	1102	5/5	0.70	0.20	70,91,121,132	0
5	PO4	H	1102	5/5	0.73	0.17	58,70,91,138	0
5	PO4	F	1102	5/5	0.79	0.17	67,80,101,127	0
5	PO4	J	1102	5/5	0.82	0.16	54,71,85,106	0
5	PO4	N	1102	5/5	0.85	0.14	78,89,102,114	0
5	PO4	D	1102	5/5	0.87	0.13	48,60,103,128	0
5	PO4	H	1101	5/5	0.87	0.09	65,65,83,99	0
5	PO4	L	1102	5/5	0.88	0.11	56,67,112,139	0
5	PO4	P	1104	5/5	0.89	0.10	30,51,77,101	0
5	PO4	L	1104	5/5	0.90	0.09	54,54,85,104	0
5	PO4	N	1104	5/5	0.91	0.08	32,59,102,105	0
4	OGK	N	1100	23/23	0.91	0.11	33,54,73,77	0
5	PO4	B	1102	5/5	0.91	0.11	51,71,81,85	0
5	PO4	D	1104	5/5	0.92	0.09	32,38,82,83	0
5	PO4	N	1101	5/5	0.93	0.07	47,54,57,87	0
5	PO4	L	1101	5/5	0.93	0.09	34,39,58,68	0
5	PO4	N	1103	5/5	0.93	0.09	40,60,78,102	0

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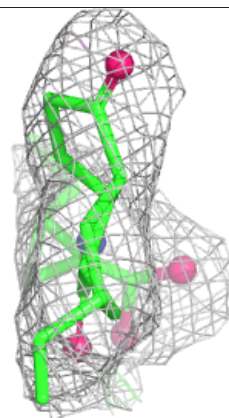
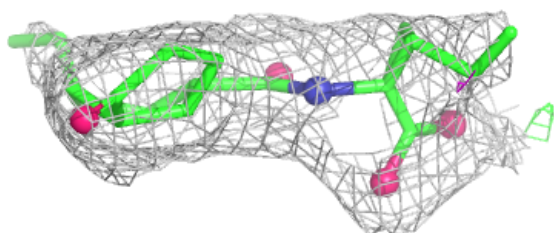
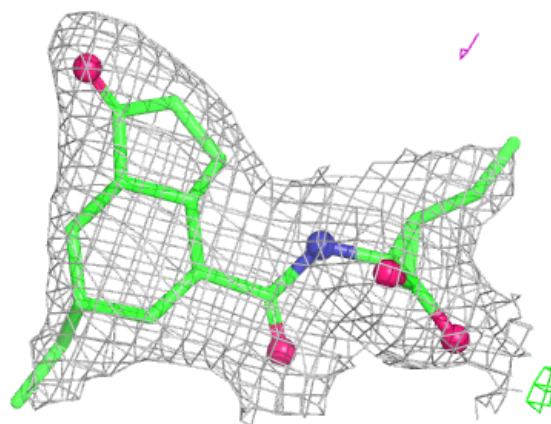
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	PO4	H	1104	5/5	0.94	0.06	23,27,62,87	0
5	PO4	J	1101	5/5	0.94	0.09	42,53,62,65	0
4	OGK	H	1100	23/23	0.94	0.08	23,41,56,62	0
5	PO4	P	1103	5/5	0.94	0.07	55,56,64,76	0
4	OGK	P	1100	23/23	0.94	0.09	40,52,64,68	0
5	PO4	F	1104	5/5	0.95	0.08	28,33,60,69	0
5	PO4	H	1103	5/5	0.95	0.07	45,60,71,83	0
4	OGK	J	1100	23/23	0.95	0.09	24,36,51,65	0
4	OGK	F	1100	23/23	0.96	0.08	23,41,50,70	0
5	PO4	B	1104	5/5	0.96	0.08	23,44,66,67	0
5	PO4	P	1101	5/5	0.96	0.06	47,50,65,73	0
4	OGK	L	1100	23/23	0.96	0.08	31,43,62,67	0
5	PO4	B	1101	5/5	0.96	0.08	31,37,44,44	0
5	PO4	J	1104	5/5	0.96	0.07	44,46,72,76	0
5	PO4	L	1103	5/5	0.97	0.06	31,41,62,72	0
4	OGK	D	1100	23/23	0.97	0.06	24,32,41,45	0
5	PO4	F	1103	5/5	0.97	0.06	32,36,48,80	0
5	PO4	D	1101	5/5	0.97	0.07	29,32,43,57	0
5	PO4	F	1101	5/5	0.97	0.08	25,37,47,70	0
5	PO4	B	1103	5/5	0.98	0.05	23,25,30,45	0
4	OGK	B	1100	23/23	0.98	0.06	14,26,38,48	0
5	PO4	D	1103	5/5	0.98	0.06	28,30,38,79	0
5	PO4	J	1103	5/5	0.99	0.04	34,39,48,64	0

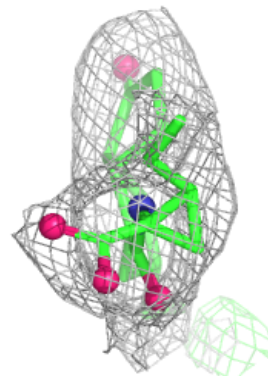
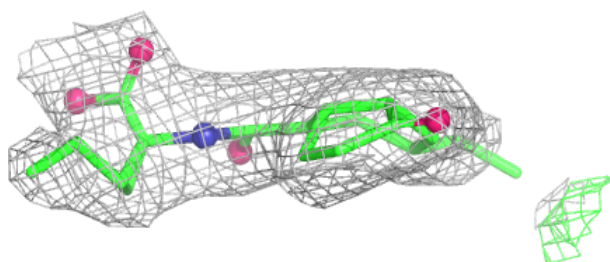
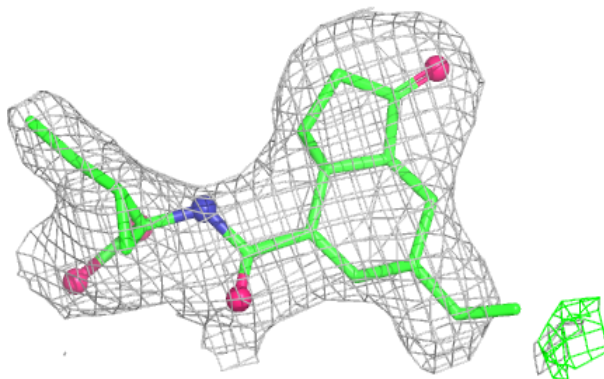
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around OGK N 1100:

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

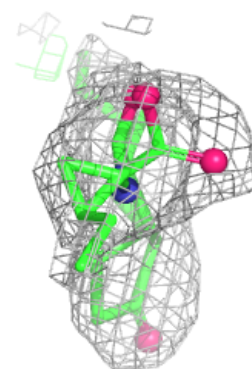
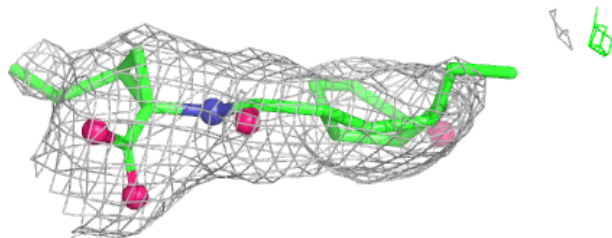
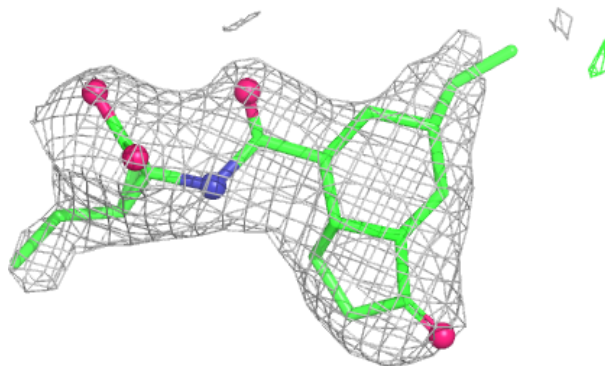
**Electron density around OGK H 1100:**

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

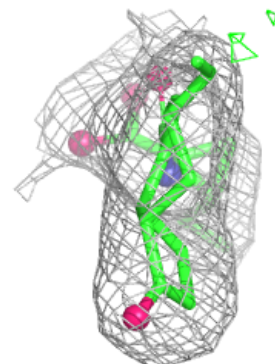
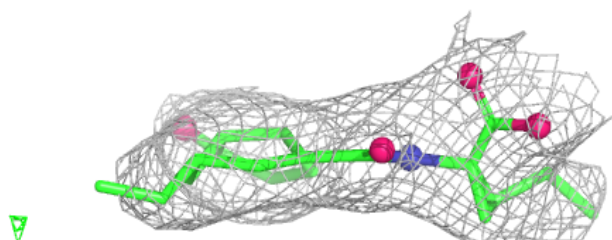
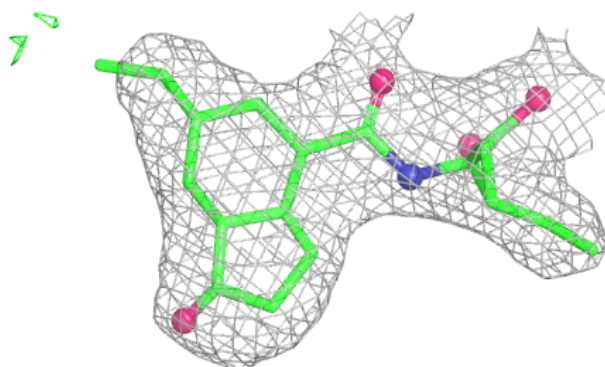


Electron density around OGK P 1100:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

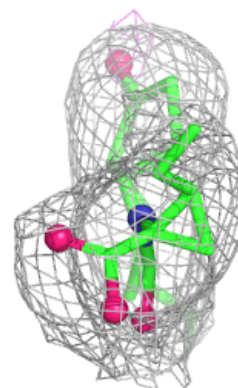
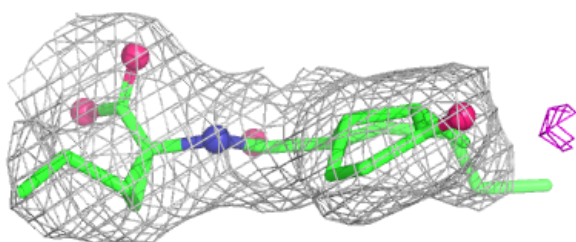
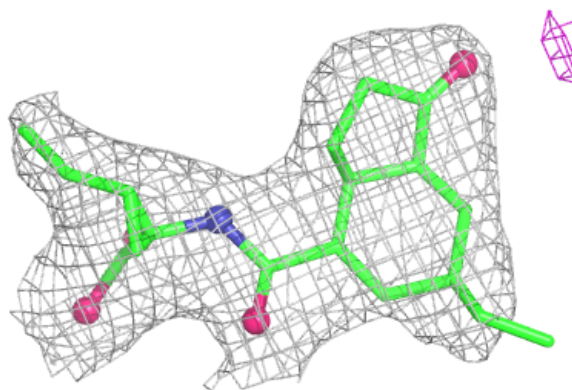
**Electron density around OGK J 1100:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

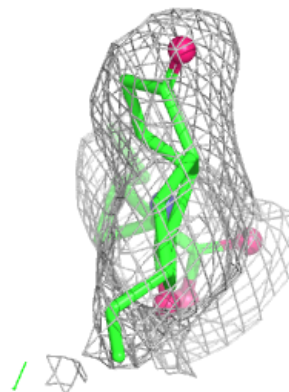
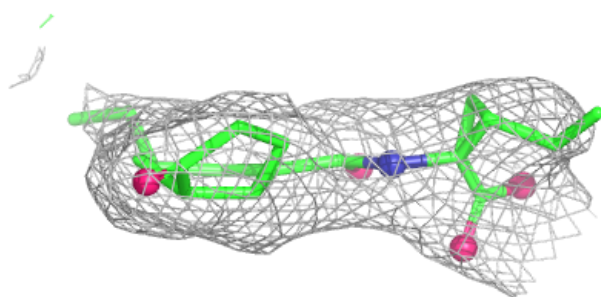
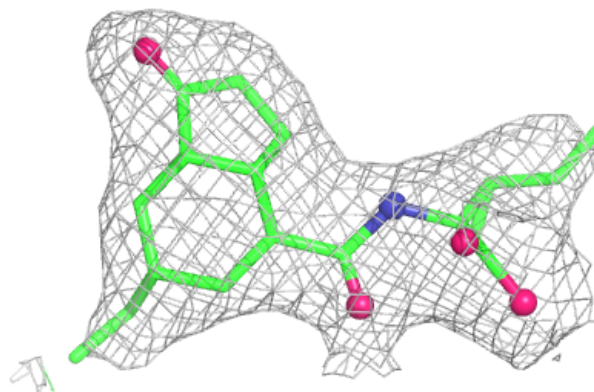


Electron density around OGK F 1100:

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

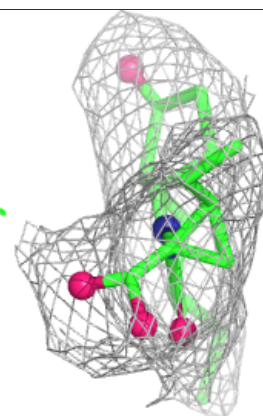
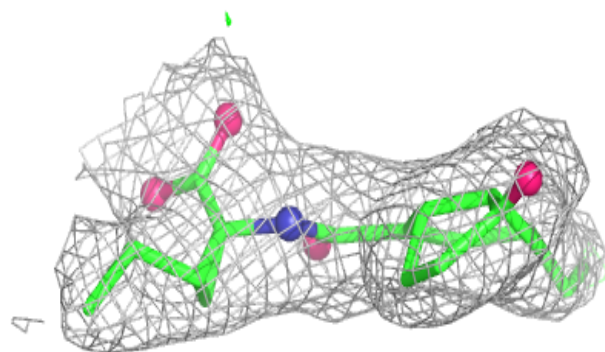
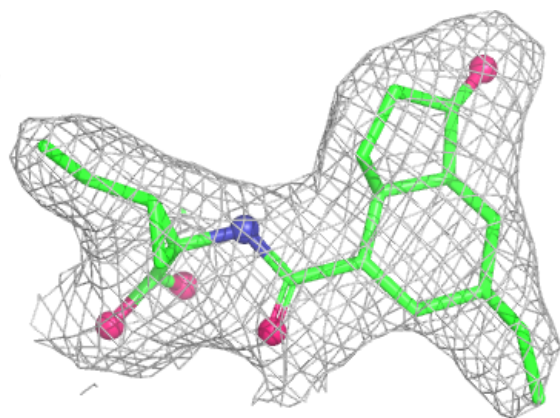
**Electron density around OGK L 1100:**

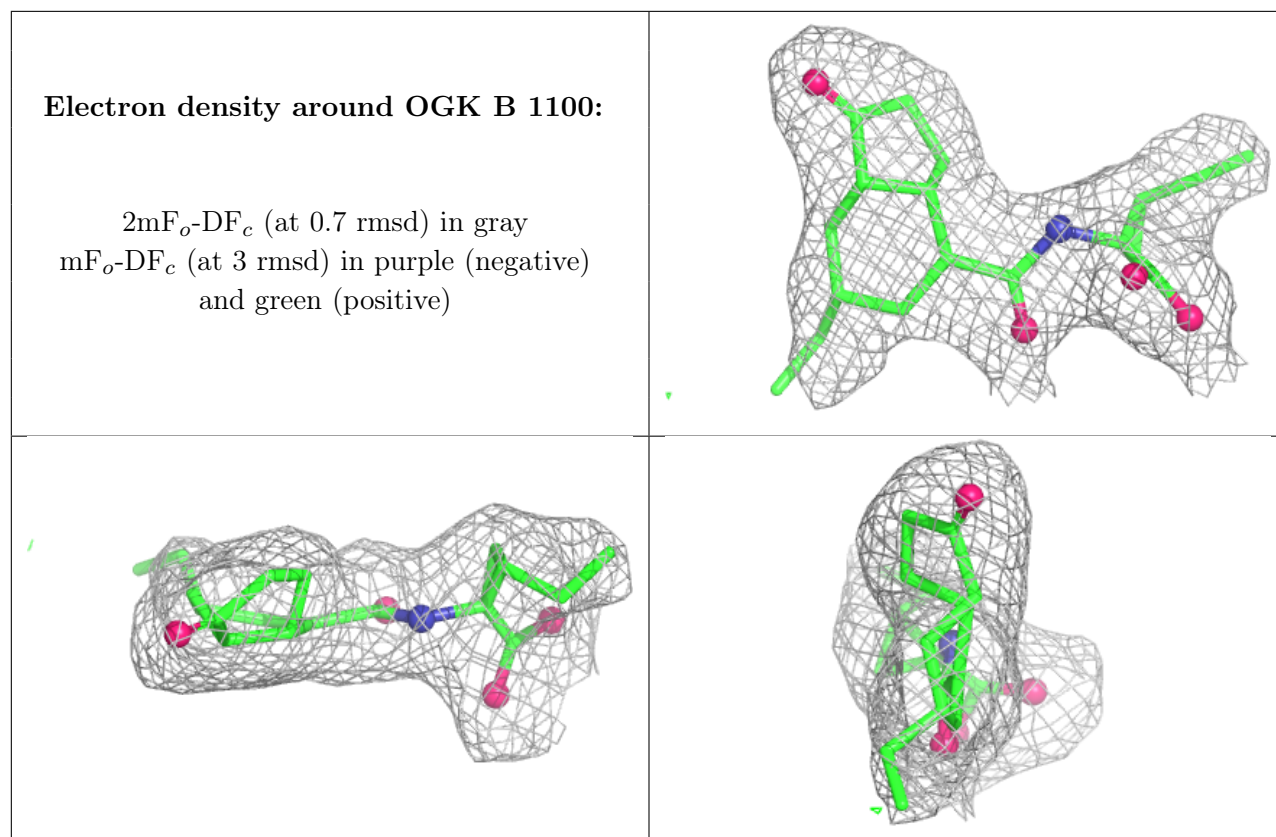
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around OGK D 1100:

$2mF_o-DF_c$ (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.