



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 08:26 AM UTC

PDB ID : 8PYI / pdb_00008pyi
Title : Human IGF1R with inhibitor 6
Authors : Dreyer, M.K.; Wang, J.; Elkins, J.M.
Deposited on : 2023-07-25
Resolution : 3.06 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)
Xtrriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

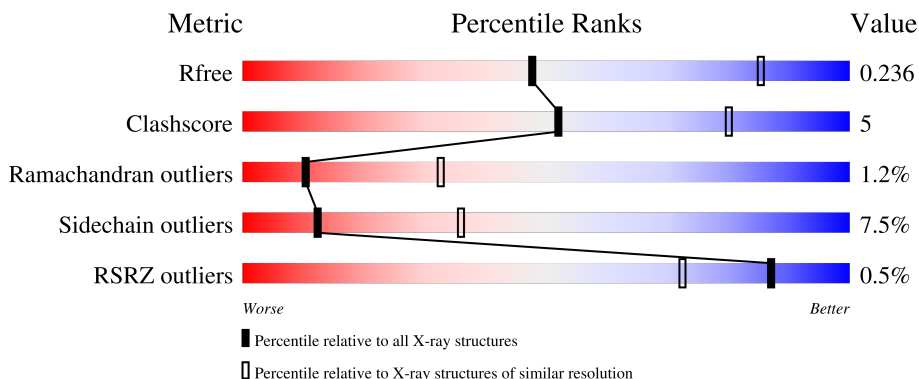
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.06 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.



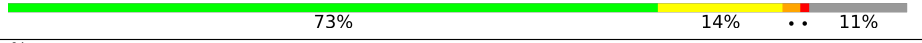


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)

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	AAA	321	 71% 16% • 10%
1	BBB	321	 74% 13% •• 11%
1	CCC	321	 74% 13% • 11%
1	DDD	321	 74% 14% • 11%
1	EEE	321	 74% 13% • 11%

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Mol	Chain	Length	Quality of chain
1	FFF	321	 73% 14% •• 11%
1	GGG	321	%  72% 15% • 12%
1	HHH	321	%  74% 12% • 11%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 18860 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 Insulin-like growth factor 1 receptor beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	AAA	288	2311	1471	384	434	22	0	0	0
1	BBB	287	2306	1468	383	433	22	0	0	0
1	CCC	286	2296	1461	379	434	22	0	0	0
1	DDD	287	2307	1467	383	435	22	0	0	0
1	EEE	285	2292	1459	378	433	22	0	0	0
1	FFF	287	2307	1468	384	433	22	0	0	0
1	GGG	284	2285	1454	377	432	22	0	0	0
1	HHH	285	2294	1460	381	431	22	0	0	0

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	973	MET	-	initiating methionine	UNP P08069
AAA	1287	ALA	-	expression tag	UNP P08069
AAA	1288	GLU	-	expression tag	UNP P08069
AAA	1289	ASN	-	expression tag	UNP P08069
AAA	1290	LEU	-	expression tag	UNP P08069
AAA	1291	TYR	-	expression tag	UNP P08069
AAA	1292	PHE	-	expression tag	UNP P08069
AAA	1293	GLN	-	expression tag	UNP P08069
BBB	973	MET	-	initiating methionine	UNP P08069
BBB	1287	ALA	-	expression tag	UNP P08069
BBB	1288	GLU	-	expression tag	UNP P08069
BBB	1289	ASN	-	expression tag	UNP P08069
BBB	1290	LEU	-	expression tag	UNP P08069

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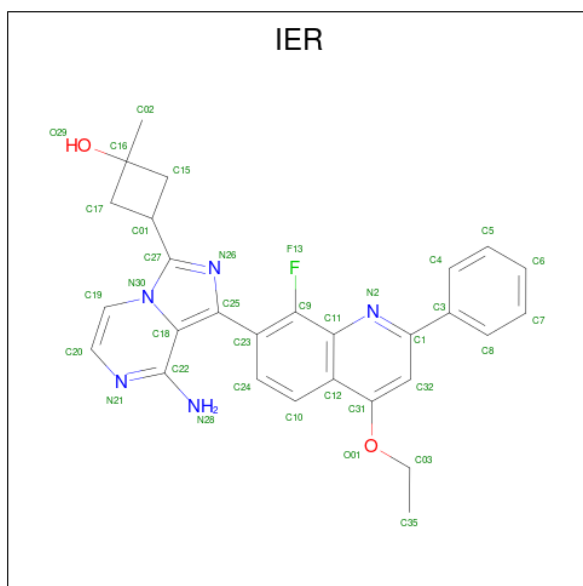
Chain	Residue	Modelled	Actual	Comment	Reference
BBB	1291	TYR	-	expression tag	UNP P08069
BBB	1292	PHE	-	expression tag	UNP P08069
BBB	1293	GLN	-	expression tag	UNP P08069
CCC	973	MET	-	initiating methionine	UNP P08069
CCC	1287	ALA	-	expression tag	UNP P08069
CCC	1288	GLU	-	expression tag	UNP P08069
CCC	1289	ASN	-	expression tag	UNP P08069
CCC	1290	LEU	-	expression tag	UNP P08069
CCC	1291	TYR	-	expression tag	UNP P08069
CCC	1292	PHE	-	expression tag	UNP P08069
CCC	1293	GLN	-	expression tag	UNP P08069
DDD	973	MET	-	initiating methionine	UNP P08069
DDD	1287	ALA	-	expression tag	UNP P08069
DDD	1288	GLU	-	expression tag	UNP P08069
DDD	1289	ASN	-	expression tag	UNP P08069
DDD	1290	LEU	-	expression tag	UNP P08069
DDD	1291	TYR	-	expression tag	UNP P08069
DDD	1292	PHE	-	expression tag	UNP P08069
DDD	1293	GLN	-	expression tag	UNP P08069
EEE	973	MET	-	initiating methionine	UNP P08069
EEE	1287	ALA	-	expression tag	UNP P08069
EEE	1288	GLU	-	expression tag	UNP P08069
EEE	1289	ASN	-	expression tag	UNP P08069
EEE	1290	LEU	-	expression tag	UNP P08069
EEE	1291	TYR	-	expression tag	UNP P08069
EEE	1292	PHE	-	expression tag	UNP P08069
EEE	1293	GLN	-	expression tag	UNP P08069
FFF	973	MET	-	initiating methionine	UNP P08069
FFF	1287	ALA	-	expression tag	UNP P08069
FFF	1288	GLU	-	expression tag	UNP P08069
FFF	1289	ASN	-	expression tag	UNP P08069
FFF	1290	LEU	-	expression tag	UNP P08069
FFF	1291	TYR	-	expression tag	UNP P08069
FFF	1292	PHE	-	expression tag	UNP P08069
FFF	1293	GLN	-	expression tag	UNP P08069
GGG	973	MET	-	initiating methionine	UNP P08069
GGG	1287	ALA	-	expression tag	UNP P08069
GGG	1288	GLU	-	expression tag	UNP P08069
GGG	1289	ASN	-	expression tag	UNP P08069
GGG	1290	LEU	-	expression tag	UNP P08069
GGG	1291	TYR	-	expression tag	UNP P08069
GGG	1292	PHE	-	expression tag	UNP P08069

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Chain	Residue	Modelled	Actual	Comment	Reference
GGG	1293	GLN	-	expression tag	UNP P08069
HHH	973	MET	-	initiating methionine	UNP P08069
HHH	1287	ALA	-	expression tag	UNP P08069
HHH	1288	GLU	-	expression tag	UNP P08069
HHH	1289	ASN	-	expression tag	UNP P08069
HHH	1290	LEU	-	expression tag	UNP P08069
HHH	1291	TYR	-	expression tag	UNP P08069
HHH	1292	PHE	-	expression tag	UNP P08069
HHH	1293	GLN	-	expression tag	UNP P08069

- Molecule 2 is 3-[8-azanyl-1-(4-ethoxy-8-fluoranyl-2-phenyl-quinolin-7-yl)imidazo[1,5-a]pyrazin-3-yl]-1-methyl-cyclobutan-1-ol (CCD ID: IER) (formula: C₂₈H₂₆FN₅O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	F	N	O		
2	AAA	1	Total	C	F	N	O	0	0
			36	28	1	5	2		
2	BBB	1	Total	C	F	N	O	0	0
			36	28	1	5	2		
2	CCC	1	Total	C	F	N	O	0	0
			36	28	1	5	2		
2	DDD	1	Total	C	F	N	O	0	0
			36	28	1	5	2		
2	EEE	1	Total	C	F	N	O	0	0
			36	28	1	5	2		
2	FFF	1	Total	C	F	N	O	0	0
			36	28	1	5	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	GGG	1	Total	C	F	N	O	0	0
			36	28	1	5	2		
2	HHH	1	Total	C	F	N	O	0	0
			36	28	1	5	2		

- Molecule 3 is water.

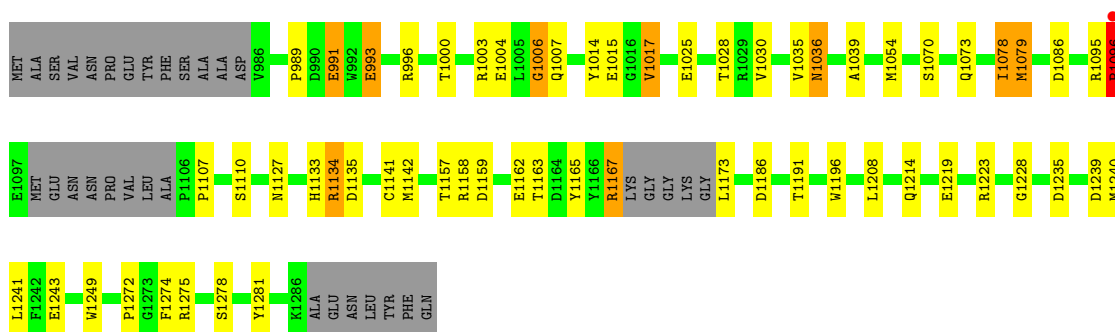
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	AAA	19	Total	O	0	0
			19	19		
3	BBB	27	Total	O	0	0
			27	27		
3	CCC	24	Total	O	0	0
			24	24		
3	DDD	27	Total	O	0	0
			27	27		
3	EEE	19	Total	O	0	0
			19	19		
3	FFF	21	Total	O	0	0
			21	21		
3	GGG	24	Total	O	0	0
			24	24		
3	HHH	13	Total	O	0	0
			13	13		

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.

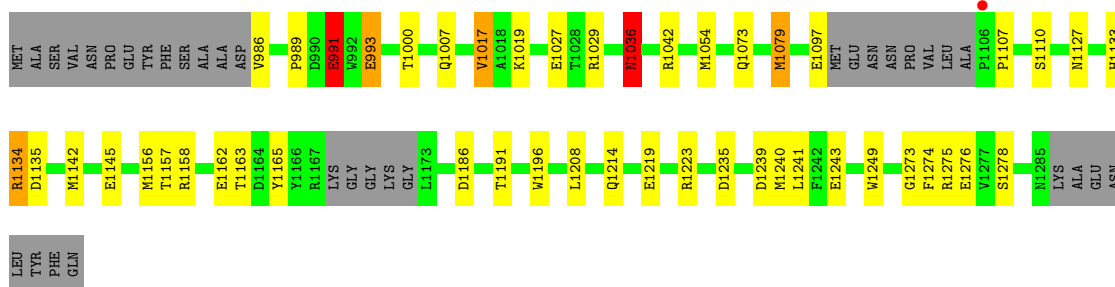
- Molecule 1: Insulin-like growth factor 1 receptor beta chain

Chain AAA: 




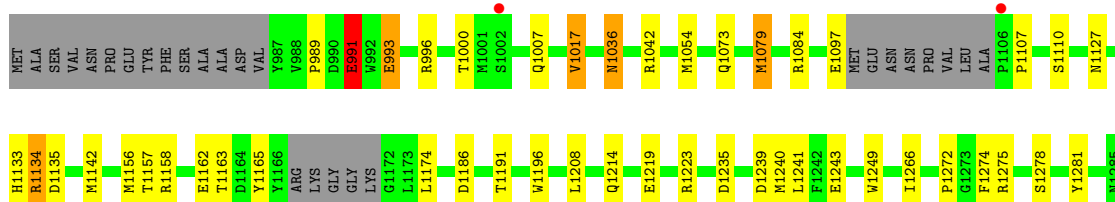
- Molecule 1: Insulin-like growth factor 1 receptor beta chain

Chain BBB: 



- Molecule 1: Insulin-like growth factor 1 receptor beta chain

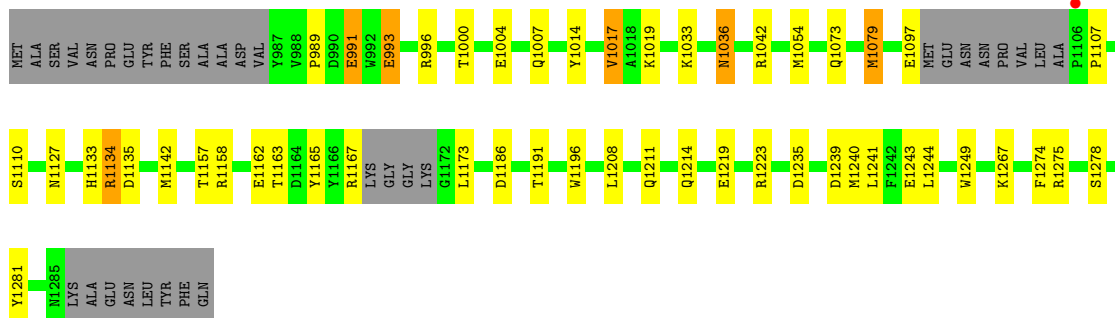
Chain CCC: 



LYS
ALA
GLU
ASN
LEU
TYR
PHE
GLN

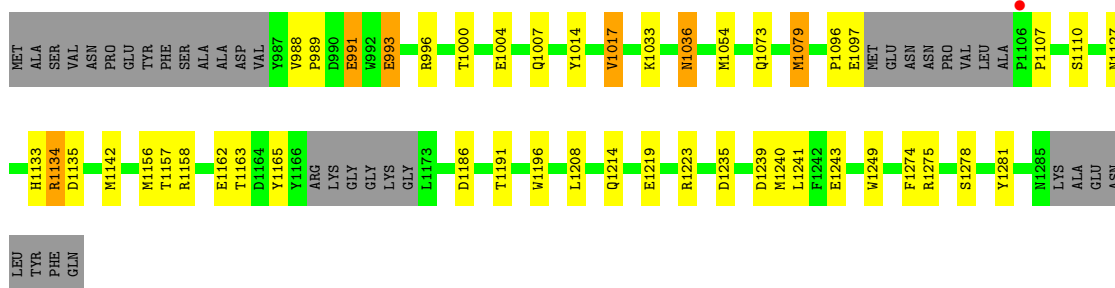
• Molecule 1: Insulin-like growth factor 1 receptor beta chain

Chain DDD: 74% 14% 11%



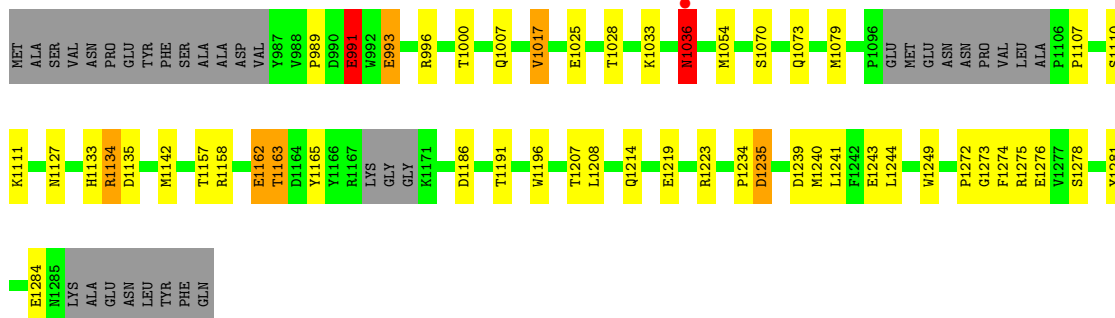
• Molecule 1: Insulin-like growth factor 1 receptor beta chain

Chain EEE: 74% 13% 11%



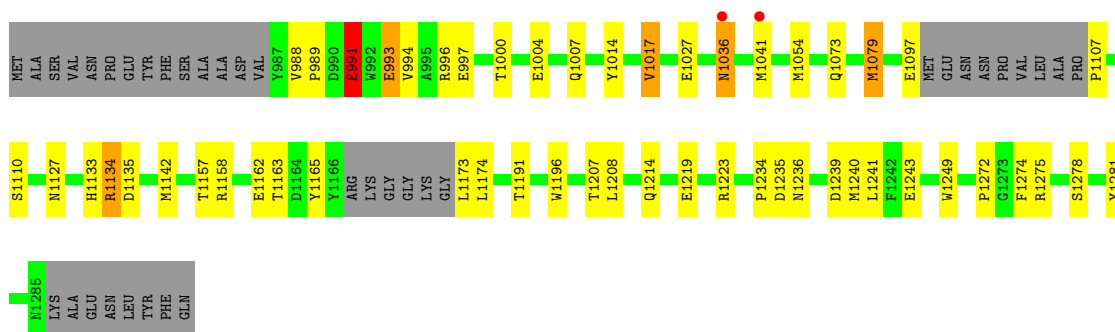
• Molecule 1: Insulin-like growth factor 1 receptor beta chain

Chain FFF: 73% 14% 11%



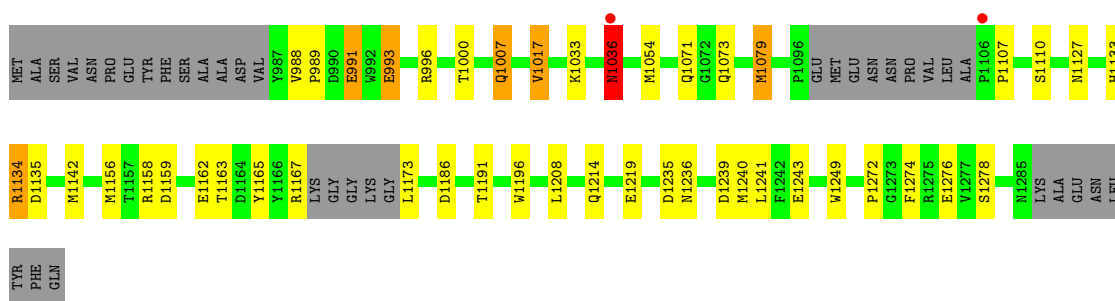
• Molecule 1: Insulin-like growth factor 1 receptor beta chain

Chain GGG: 72% 15% 12%



- Molecule 1: Insulin-like growth factor 1 receptor beta chain

Chain HHH: %



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	128.59Å 103.95Å 191.82Å 90.00° 100.17° 90.00°	Depositor
Resolution (Å)	63.47 – 3.06 63.47 – 3.06	Depositor EDS
% Data completeness (in resolution range)	99.6 (63.47-3.06) 99.6 (63.47-3.06)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.38 (at 3.07Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.191 , 0.235 0.195 , 0.236	Depositor DCC
R_{free} test set	2372 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	52.3	Xtrriage
Anisotropy	0.150	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 64.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18860	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.79% 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 i

5.1 Standard geometry i

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

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	AAA	0.98	0/2360	1.45	9/3183 (0.3%)
1	BBB	0.99	0/2355	1.42	0/3177
1	CCC	0.97	1/2345 (0.0%)	1.41	4/3163 (0.1%)
1	DDD	0.96	0/2356	1.40	2/3177 (0.1%)
1	EEE	0.98	0/2341	1.41	3/3158 (0.1%)
1	FFF	0.97	0/2356	1.42	3/3176 (0.1%)
1	GGG	0.97	0/2333	1.42	4/3146 (0.1%)
1	HHH	0.97	0/2343	1.41	4/3160 (0.1%)
All	All	0.98	1/18789 (0.0%)	1.42	29/25340 (0.1%)

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

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CCC	1266	ILE	N-CA	5.06	1.50	1.46

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	FFF	1158	ARG	CG-CD-NE	-7.23	96.10	112.00
1	AAA	1158	ARG	CG-CD-NE	-7.11	96.36	112.00
1	EEE	1158	ARG	CG-CD-NE	-6.99	96.61	112.00
1	EEE	996	ARG	CA-C-N	6.00	128.60	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	EEE	996	ARG	C-N-CA	6.00	128.60	120.38

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	EEE	1096	PRO	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	AAA	2311	0	2263	33	0
1	BBB	2306	0	2264	25	3
1	CCC	2296	0	2249	22	1
1	DDD	2307	0	2262	28	0
1	EEE	2292	0	2246	24	0
1	FFF	2307	0	2269	28	3
1	GGG	2285	0	2239	25	5
1	HHH	2294	0	2253	22	5
2	AAA	36	0	0	0	0
2	BBB	36	0	0	1	0
2	CCC	36	0	0	1	0
2	DDD	36	0	0	2	0
2	EEE	36	0	0	3	0
2	FFF	36	0	0	2	0
2	GGG	36	0	0	1	0
2	HHH	36	0	0	2	0
3	AAA	19	0	0	0	0
3	BBB	27	0	0	3	0
3	CCC	24	0	0	2	0
3	DDD	27	0	0	3	1
3	EEE	19	0	0	0	0
3	FFF	21	0	0	1	0
3	GGG	24	0	0	1	0
3	HHH	13	0	0	3	0
All	All	18860	0	18045	187	10

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 5.

The worst 5 of 187 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:CCC:1127:ASN:HB3	3:CCC:3114:HOH:O	1.07	1.22
1:AAA:1141:CYS:O	1:AAA:1142:MET:HE2	1.75	0.86
1:DDD:1211:GLN:HG3	3:HHH:3110:HOH:O	1.85	0.77
1:AAA:1141:CYS:C	1:AAA:1142:MET:HE2	2.13	0.74
1:AAA:1006:GLY:HA2	1:BBB:986:VAL:HB	1.72	0.71

The worst 5 of 10 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)
1:GGG:1236:ASN:OD1	1:HHH:1276:GLU:O[3_455]	1.35	0.85
1:GGG:1236:ASN:CG	1:HHH:1276:GLU:O[3_455]	1.62	0.58
1:BBB:1275:ARG:NH1	1:FFF:1272:PRO:CB[1_565]	1.76	0.44
1:GGG:1236:ASN:CB	1:HHH:1276:GLU:O[3_455]	1.77	0.43
1:GGG:1027:GLU:OE2	1:GGG:1027:GLU:OE2[2_656]	1.82	0.38

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	AAA	282/321 (88%)	267 (95%)	11 (4%)	4 (1%)	9	29
1	BBB	281/321 (88%)	269 (96%)	8 (3%)	4 (1%)	9	29
1	CCC	280/321 (87%)	266 (95%)	11 (4%)	3 (1%)	11	34
1	DDD	281/321 (88%)	268 (95%)	10 (4%)	3 (1%)	11	34
1	EEE	279/321 (87%)	266 (95%)	10 (4%)	3 (1%)	11	34
1	FFF	281/321 (88%)	268 (95%)	9 (3%)	4 (1%)	9	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	GGG	278/321 (87%)	266 (96%)	9 (3%)	3 (1%)	11	34
1	HHH	279/321 (87%)	267 (96%)	8 (3%)	4 (1%)	9	29
All	All	2241/2568 (87%)	2137 (95%)	76 (3%)	28 (1%)	10	32

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	1096	PRO
1	AAA	1162	GLU
1	AAA	1163	THR
1	BBB	1162	GLU
1	BBB	1163	THR

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AAA	252/280 (90%)	232 (92%)	20 (8%)	11	34
1	BBB	253/280 (90%)	234 (92%)	19 (8%)	12	36
1	CCC	252/280 (90%)	233 (92%)	19 (8%)	12	36
1	DDD	253/280 (90%)	232 (92%)	21 (8%)	10	32
1	EEE	252/280 (90%)	234 (93%)	18 (7%)	13	37
1	FFF	253/280 (90%)	237 (94%)	16 (6%)	16	41
1	GGG	251/280 (90%)	230 (92%)	21 (8%)	10	31
1	HHH	252/280 (90%)	234 (93%)	18 (7%)	13	37
All	All	2018/2240 (90%)	1866 (92%)	152 (8%)	12	36

5 of 152 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	GGG	993	GLU
1	HHH	1134	ARG

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Mol	Chain	Res	Type
1	GGG	1036	ASN
1	GGG	1239	ASP
1	HHH	1241	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

8 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
2	IER	CCC	3000	-	39,41,41	1.79	4 (10%)	45,62,62	2.82	18 (40%)
2	IER	AAA	3000	-	39,41,41	1.98	8 (20%)	45,62,62	2.25	10 (22%)
2	IER	DDD	3000	-	39,41,41	1.70	5 (12%)	45,62,62	2.10	14 (31%)
2	IER	FFF	3000	-	39,41,41	1.96	5 (12%)	45,62,62	2.53	15 (33%)
2	IER	GGG	3000	-	39,41,41	1.72	5 (12%)	45,62,62	2.71	12 (26%)
2	IER	EEE	3000	-	39,41,41	1.94	5 (12%)	45,62,62	2.27	15 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	IER	HHH	3000	-	39,41,41	1.67	7 (17%)	45,62,62	2.16	14 (31%)
2	IER	BBB	3000	-	39,41,41	1.89	6 (15%)	45,62,62	1.97	9 (20%)

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
2	IER	CCC	3000	-	-	4/13/25/25	0/6/6/6
2	IER	AAA	3000	-	-	4/13/25/25	0/6/6/6
2	IER	DDD	3000	-	-	3/13/25/25	0/6/6/6
2	IER	FFF	3000	-	-	4/13/25/25	0/6/6/6
2	IER	GGG	3000	-	-	2/13/25/25	0/6/6/6
2	IER	EEE	3000	-	-	4/13/25/25	0/6/6/6
2	IER	HHH	3000	-	-	3/13/25/25	0/6/6/6
2	IER	BBB	3000	-	-	4/13/25/25	0/6/6/6

The worst 5 of 45 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	EEE	3000	IER	C3-C1	-6.80	1.38	1.49
2	EEE	3000	IER	C23-C25	-6.50	1.37	1.48
2	FFF	3000	IER	C3-C1	-6.45	1.39	1.49
2	AAA	3000	IER	C3-C1	-6.16	1.39	1.49
2	BBB	3000	IER	C3-C1	-6.01	1.39	1.49

The worst 5 of 107 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	GGG	3000	IER	C17-C01-C27	-9.84	106.85	118.04
2	FFF	3000	IER	C15-C01-C27	-9.57	107.15	118.04
2	GGG	3000	IER	C1-N2-C11	8.54	124.63	118.28
2	AAA	3000	IER	C25-N26-C27	7.87	112.65	105.38
2	CCC	3000	IER	C17-C01-C27	-7.79	109.18	118.04

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

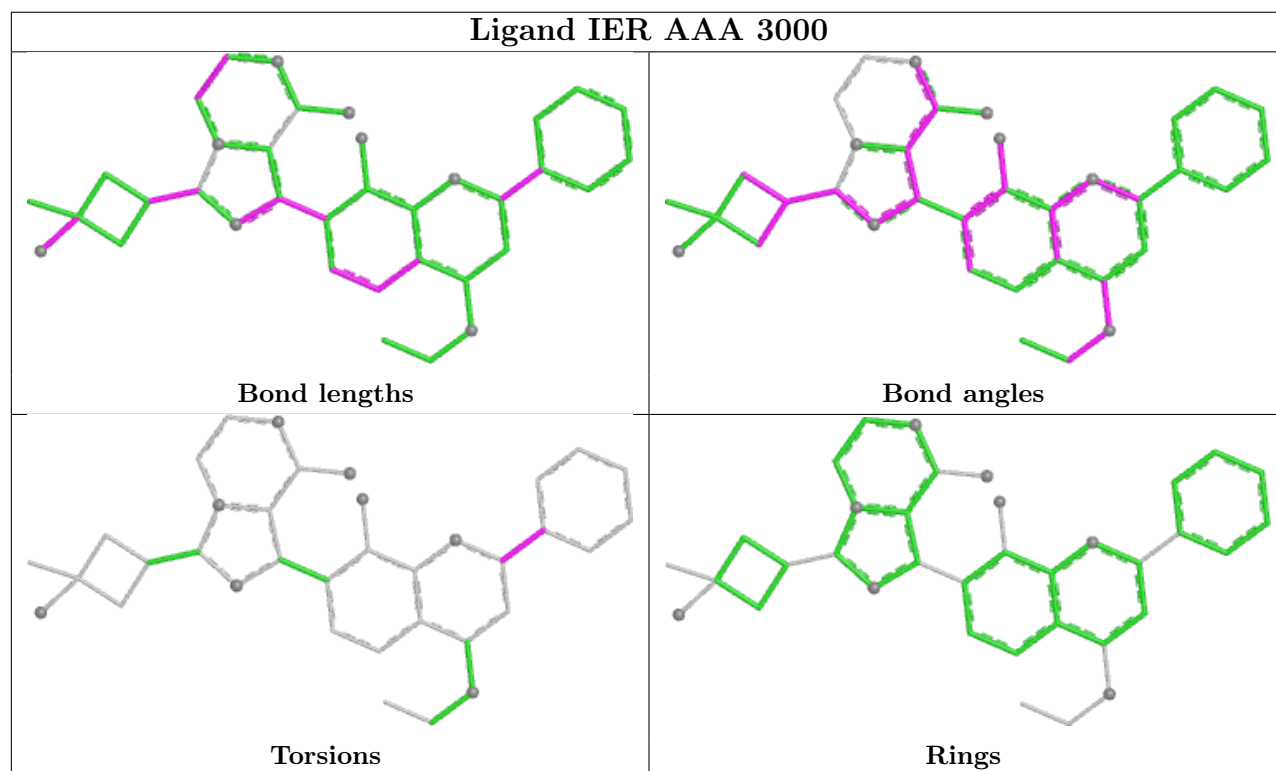
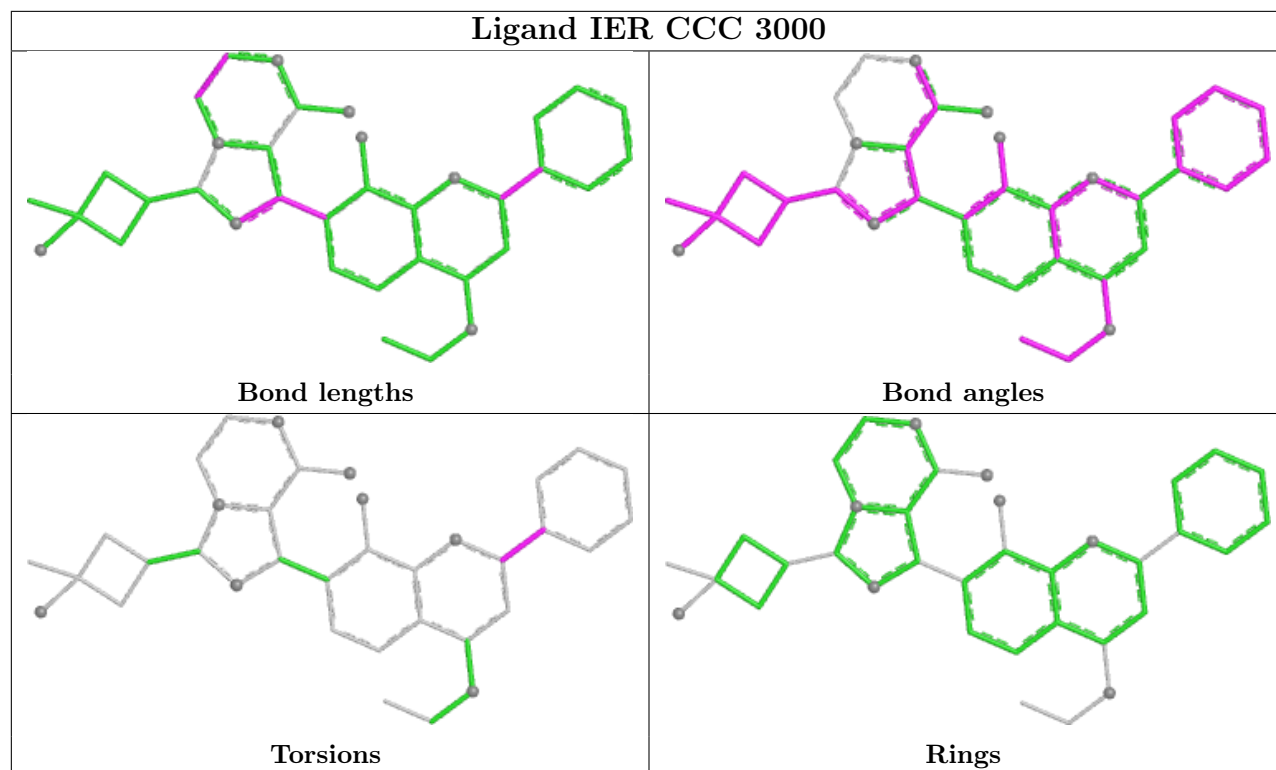
Mol	Chain	Res	Type	Atoms
2	EEE	3000	IER	N2-C1-C3-C4
2	EEE	3000	IER	C32-C1-C3-C4
2	EEE	3000	IER	C32-C1-C3-C8
2	EEE	3000	IER	N2-C1-C3-C8
2	FFF	3000	IER	N2-C1-C3-C4

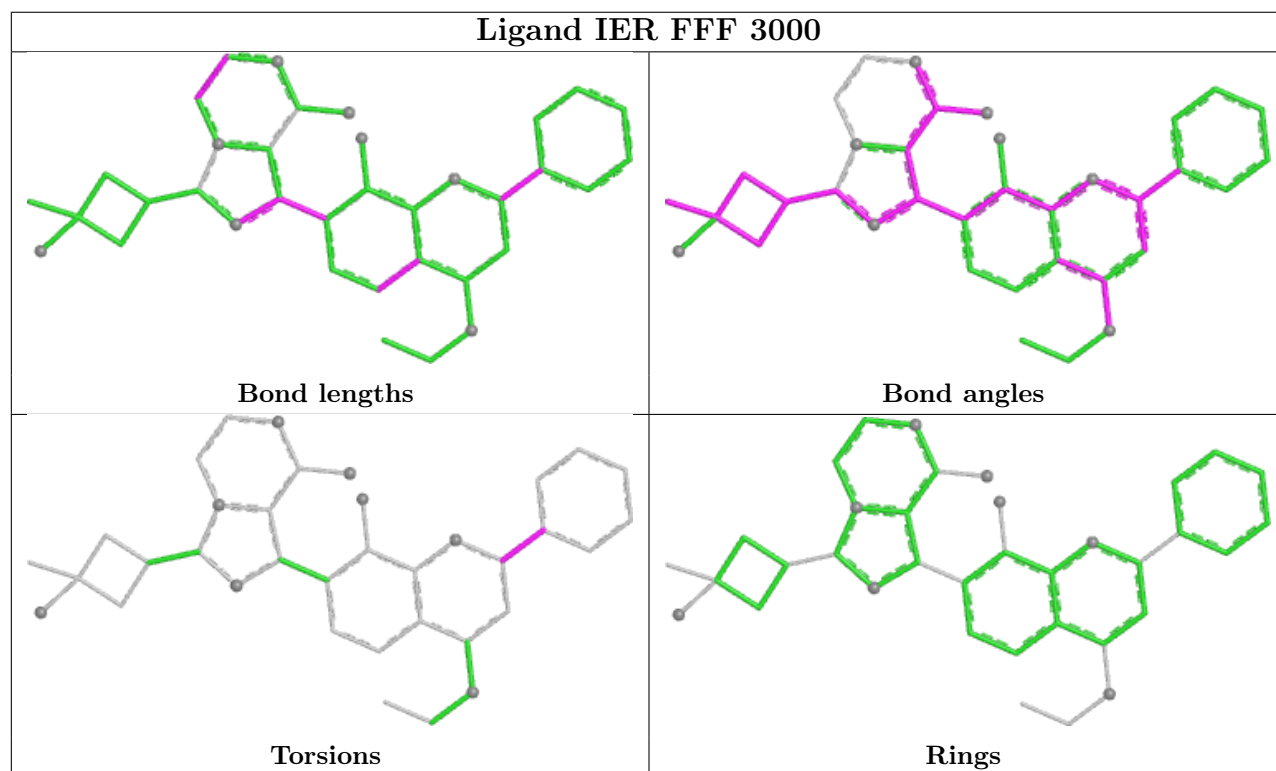
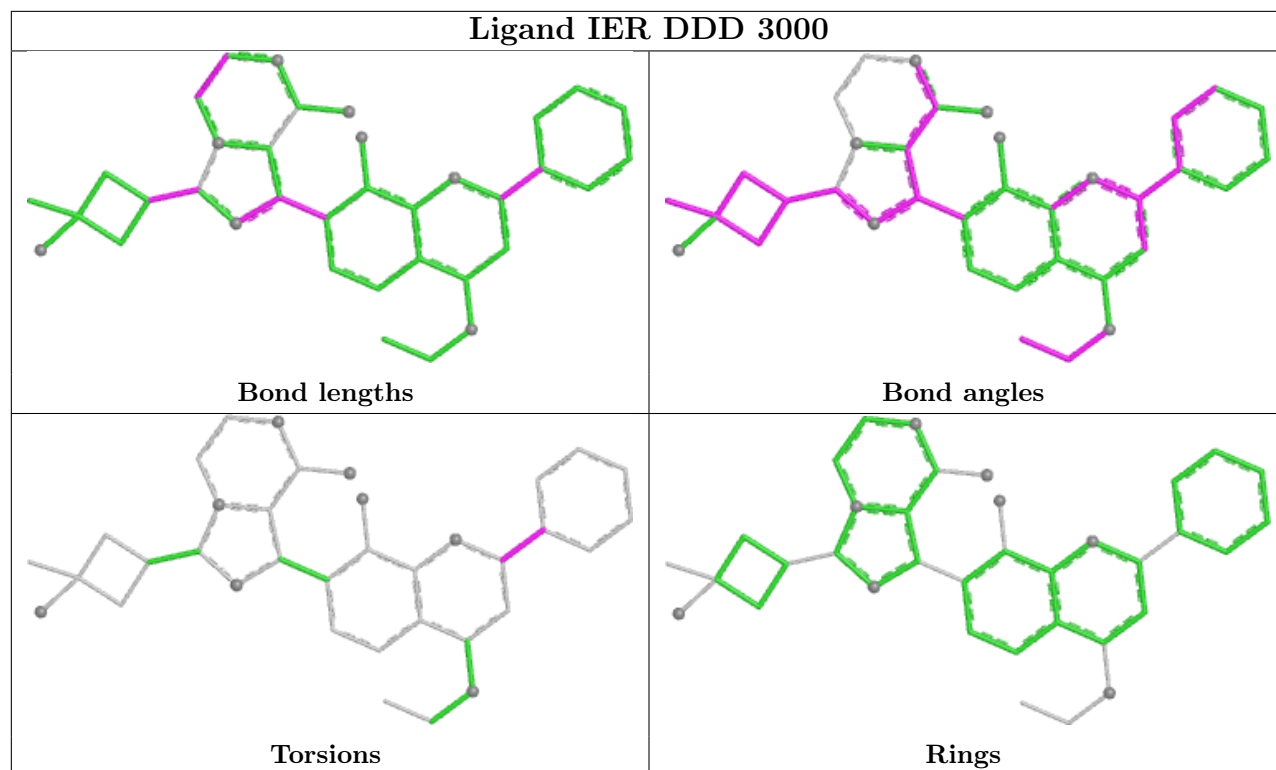
There are no ring outliers.

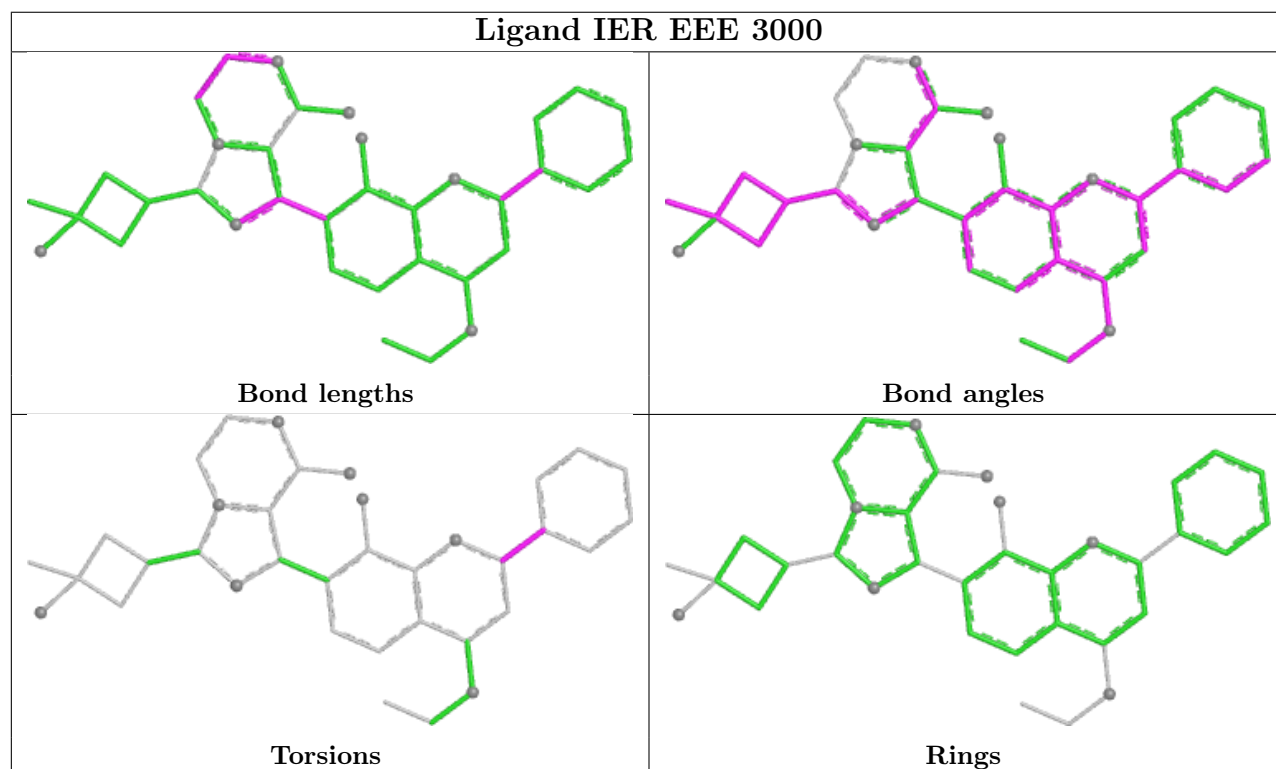
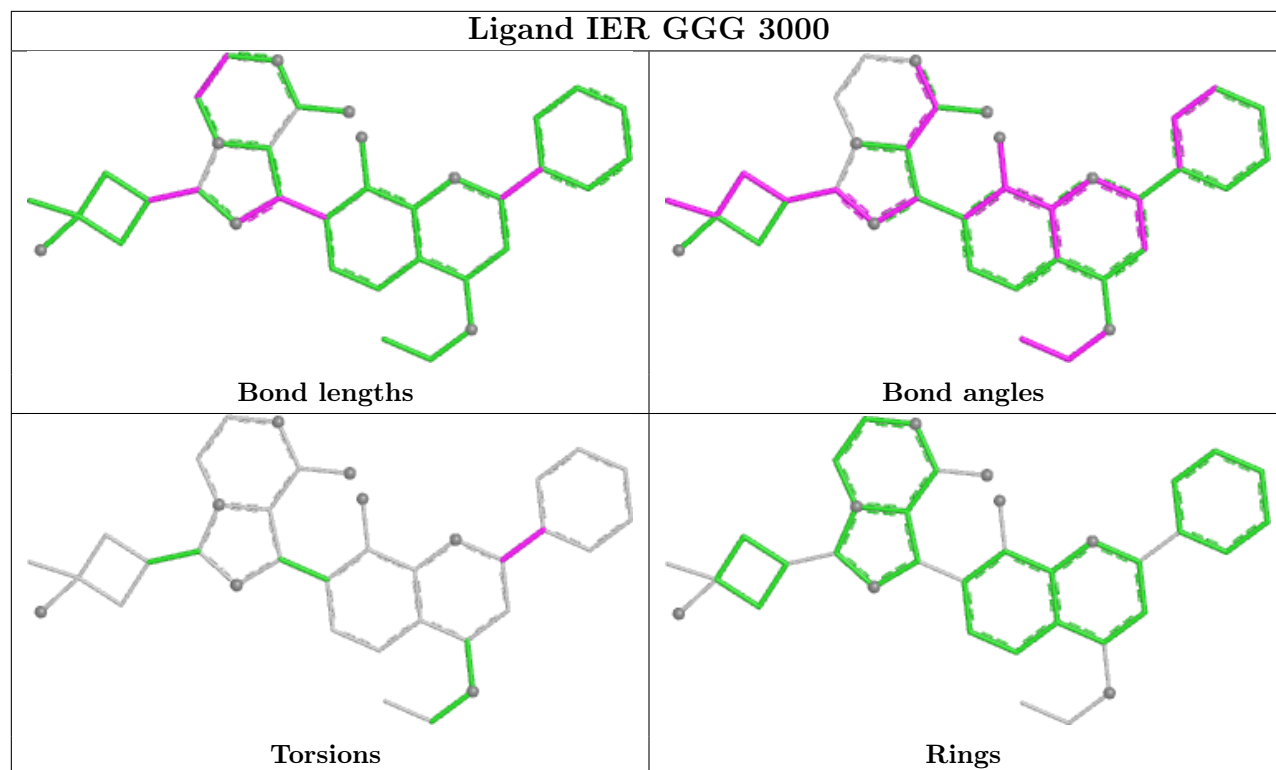
7 monomers are involved in 12 short contacts:

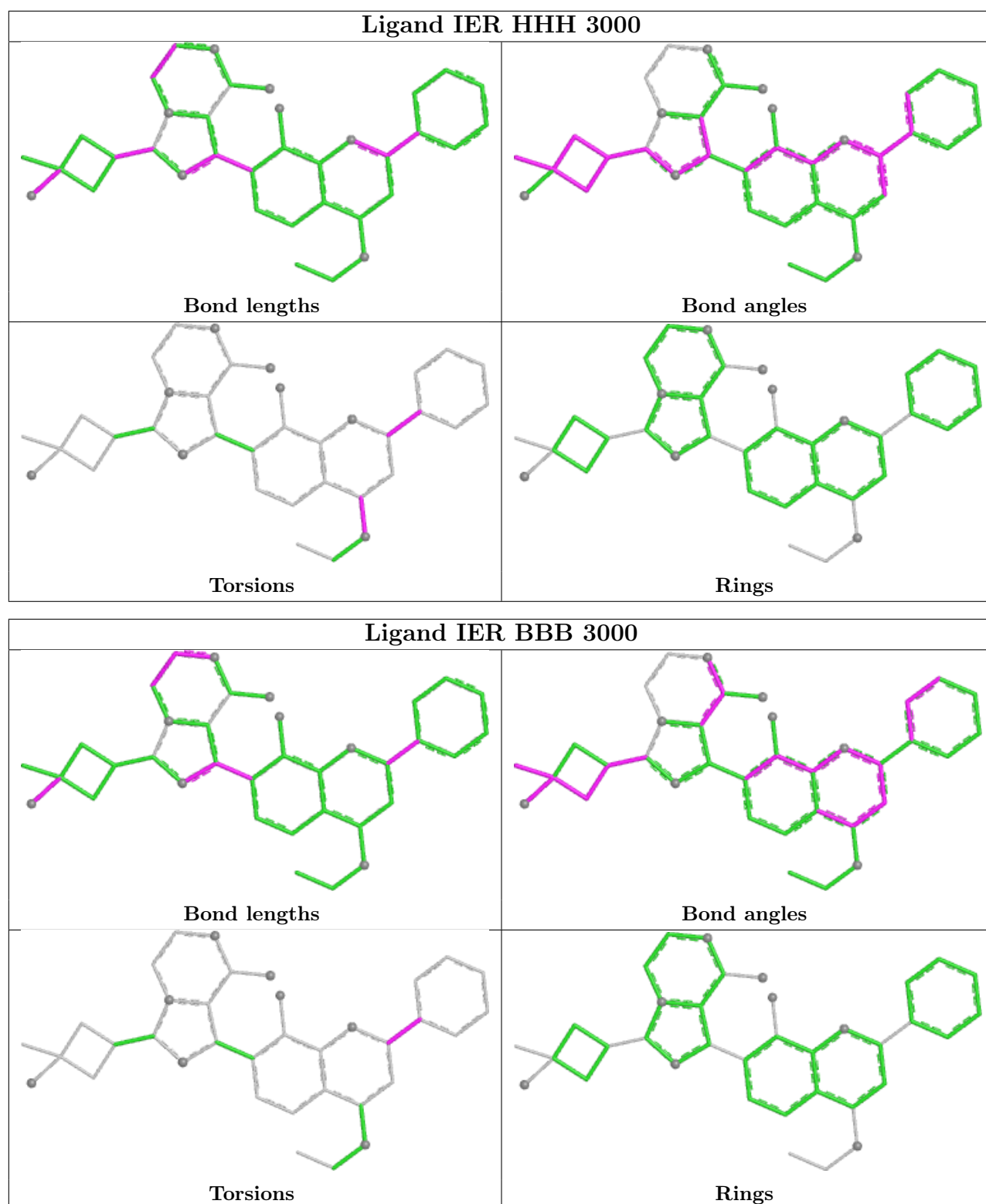
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	CCC	3000	IER	1	0
2	DDD	3000	IER	2	0
2	FFF	3000	IER	2	0
2	GGG	3000	IER	1	0
2	EEE	3000	IER	3	0
2	HHH	3000	IER	2	0
2	BBB	3000	IER	1	0

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

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, 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	AAA	288/321 (89%)	-0.29	1 (0%) 90 80	29, 52, 91, 128	0
1	BBB	287/321 (89%)	-0.40	1 (0%) 90 80	27, 44, 85, 134	0
1	CCC	286/321 (89%)	-0.27	2 (0%) 84 66	28, 50, 86, 143	0
1	DDD	287/321 (89%)	-0.28	1 (0%) 90 80	28, 52, 96, 171	0
1	EEE	285/321 (88%)	-0.22	1 (0%) 88 75	28, 56, 96, 131	0
1	FFF	287/321 (89%)	-0.21	1 (0%) 90 80	26, 52, 89, 161	0
1	GGG	284/321 (88%)	-0.16	2 (0%) 84 66	32, 60, 105, 137	0
1	HHH	285/321 (88%)	0.02	2 (0%) 84 66	34, 68, 124, 162	0
All	All	2289/2568 (89%)	-0.23	11 (0%) 87 72	26, 54, 101, 171	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	DDD	1106	PRO	3.6
1	CCC	1106	PRO	3.1
1	FFF	1036	ASN	2.9
1	BBB	1106	PRO	2.5
1	HHH	1036	ASN	2.4

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

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

6.3 Carbohydrates [i](#)

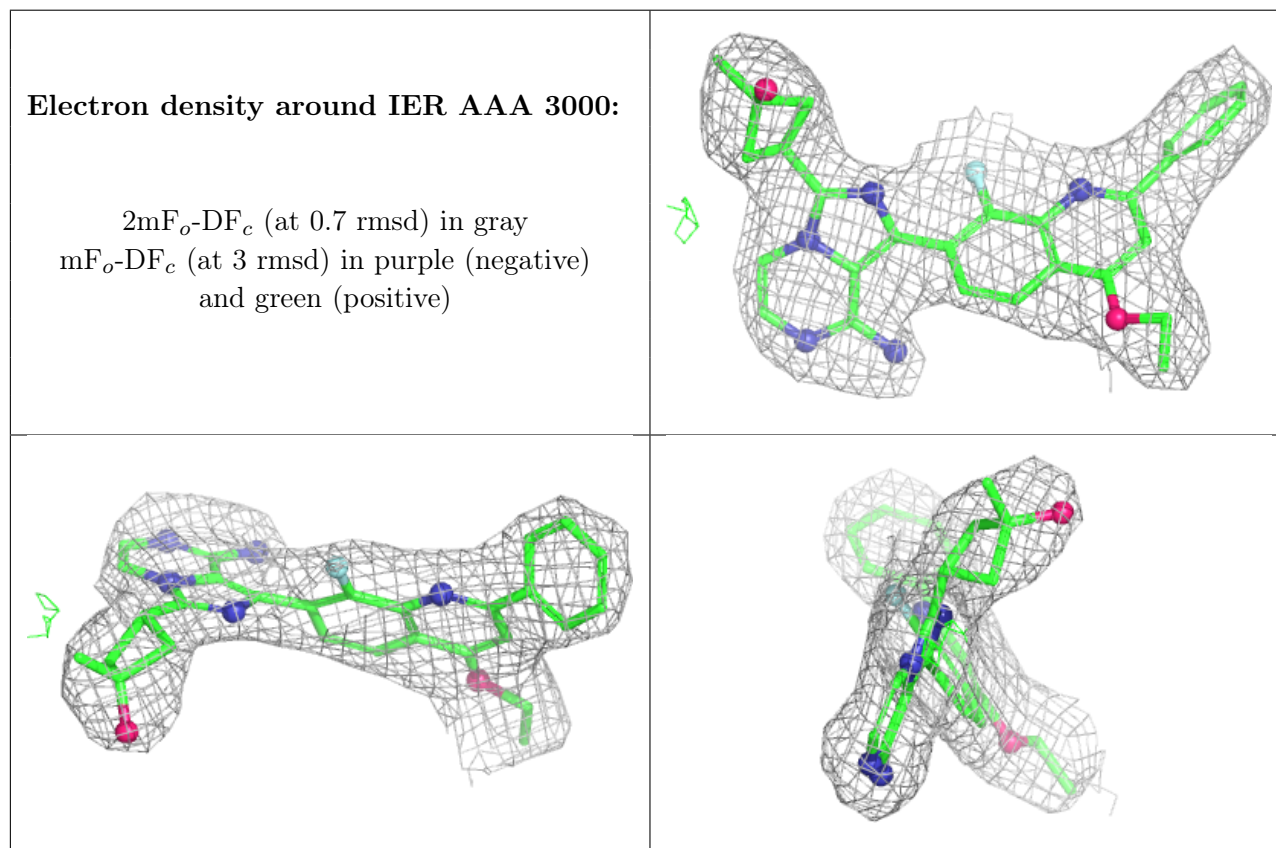
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

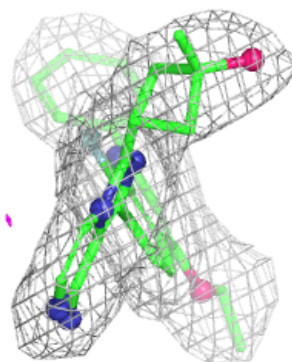
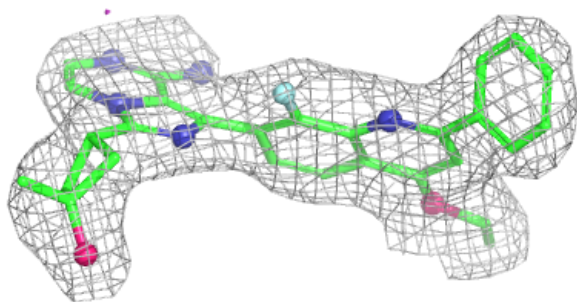
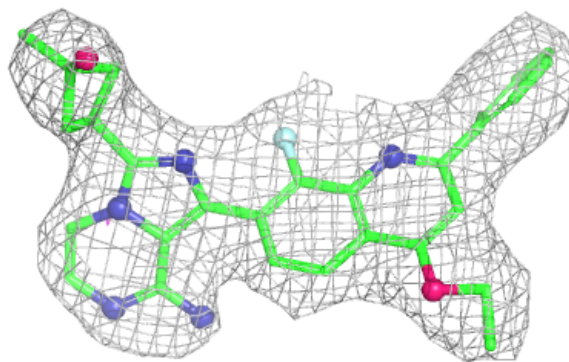
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	IER	AAA	3000	36/36	0.96	0.07	33,39,49,52	0
2	IER	CCC	3000	36/36	0.96	0.07	33,35,39,44	0
2	IER	DDD	3000	36/36	0.96	0.07	29,39,48,57	0
2	IER	GGG	3000	36/36	0.96	0.07	34,45,59,62	0
2	IER	HHH	3000	36/36	0.96	0.07	38,45,57,60	0
2	IER	BBB	3000	36/36	0.97	0.06	27,31,37,42	0
2	IER	EEE	3000	36/36	0.97	0.06	34,39,50,53	0
2	IER	FFF	3000	36/36	0.98	0.06	30,36,42,44	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.

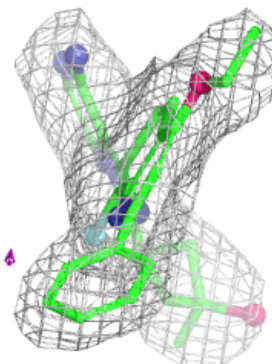
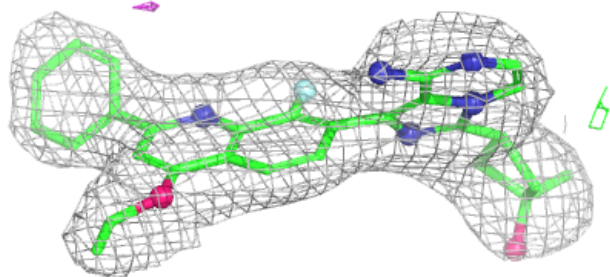
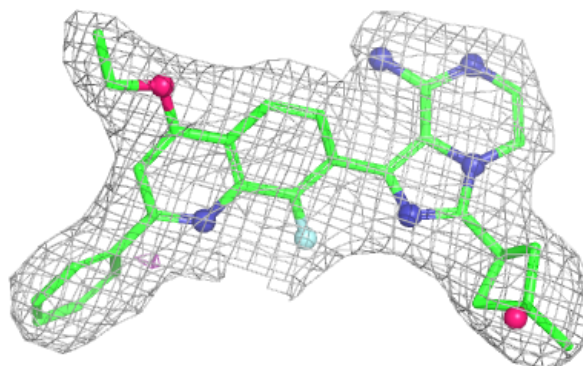


Electron density around IER CCC 3000:

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

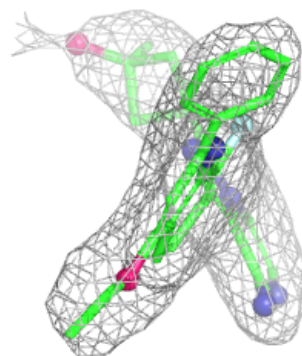
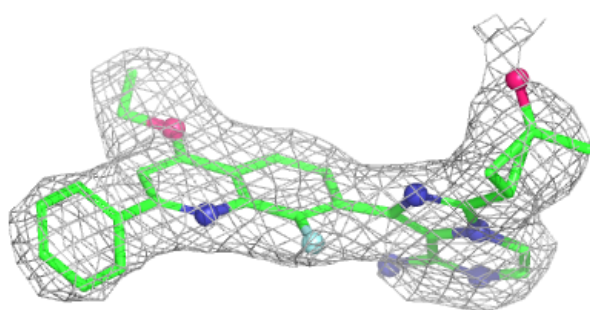
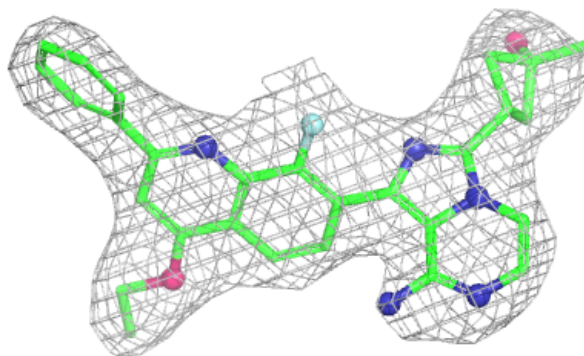
**Electron density around IER DDD 3000:**

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

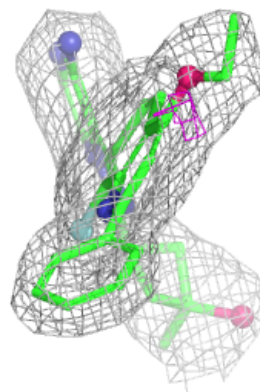
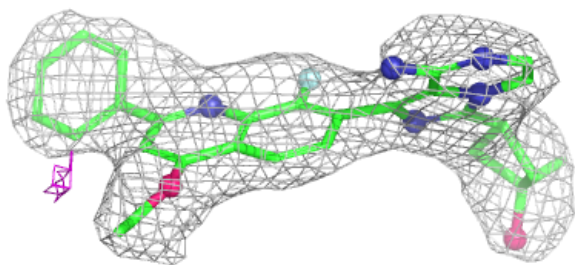
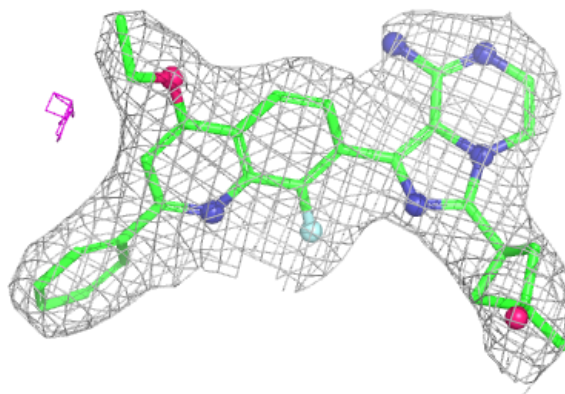


Electron density around IER GGG 3000:

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

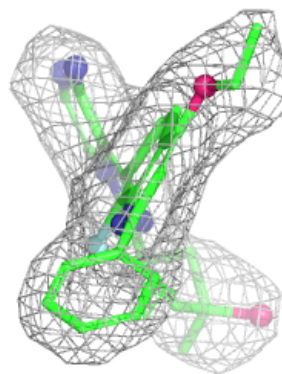
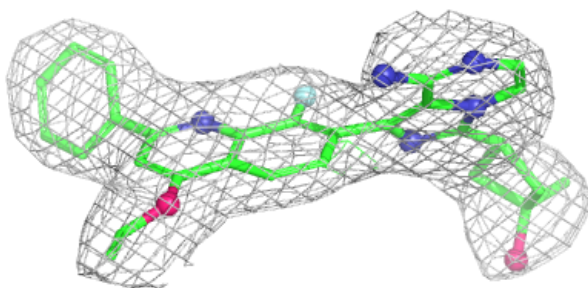
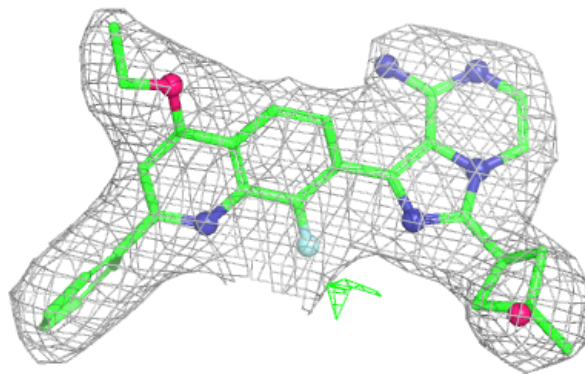
**Electron density around IER HHH 3000:**

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

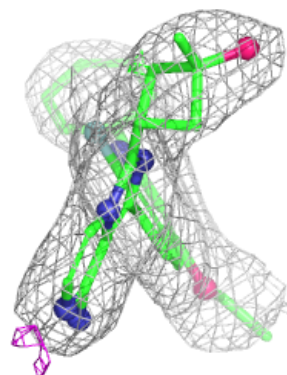
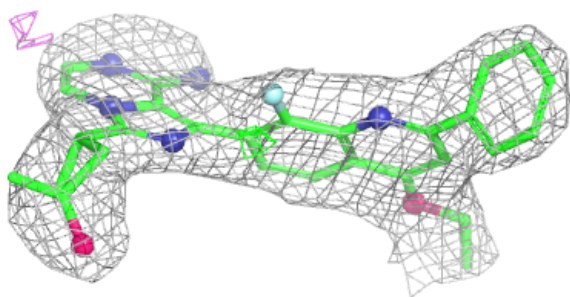
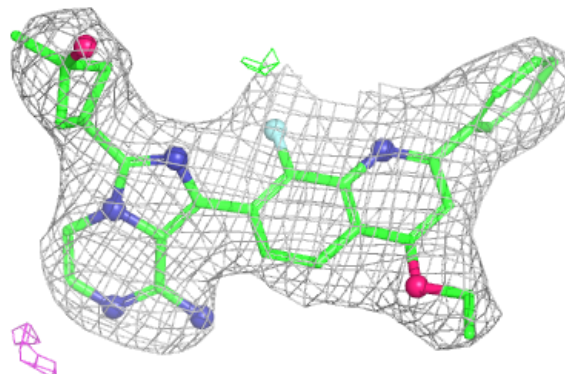


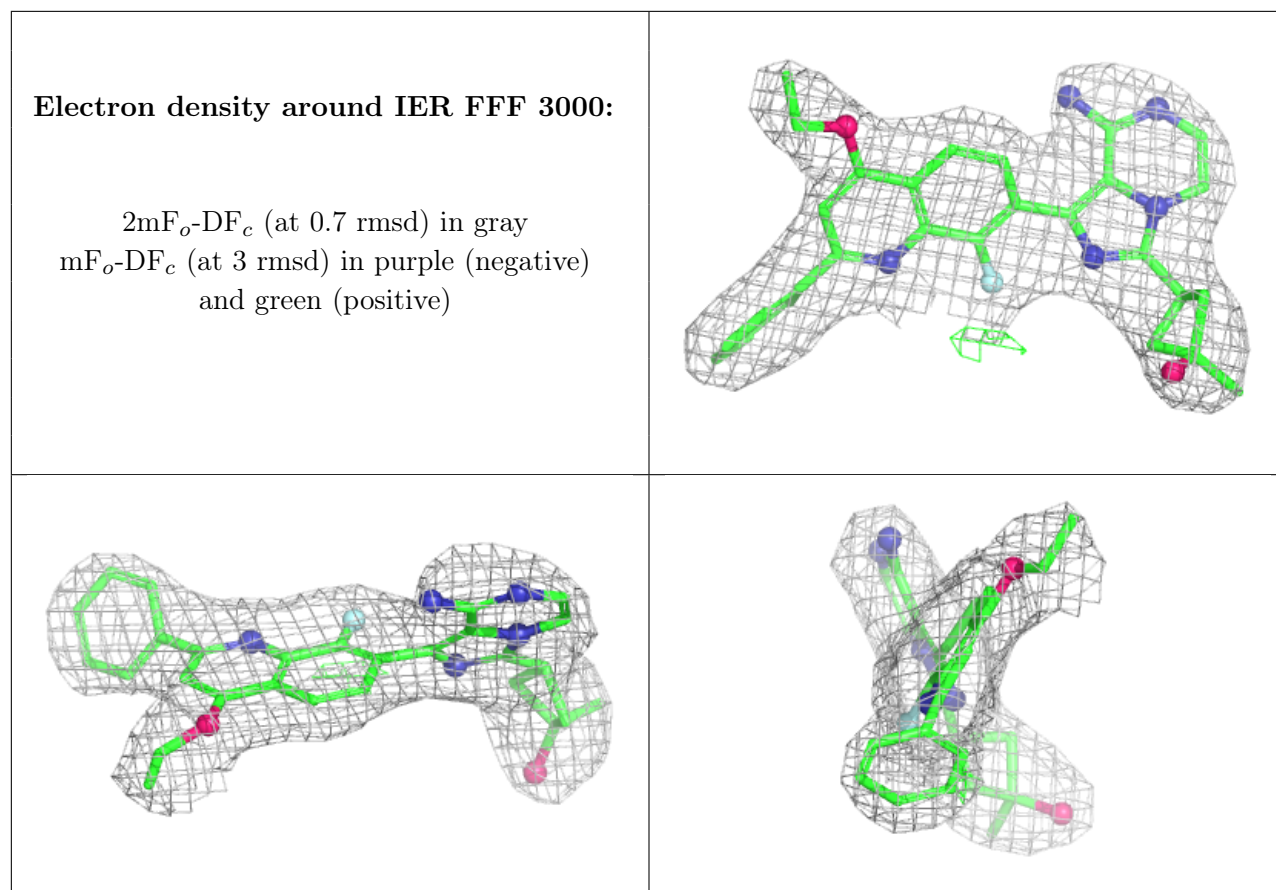
Electron density around IER BBB 3000:

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

**Electron density around IER EEE 3000:**

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





6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.