



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 03:10 AM UTC

PDB ID : 3NSH / pdb_00003nsh
Title : BACE-1 in complex with ELN475957
Authors : Probst, G.D.; Bowers, S.; Sealy, J.M.; Brecht, E.; Yao, N.
Deposited on : 2010-07-01
Resolution : 2.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

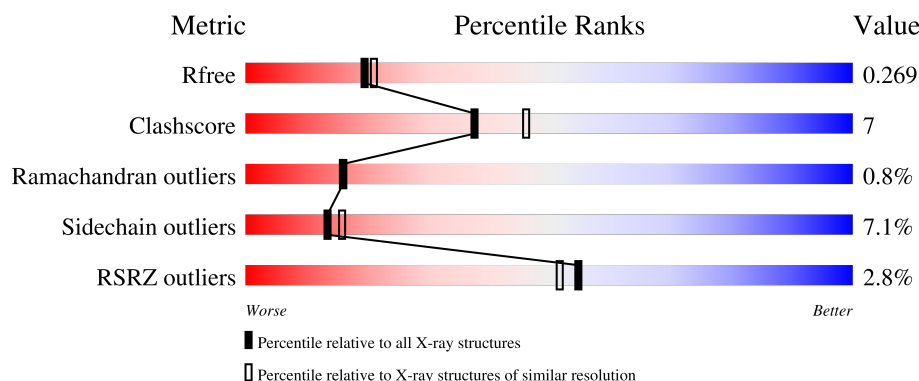
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	406	3% 71% 17% 8%
1	B	406	3% 68% 21% 7%
1	C	406	% 79% 11% 7%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9293 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 Beta-secretase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	372	Total	C	N	O	S	0	0	0
			2928	1876	487	551	14			
1	B	376	Total	C	N	O	S	0	0	0
			2958	1900	491	553	14			
1	C	376	Total	C	N	O	S	0	0	0
			2958	1898	492	554	14			

There are 27 discrepancies between the modelled and reference sequences:

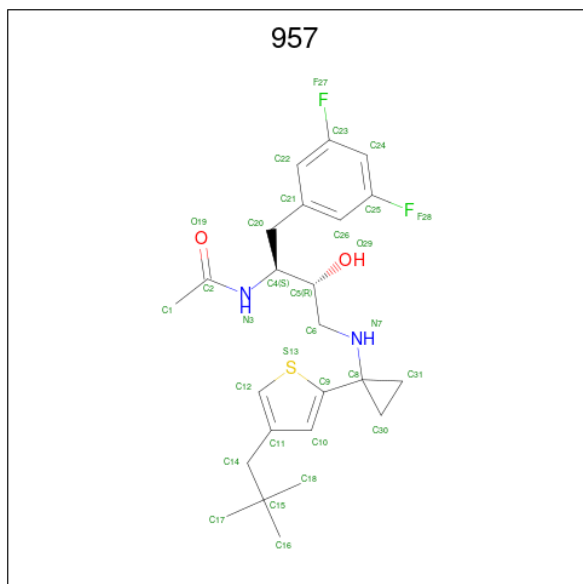
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P56817
A	399	ARG	-	expression tag	UNP P56817
A	400	SER	-	expression tag	UNP P56817
A	401	HIS	-	expression tag	UNP P56817
A	402	HIS	-	expression tag	UNP P56817
A	403	HIS	-	expression tag	UNP P56817
A	404	HIS	-	expression tag	UNP P56817
A	405	HIS	-	expression tag	UNP P56817
A	406	HIS	-	expression tag	UNP P56817
B	1	MET	-	initiating methionine	UNP P56817
B	399	ARG	-	expression tag	UNP P56817
B	400	SER	-	expression tag	UNP P56817
B	401	HIS	-	expression tag	UNP P56817
B	402	HIS	-	expression tag	UNP P56817
B	403	HIS	-	expression tag	UNP P56817
B	404	HIS	-	expression tag	UNP P56817
B	405	HIS	-	expression tag	UNP P56817
B	406	HIS	-	expression tag	UNP P56817
C	1	MET	-	initiating methionine	UNP P56817
C	399	ARG	-	expression tag	UNP P56817
C	400	SER	-	expression tag	UNP P56817
C	401	HIS	-	expression tag	UNP P56817
C	402	HIS	-	expression tag	UNP P56817

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Chain	Residue	Modelled	Actual	Comment	Reference
C	403	HIS	-	expression tag	UNP P56817
C	404	HIS	-	expression tag	UNP P56817
C	405	HIS	-	expression tag	UNP P56817
C	406	HIS	-	expression tag	UNP P56817

- Molecule 2 is N-[(1S,2R)-1-(3,5-difluorobenzyl)-3-({1-[4-(2,2-dimethylpropyl)thiophen-2-yl]cyclopropyl}amino)-2-hydroxypropyl]acetamide (CCD ID: 957) (formula: C₂₄H₃₂F₂N₂O₂S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	S	0	0
			31	24	2	2	2	1		
2	B	1	Total	C	F	N	O	S	0	0
			31	24	2	2	2	1		
2	C	1	Total	C	F	N	O	S	0	0
			31	24	2	2	2	1		

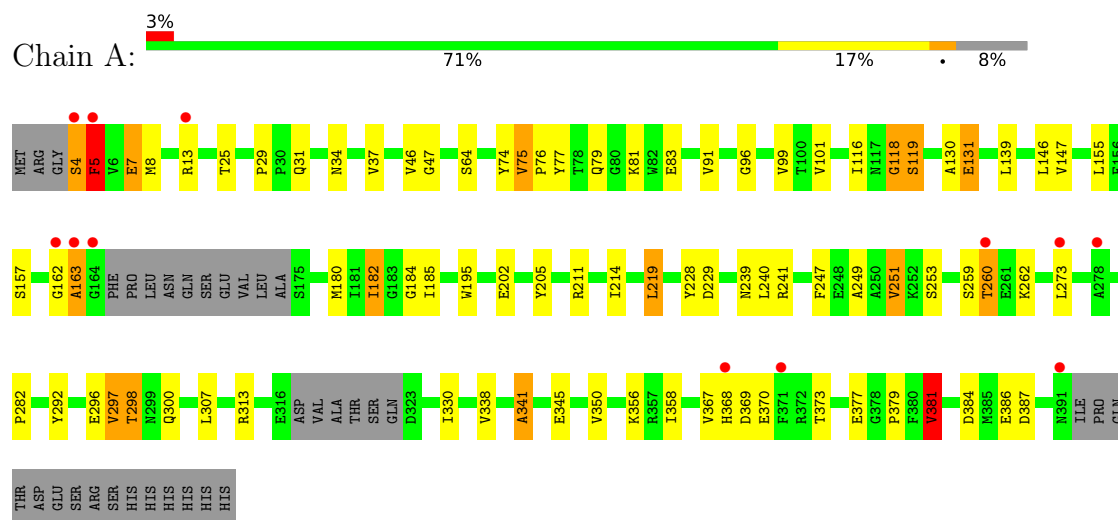
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	121	Total	O	0	0
			121	121		
3	B	108	Total	O	0	0
			108	108		
3	C	127	Total	O	0	0
			127	127		

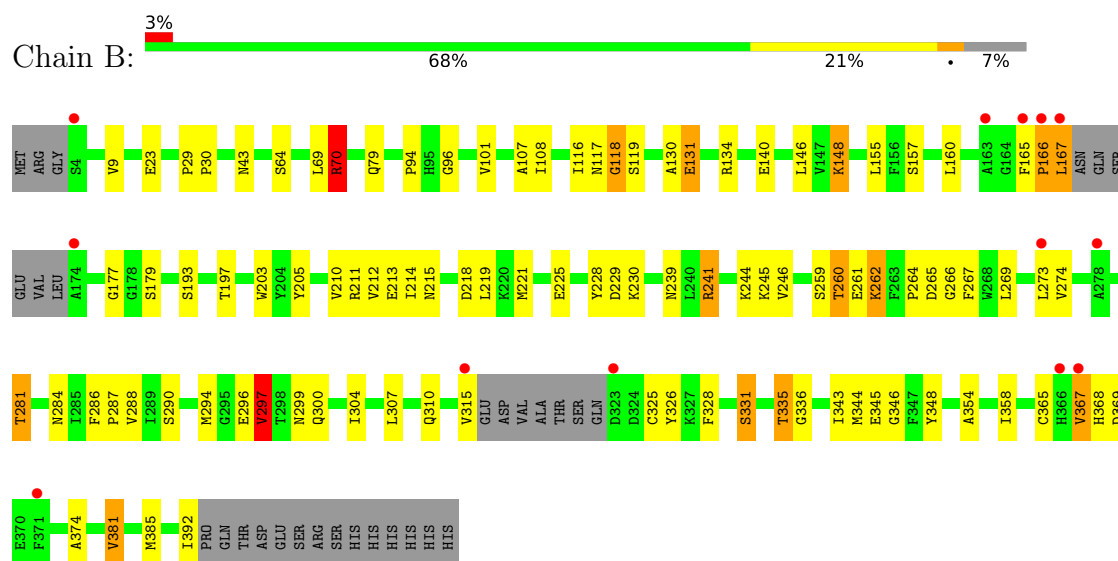
3 Residue-property plots

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.

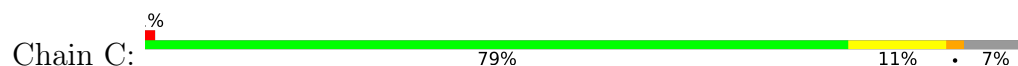
• Molecule 1: Beta-secretase 1

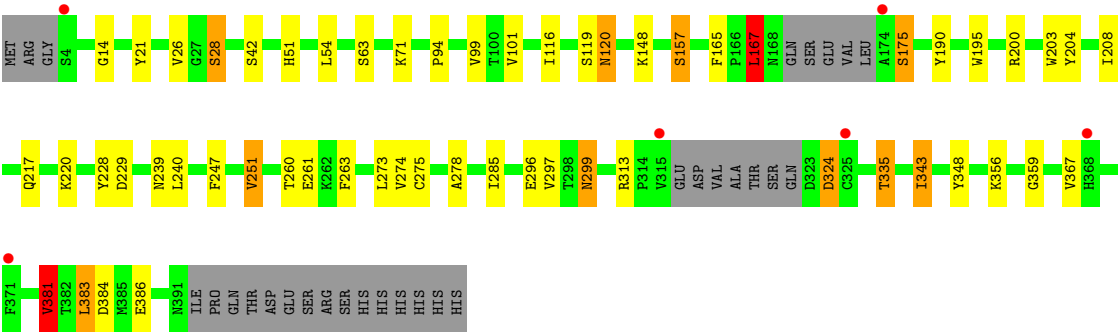


• Molecule 1: Beta-secretase 1



• Molecule 1: Beta-secretase 1





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.16Å 104.59Å 100.16Å 90.00° 104.50° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 20.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.5 (20.00-2.20) 96.4 (20.00-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.61 (at 2.19Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.231 , 0.279 (Not available) , 0.269	Depositor DCC
R_{free} test set	4011 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	57.3	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 31.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.54$, $\langle L^2 \rangle = 0.38$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9293	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.48% 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: 957

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	1.26	7/3002 (0.2%)	1.26	14/4077 (0.3%)
1	B	1.28	6/3034 (0.2%)	1.30	17/4122 (0.4%)
1	C	1.23	3/3034 (0.1%)	1.23	9/4122 (0.2%)
All	All	1.26	16/9070 (0.2%)	1.26	40/12321 (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
1	A	0	2
1	B	0	3
All	All	0	5

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	367	VAL	CA-CB	7.51	1.62	1.53
1	B	354	ALA	CA-CB	7.35	1.64	1.53
1	A	249	ALA	CA-CB	6.55	1.63	1.53
1	A	91	VAL	C-O	6.35	1.30	1.24
1	A	75	VAL	CA-C	-5.56	1.47	1.52
1	C	42	SER	CA-C	-5.56	1.45	1.52
1	A	34	ASN	CA-C	5.51	1.60	1.52
1	A	282	PRO	CA-C	5.49	1.57	1.52
1	C	175	SER	CA-C	5.42	1.60	1.52
1	B	107	ALA	CA-CB	5.36	1.59	1.52
1	B	108	ILE	C-O	5.21	1.28	1.23
1	B	118	GLY	C-O	5.17	1.30	1.23
1	B	177	GLY	N-CA	5.13	1.50	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	190	TYR	CA-C	-5.06	1.46	1.52
1	A	377	GLU	CA-C	-5.01	1.46	1.52
1	A	341	ALA	CA-CB	5.00	1.61	1.53

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	119	SER	N-CA-C	12.79	125.22	111.03
1	A	381	VAL	CB-CA-C	-9.49	98.21	111.21
1	C	381	VAL	CB-CA-C	-9.19	98.61	111.21
1	C	175	SER	N-CA-C	8.45	128.79	110.80
1	A	99	VAL	N-CA-C	7.63	119.71	108.65
1	B	344	MET	N-CA-C	7.15	119.15	111.36
1	B	96	GLY	CA-C-N	-7.12	113.33	120.31
1	B	96	GLY	C-N-CA	-7.12	113.33	120.31
1	A	75	VAL	CA-C-N	7.07	128.67	119.84
1	A	75	VAL	C-N-CA	7.07	128.67	119.84
1	B	165	PHE	CA-C-N	6.68	128.19	119.84
1	B	165	PHE	C-N-CA	6.68	128.19	119.84
1	A	370	GLU	N-CA-C	-6.58	105.25	113.28
1	C	343	ILE	N-CA-C	-6.55	103.86	111.00
1	A	147	VAL	N-CA-C	6.47	116.63	110.42
1	B	70	ARG	N-CA-C	6.47	120.49	112.47
1	C	324	ASP	N-CA-C	6.35	118.88	108.52
1	B	297	VAL	N-CA-CB	-6.31	101.87	112.47
1	B	118	GLY	N-CA-C	-6.20	98.49	113.18
1	A	29	PRO	CA-C-N	5.93	126.86	119.98
1	A	29	PRO	C-N-CA	5.93	126.86	119.98
1	C	296	GLU	N-CA-C	-5.93	104.94	111.82
1	A	369	ASP	N-CA-C	-5.91	100.32	109.24
1	C	239	ASN	N-CA-C	5.89	118.51	110.55
1	A	239	ASN	N-CA-C	5.83	118.05	110.53
1	B	328	PHE	N-CA-C	-5.74	100.63	109.76
1	B	367	VAL	CB-CA-C	5.61	117.28	111.23
1	C	99	VAL	N-CA-C	5.40	116.48	108.65
1	B	246	VAL	N-CA-C	-5.33	105.93	111.58
1	C	167	LEU	CA-CB-CG	5.32	134.92	116.30
1	A	202	GLU	N-CA-C	5.31	118.00	108.17
1	C	208	ILE	CB-CA-C	-5.21	103.39	110.42
1	B	374	ALA	N-CA-C	-5.19	103.29	110.35
1	B	297	VAL	CB-CA-C	5.15	118.31	110.90
1	A	368	HIS	N-CA-C	5.14	118.19	109.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	343	ILE	N-CA-C	-5.12	105.72	110.53
1	A	37	VAL	N-CA-CB	-5.06	105.29	111.21
1	B	365	CYS	CB-CA-C	5.05	119.91	112.03
1	B	197	THR	CA-C-N	-5.00	114.80	119.85
1	B	197	THR	C-N-CA	-5.00	114.80	119.85

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	118	GLY	Peptide
1	A	4	SER	Peptide
1	B	117	ASN	Peptide
1	B	203	TRP	Peptide
1	B	346	GLY	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	2928	0	2839	46	0
1	B	2958	0	2876	58	0
1	C	2958	0	2871	24	0
2	A	31	0	32	1	0
2	B	31	0	32	1	0
2	C	31	0	32	0	0
3	A	121	0	0	5	0
3	B	108	0	0	9	1
3	C	127	0	0	2	1
All	All	9293	0	8682	123	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 7.

All (123) 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:A:5:PHE:HB3	3:A:502:HOH:O	1.48	1.10
1:B:215:ASN:HA	3:B:411:HOH:O	1.58	1.01
1:B:166:PRO:O	1:B:167:LEU:HB2	1.70	0.91
1:C:335:THR:HG23	3:C:511:HOH:O	1.69	0.91
1:A:381:VAL:HG22	1:C:381:VAL:HG22	1.56	0.88
1:B:118:GLY:CA	3:B:439:HOH:O	2.21	0.88
1:B:119:SER:HA	3:B:439:HOH:O	1.78	0.84
1:A:155:LEU:HD22	1:A:184:GLY:HA2	1.61	0.83
1:B:214:ILE:HD12	1:B:219:LEU:HD13	1.62	0.79
1:B:43:ASN:HD21	1:B:134:ARG:H	1.33	0.75
1:B:118:GLY:HA3	3:B:439:HOH:O	1.85	0.70
1:A:296:GLU:H	1:A:300:GLN:HE22	1.39	0.70
1:B:119:SER:CA	3:B:439:HOH:O	2.39	0.69
1:B:23:GLU:HG2	1:B:94:PRO:HG2	1.74	0.69
1:C:260:THR:O	1:C:261:GLU:HG3	1.92	0.67
1:A:155:LEU:CD2	1:A:184:GLY:HA2	2.24	0.67
1:A:247:PHE:O	1:A:251:VAL:CG1	2.45	0.65
1:B:213:GLU:OE1	3:B:434:HOH:O	2.13	0.64
1:C:275:CYS:HA	1:C:324:ASP:O	1.99	0.62
1:B:214:ILE:HD12	1:B:219:LEU:CD1	2.30	0.62
1:A:116:ILE:O	1:A:119:SER:HB2	1.98	0.62
1:A:8:MET:HG2	1:A:96:GLY:HA2	1.83	0.61
1:B:166:PRO:O	1:B:167:LEU:CB	2.46	0.61
1:A:247:PHE:O	1:A:251:VAL:HG13	2.01	0.59
1:B:211:ARG:NH1	1:C:384:ASP:OD1	2.35	0.59
1:A:4:SER:O	1:A:4:SER:OG	2.01	0.59
1:A:162:GLY:O	1:A:163:ALA:HB3	2.04	0.58
1:A:356:LYS:HD3	3:A:473:HOH:O	2.03	0.58
1:B:315:VAL:O	1:B:325:CYS:HB2	2.04	0.57
1:A:7:GLU:HB2	3:A:502:HOH:O	2.04	0.56
1:C:119:SER:O	1:C:120:ASN:HB2	2.06	0.56
1:C:247:PHE:O	1:C:251:VAL:HG13	2.06	0.56
1:B:335:THR:HG23	3:B:486:HOH:O	2.05	0.56
1:C:157:SER:HB2	1:C:348:TYR:CE1	2.40	0.56
1:B:296:GLU:H	1:B:300:GLN:HE22	1.53	0.55
1:B:281:THR:HG21	1:B:326:TYR:CE1	2.41	0.54
1:B:335:THR:CG2	3:B:486:HOH:O	2.55	0.54
1:B:239:ASN:HD22	1:B:331:SER:HB3	1.72	0.54
1:A:5:PHE:CB	3:A:502:HOH:O	2.27	0.54
1:C:299:ASN:HB3	1:C:381:VAL:HG13	1.89	0.54
1:A:180:MET:HE3	1:A:182:ILE:HD11	1.90	0.53
1:B:294:MET:HE2	1:B:385:MET:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:116:ILE:O	1:B:119:SER:HB3	2.08	0.52
1:C:299:ASN:HA	1:C:381:VAL:HA	1.91	0.52
1:B:210:VAL:HG11	1:B:385:MET:HG2	1.92	0.52
1:B:140:GLU:OE1	1:B:148:LYS:HE3	2.09	0.52
1:C:28:SER:O	1:C:63:SER:HA	2.09	0.52
1:A:195:TRP:CZ3	1:B:297:VAL:HG13	2.45	0.52
1:A:241:ARG:HB2	1:A:338:VAL:HB	1.92	0.52
1:A:25:THR:HA	1:A:31:GLN:O	2.11	0.51
1:A:247:PHE:O	1:A:251:VAL:HG12	2.11	0.51
1:A:240:LEU:O	1:A:330:ILE:HA	2.12	0.50
1:A:162:GLY:O	1:A:163:ALA:CB	2.59	0.50
1:A:46:VAL:O	1:A:47:GLY:C	2.52	0.50
1:A:101:VAL:HG11	1:A:146:LEU:HA	1.93	0.50
2:B:407:957:H18A	2:B:407:957:C10	2.42	0.50
1:B:211:ARG:HG2	1:B:212:VAL:N	2.26	0.49
1:B:264:PRO:C	1:B:266:GLY:H	2.20	0.49
1:A:4:SER:N	1:A:185:ILE:O	2.45	0.49
1:A:5:PHE:HD1	3:A:502:HOH:O	1.96	0.49
1:B:211:ARG:NH2	1:B:218:ASP:HB2	2.27	0.49
1:B:160:LEU:O	1:B:345:GLU:HA	2.13	0.49
1:B:288:VAL:HG12	1:B:307:LEU:HD23	1.94	0.48
1:A:155:LEU:CD2	1:A:184:GLY:CA	2.91	0.48
1:C:165:PHE:O	1:C:167:LEU:HD22	2.13	0.47
1:C:299:ASN:HD22	1:C:299:ASN:C	2.22	0.47
1:C:14:GLY:HA2	1:C:21:TYR:CE2	2.49	0.47
1:B:130:ALA:O	1:B:131:GLU:C	2.57	0.47
1:C:195:TRP:O	1:C:359:GLY:HA2	2.16	0.46
1:A:384:ASP:HB3	1:A:387:ASP:OD1	2.14	0.46
1:A:298:THR:HG23	3:B:464:HOH:O	2.15	0.46
1:B:281:THR:CG2	1:B:326:TYR:CE1	2.98	0.46
1:B:392:ILE:H	1:B:392:ILE:HD12	1.80	0.46
1:C:116:ILE:HB	1:C:119:SER:HB3	1.98	0.46
1:A:298:THR:HG21	1:B:193:SER:HB3	1.98	0.46
1:B:267:PHE:CD1	1:B:274:VAL:HG23	2.51	0.46
1:A:77:TYR:CG	2:A:407:957:H26	2.52	0.45
1:B:221:MET:CE	1:B:225:GLU:HG3	2.46	0.45
1:A:297:VAL:H	1:A:300:GLN:NE2	2.13	0.45
1:B:221:MET:HE2	1:B:225:GLU:HG3	1.97	0.45
1:B:262:LYS:N	1:B:262:LYS:HD2	2.31	0.45
1:B:273:LEU:H	1:B:273:LEU:HD12	1.81	0.45
1:C:299:ASN:CB	1:C:381:VAL:HG13	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:221:MET:HE2	1:B:225:GLU:CB	2.47	0.44
1:B:307:LEU:N	1:B:310:GLN:OE1	2.49	0.44
1:C:228:TYR:HA	1:C:229:ASP:HA	1.73	0.44
1:A:76:PRO:HA	1:A:81:LYS:HB3	2.00	0.43
1:B:335:THR:HG23	1:B:335:THR:O	2.18	0.43
1:A:211:ARG:HB3	1:A:292:TYR:HB2	2.00	0.43
1:A:219:LEU:HA	1:A:219:LEU:HD12	1.60	0.43
1:B:230:LYS:O	1:B:336:GLY:HA3	2.19	0.43
1:B:273:LEU:HD12	1:B:273:LEU:N	2.33	0.43
1:B:259:SER:O	1:B:261:GLU:N	2.51	0.43
1:A:74:TYR:HA	1:A:83:GLU:HA	2.01	0.43
1:B:241:ARG:HA	1:B:331:SER:O	2.19	0.43
1:A:259:SER:O	1:A:260:THR:C	2.61	0.43
1:B:381:VAL:CG2	1:C:383:LEU:HD13	2.49	0.43
1:B:286:PHE:HA	1:B:287:PRO:HD3	1.89	0.42
1:B:101:VAL:HG11	1:B:146:LEU:HA	2.01	0.42
1:B:264:PRO:C	1:B:266:GLY:N	2.77	0.42
1:A:139:LEU:HD12	1:A:139:LEU:HA	1.91	0.42
1:B:157:SER:HB2	1:B:348:TYR:CE1	2.54	0.42
1:B:299:ASN:O	1:B:381:VAL:HA	2.19	0.42
1:B:205:TYR:HB3	1:B:358:ILE:HD11	2.00	0.42
1:A:379:PRO:HG2	1:B:381:VAL:HG12	2.00	0.42
1:B:228:TYR:HA	1:B:229:ASP:HA	1.77	0.42
1:A:228:TYR:HA	1:A:229:ASP:HA	1.74	0.42
1:B:155:LEU:C	1:B:155:LEU:HD23	2.44	0.42
1:A:296:GLU:N	1:A:300:GLN:HE22	2.12	0.41
1:A:205:TYR:HB3	1:A:358:ILE:HD11	2.02	0.41
1:B:290:SER:HA	1:B:304:ILE:O	2.20	0.41
1:C:263:PHE:CD2	1:C:274:VAL:HG21	2.56	0.41
1:A:75:VAL:HA	1:A:76:PRO:HD3	1.78	0.41
1:C:51:HIS:HB3	1:C:54:LEU:HG	2.03	0.41
1:C:203:TRP:CG	1:C:204:TYR:H	2.39	0.41
1:C:335:THR:CG2	3:C:511:HOH:O	2.46	0.41
1:A:341:ALA:O	1:A:345:GLU:HG3	2.21	0.40
1:A:350:VAL:O	1:A:358:ILE:HA	2.21	0.40
1:A:307:LEU:HD12	1:A:367:VAL:HG23	2.02	0.40
1:B:29:PRO:HA	1:B:30:PRO:HD3	1.96	0.40
1:A:130:ALA:O	1:A:131:GLU:C	2.65	0.40
1:B:69:LEU:HD23	1:B:69:LEU:HA	1.84	0.40
1:C:240:LEU:HB2	1:C:343:ILE:HD11	2.02	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:478:HOH:O	3:C:463:HOH:O[1_455]	2.04	0.16

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	366/406 (90%)	347 (95%)	16 (4%)	3 (1%)	16	16
1	B	370/406 (91%)	349 (94%)	16 (4%)	5 (1%)	9	7
1	C	370/406 (91%)	343 (93%)	26 (7%)	1 (0%)	36	42
All	All	1106/1218 (91%)	1039 (94%)	58 (5%)	9 (1%)	16	16

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	166	PRO
1	A	118	GLY
1	B	260	THR
1	B	265	ASP
1	C	278	ALA
1	A	163	ALA
1	A	5	PHE
1	B	70	ARG
1	B	369	ASP

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	A	317/348 (91%)	296 (93%)	21 (7%)	15	18
1	B	320/348 (92%)	298 (93%)	22 (7%)	14	16
1	C	320/348 (92%)	295 (92%)	25 (8%)	11	13
All	All	957/1044 (92%)	889 (93%)	68 (7%)	13	16

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	PHE
1	A	7	GLU
1	A	13	ARG
1	A	64	SER
1	A	79	GLN
1	A	131	GLU
1	A	157	SER
1	A	182	ILE
1	A	214	ILE
1	A	219	LEU
1	A	251	VAL
1	A	253	SER
1	A	260	THR
1	A	262	LYS
1	A	273	LEU
1	A	297	VAL
1	A	298	THR
1	A	313	ARG
1	A	373	THR
1	A	381	VAL
1	A	386	GLU
1	B	9	VAL
1	B	64	SER
1	B	70	ARG
1	B	79	GLN
1	B	131	GLU
1	B	148	LYS
1	B	167	LEU
1	B	179	SER
1	B	241	ARG
1	B	244	LYS
1	B	245	LYS

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Mol	Chain	Res	Type
1	B	260	THR
1	B	262	LYS
1	B	269	LEU
1	B	281	THR
1	B	284	ASN
1	B	297	VAL
1	B	331	SER
1	B	335	THR
1	B	367	VAL
1	B	368	HIS
1	B	381	VAL
1	C	26	VAL
1	C	28	SER
1	C	71	LYS
1	C	94	PRO
1	C	101	VAL
1	C	120	ASN
1	C	148	LYS
1	C	157	SER
1	C	167	LEU
1	C	175	SER
1	C	200	ARG
1	C	217	GLN
1	C	220	LYS
1	C	251	VAL
1	C	273	LEU
1	C	285	ILE
1	C	297	VAL
1	C	299	ASN
1	C	313	ARG
1	C	335	THR
1	C	356	LYS
1	C	367	VAL
1	C	381	VAL
1	C	383	LEU
1	C	386	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	A	284	ASN

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Mol	Chain	Res	Type
1	A	300	GLN
1	A	368	HIS
1	B	43	ASN
1	B	120	ASN
1	B	239	ASN
1	B	300	GLN
1	B	332	GLN
1	B	366	HIS
1	C	98	ASN
1	C	104	ASN
1	C	217	GLN
1	C	284	ASN
1	C	299	ASN
1	C	300	GLN
1	C	368	HIS

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 ⓘ

3 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	957	C	407	-	31,33,33	1.92	8 (25%)	42,49,49	2.02	12 (28%)
2	957	A	407	-	31,33,33	1.65	6 (19%)	42,49,49	1.91	9 (21%)
2	957	B	407	-	31,33,33	1.81	5 (16%)	42,49,49	2.09	12 (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
2	957	C	407	-	-	1/20/33/33	0/3/3/3
2	957	A	407	-	-	0/20/33/33	0/3/3/3
2	957	B	407	-	-	0/20/33/33	0/3/3/3

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	407	957	F28-C25	5.80	1.50	1.36
2	B	407	957	F28-C25	5.59	1.49	1.36
2	B	407	957	F27-C23	5.46	1.49	1.36
2	C	407	957	F28-C25	5.43	1.49	1.36
2	C	407	957	F27-C23	4.90	1.48	1.36
2	A	407	957	F27-C23	3.78	1.45	1.36
2	B	407	957	C31-C8	3.31	1.55	1.51
2	C	407	957	C14-C11	3.22	1.55	1.51
2	C	407	957	C26-C25	3.19	1.43	1.37
2	B	407	957	C12-C11	2.76	1.42	1.36
2	C	407	957	C30-C8	2.74	1.54	1.51
2	C	407	957	C31-C30	2.63	1.56	1.50
2	C	407	957	C22-C23	2.45	1.41	1.37
2	A	407	957	C30-C8	2.42	1.54	1.51
2	C	407	957	C12-C11	2.23	1.41	1.36
2	A	407	957	C31-C8	2.18	1.53	1.51
2	A	407	957	C5-C4	-2.10	1.50	1.53
2	B	407	957	C22-C23	2.07	1.41	1.37
2	A	407	957	C26-C25	2.06	1.41	1.37

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	407	957	C30-C8-N7	-5.98	111.62	117.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	407	957	C10-C11-C12	5.98	115.99	111.20
2	B	407	957	C11-C12-S13	-5.92	107.96	112.74
2	C	407	957	C31-C8-N7	5.54	122.56	117.30
2	B	407	957	C21-C20-C4	-4.92	105.06	113.40
2	A	407	957	C31-C8-N7	4.69	121.75	117.30
2	A	407	957	C21-C20-C4	-4.53	105.72	113.40
2	A	407	957	F28-C25-C26	4.52	124.70	118.28
2	C	407	957	C11-C12-S13	-3.93	109.57	112.74
2	B	407	957	C14-C11-C12	-3.70	118.35	125.60
2	A	407	957	F27-C23-C22	3.34	123.02	118.28
2	C	407	957	C30-C8-C9	-3.28	111.02	117.58
2	A	407	957	C11-C12-S13	-3.27	110.10	112.74
2	A	407	957	C26-C25-C24	-3.27	119.53	123.50
2	A	407	957	C10-C11-C12	3.23	113.79	111.20
2	B	407	957	C25-C24-C23	3.09	120.59	116.08
2	C	407	957	C10-C11-C12	3.02	113.62	111.20
2	B	407	957	F27-C23-C22	2.97	122.50	118.28
2	C	407	957	C20-C4-N3	-2.90	105.97	110.08
2	B	407	957	C24-C23-C22	-2.81	120.08	123.50
2	B	407	957	C26-C25-C24	-2.71	120.21	123.50
2	A	407	957	C25-C24-C23	2.71	120.03	116.08
2	C	407	957	C21-C20-C4	-2.57	109.03	113.40
2	C	407	957	C26-C25-C24	-2.30	120.71	123.50
2	C	407	957	F28-C25-C26	2.26	121.49	118.28
2	C	407	957	C31-C8-C30	2.26	61.08	59.00
2	A	407	957	C24-C23-C22	-2.21	120.82	123.50
2	B	407	957	O19-C2-C1	-2.19	118.15	122.05
2	C	407	957	F27-C23-C22	2.19	121.39	118.28
2	C	407	957	C31-C30-C8	-2.11	59.20	60.50
2	B	407	957	C12-S13-C9	2.10	94.48	92.40
2	B	407	957	C1-C2-N3	2.08	119.57	116.12
2	B	407	957	F28-C25-C26	2.04	121.18	118.28

There are no chirality outliers.

All (1) torsion outliers are listed below:

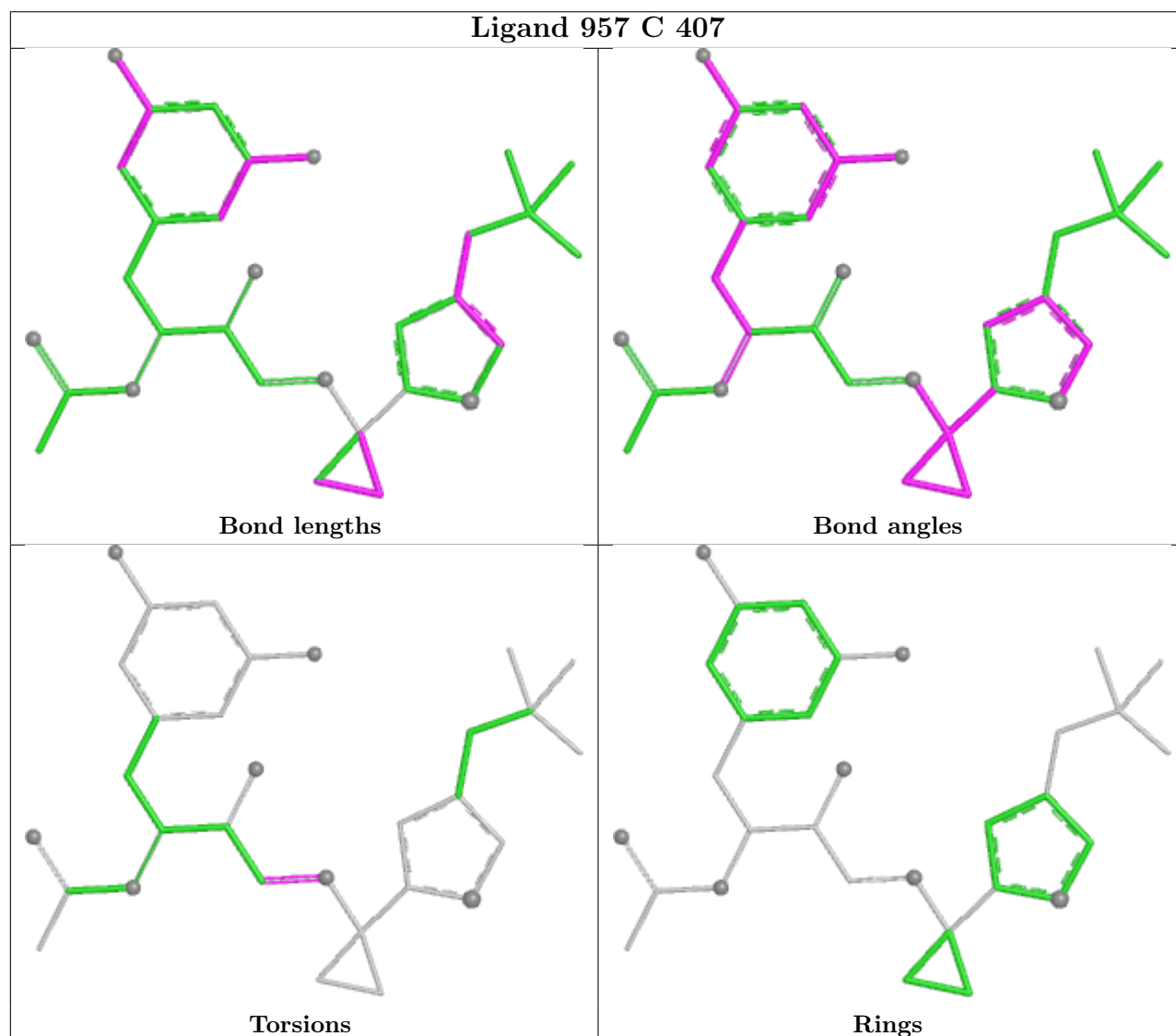
Mol	Chain	Res	Type	Atoms
2	C	407	957	C5-C6-N7-C8

There are no ring outliers.

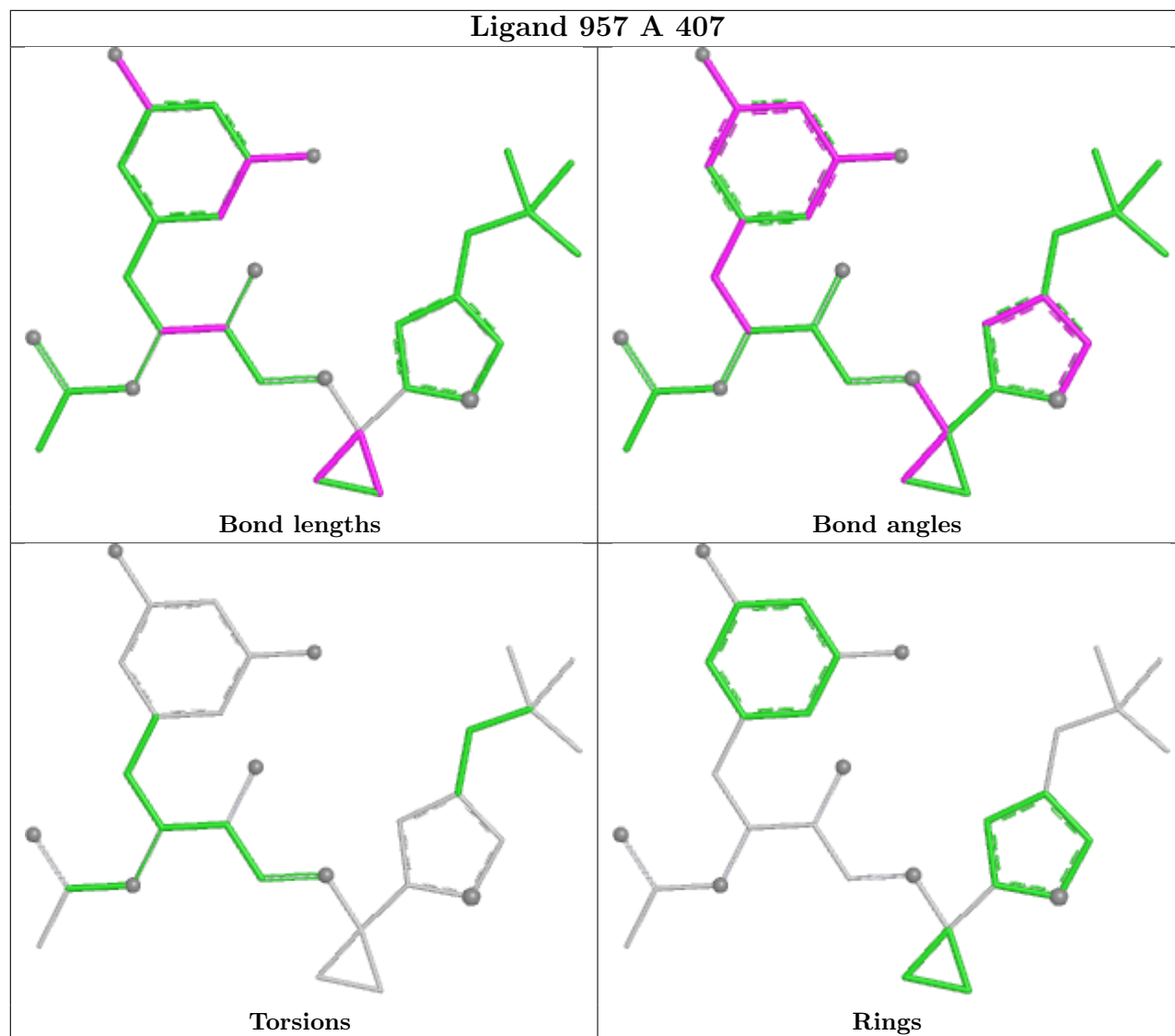
2 monomers are involved in 2 short contacts:

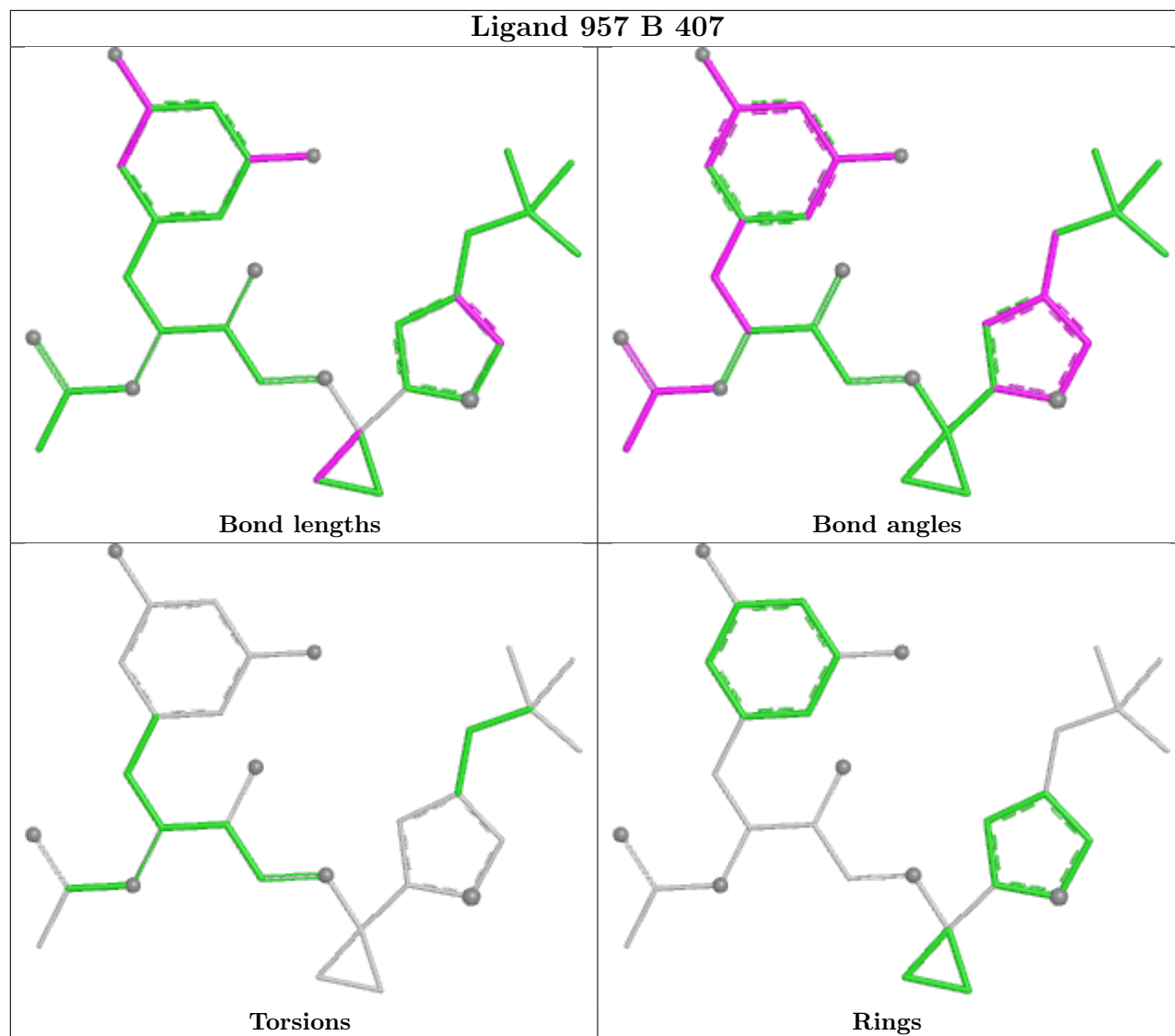
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	407	957	1	0
2	B	407	957	1	0

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.



Ligand 957 A 407





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	372/406 (91%)	0.00	12 (3%) 50 47	34, 51, 81, 89	0
1	B	376/406 (92%)	0.06	13 (3%) 47 44	33, 52, 84, 93	0
1	C	376/406 (92%)	-0.05	6 (1%) 70 67	36, 50, 81, 90	0
All	All	1124/1218 (92%)	0.01	31 (2%) 55 52	33, 51, 82, 93	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	315	VAL	3.9
1	C	174	ALA	3.9
1	C	325	CYS	3.8
1	B	165	PHE	3.7
1	B	167	LEU	3.7
1	C	371	PHE	3.1
1	C	368	HIS	3.1
1	A	164	GLY	3.0
1	A	368	HIS	2.9
1	B	367	VAL	2.8
1	B	278	ALA	2.8
1	A	273	LEU	2.7
1	B	166	PRO	2.6
1	A	260	THR	2.5
1	B	371	PHE	2.5
1	A	5	PHE	2.4
1	A	371	PHE	2.4
1	B	315	VAL	2.4
1	B	366	HIS	2.4
1	A	162	GLY	2.3
1	A	4	SER	2.3
1	A	13	ARG	2.3
1	B	4	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	391	ASN	2.3
1	B	174	ALA	2.2
1	C	4	SER	2.2
1	B	323	ASP	2.2
1	B	273	LEU	2.1
1	A	163	ALA	2.1
1	A	278	ALA	2.1
1	B	163	ALA	2.1

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](#)

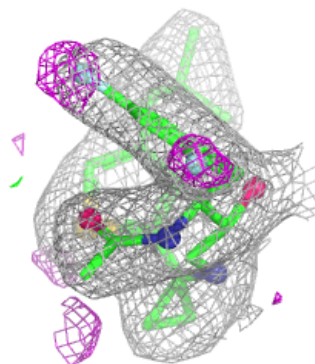
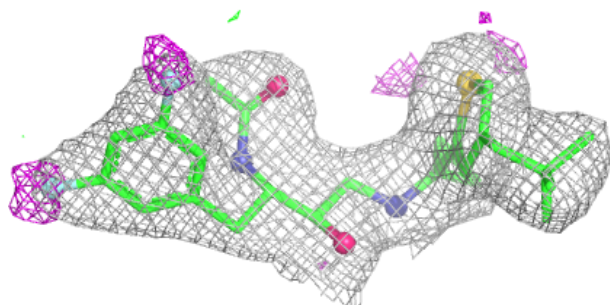
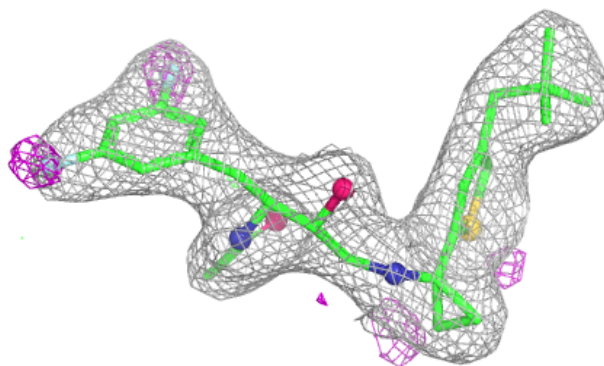
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
2	957	B	407	31/31	0.94	0.08	35,43,47,50	0
2	957	A	407	31/31	0.95	0.07	32,42,46,50	0
2	957	C	407	31/31	0.95	0.07	32,37,41,42	0

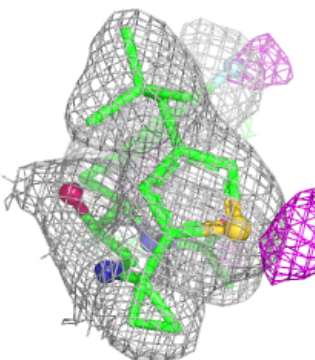
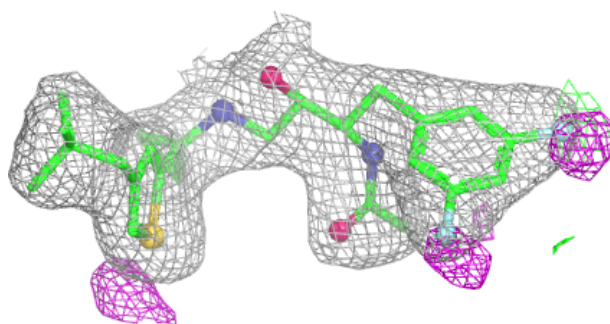
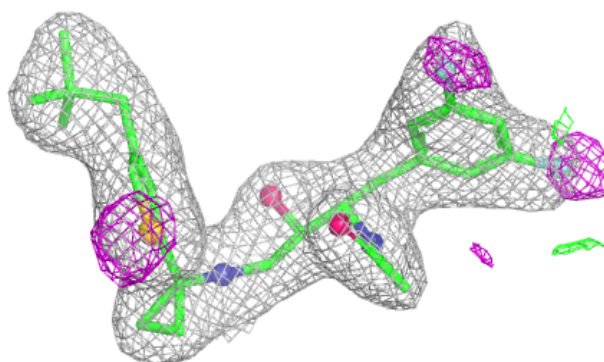
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

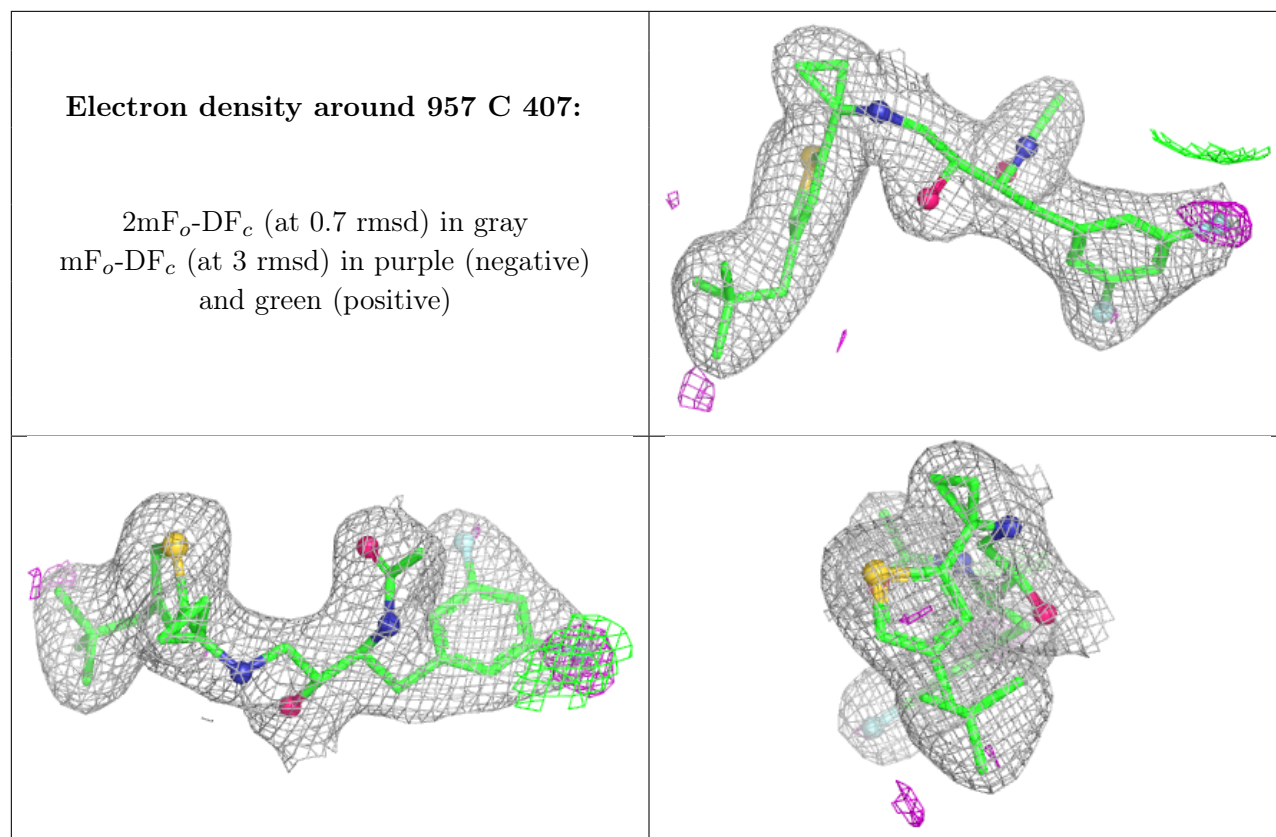
Electron density around 957 B 407:

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

**Electron density around 957 A 407:**

$2mF_o-DF_c$ (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.