



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 11, 2025 – 06:08 PM EDT

PDB ID : 8USY
Title : HIV-1 Integrase F185H N222K Complexed with Allosteric Inhibitor BI-D
Authors : Montermoso, S.; Gupta, K.; Eilers, G.; Bushman, F.D.; Van Duyne, G.D.
Deposited on : 2023-10-30
Resolution : 4.40 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.4

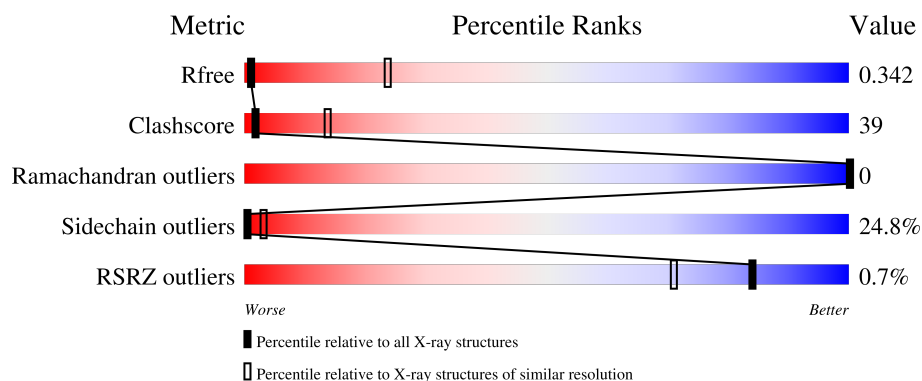
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	1013 (4.90-3.90)
Clashscore	180529	1066 (4.90-3.90)
Ramachandran outliers	177936	1019 (4.92-3.86)
Sidechain outliers	177891	1003 (4.92-3.86)
RSRZ outliers	164620	1010 (4.90-3.90)

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	293	<div> <div></div> <div> <div></div> <div>24%</div> <div>37%</div> <div>11%</div> <div>•</div> <div>27%</div> </div> </div>
1	B	293	<div> <div></div> <div> <div></div> <div>29%</div> <div>34%</div> <div>9%</div> <div>•</div> <div>26%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4324 atoms, of which 869 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.

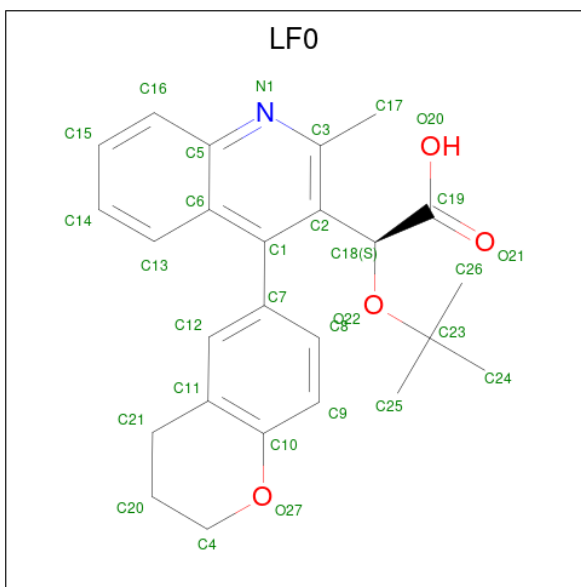
- Molecule 1 is a protein called Integrase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	214	Total	C	H	N	O	S	0	0	0
			2100	1080	407	303	304	6			
1	B	216	Total	C	H	N	O	S	0	0	0
			2112	1083	410	306	307	6			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	HIS	-	cloning artifact	UNP P12497
A	15	ALA	TYR	engineered mutation	UNP P12497
A	185	HIS	PHE	engineered mutation	UNP P12497
A	222	LYS	ASN	engineered mutation	UNP P12497
A	289	CYS	-	expression tag	UNP P12497
A	290	THR	-	expression tag	UNP P12497
A	291	LEU	-	expression tag	UNP P12497
A	292	GLU	-	expression tag	UNP P12497
A	293	TYR	-	expression tag	UNP P12497
B	1	HIS	-	cloning artifact	UNP P12497
B	15	ALA	TYR	engineered mutation	UNP P12497
B	185	HIS	PHE	engineered mutation	UNP P12497
B	222	LYS	ASN	engineered mutation	UNP P12497
B	289	CYS	-	expression tag	UNP P12497
B	290	THR	-	expression tag	UNP P12497
B	291	LEU	-	expression tag	UNP P12497
B	292	GLU	-	expression tag	UNP P12497
B	293	TYR	-	expression tag	UNP P12497

- Molecule 2 is (2S)-tert-butoxy[4-(3,4-dihydro-2H-chromen-6-yl)-2-methylquinolin-3-yl]ethanoic acid (three-letter code: LF0) (formula: C₂₅H₂₇NO₄) (labeled as "Ligand of Interest" by depositor).

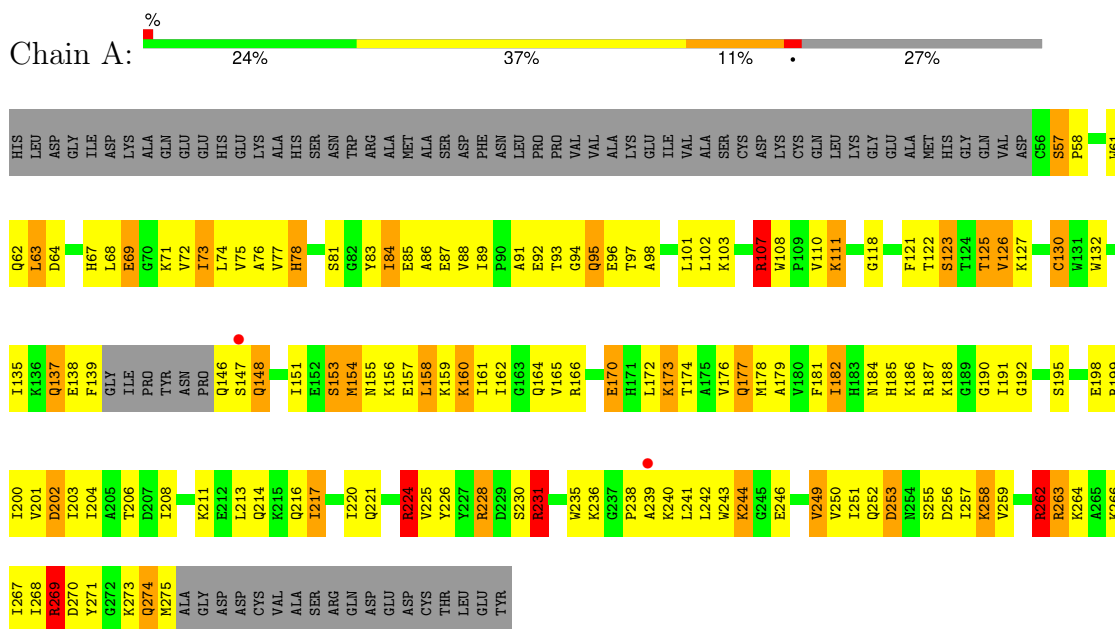


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	0	0
			56	25	26	1	4		
2	A	1	Total	C	H	N	O	0	0
			56	25	26	1	4		

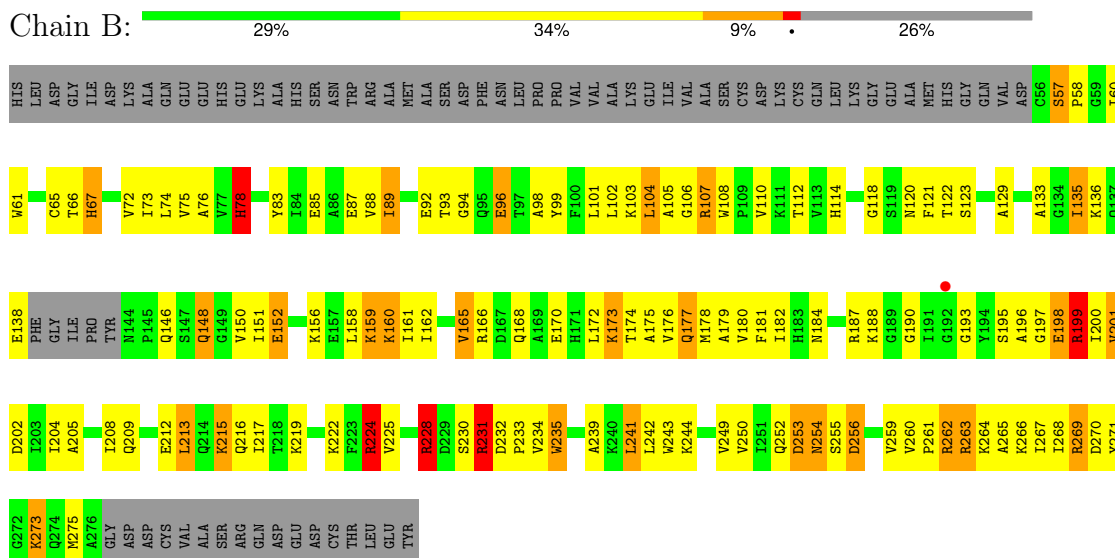
3 Residue-property plots

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: Integrase



• Molecule 1: Integrase



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	106.03Å 106.03Å 245.81Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 4.40 20.00 – 4.40	Depositor EDS
% Data completeness (in resolution range)	99.4 (20.00-4.40) 86.1 (20.00-4.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.05 (at 4.15Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.299 , 0.339 0.323 , 0.342	Depositor DCC
R_{free} test set	5035 reflections (9.92%)	wwPDB-VP
Wilson B-factor (Å ²)	221.9	Xtriage
Anisotropy	0.154	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 210.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4324	wwPDB-VP
Average B, all atoms (Å ²)	263.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.88% 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: LF0

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	0.49	0/1726	1.18	14/2327 (0.6%)
1	B	0.48	0/1735	1.12	14/2341 (0.6%)
All	All	0.49	0/3461	1.15	28/4668 (0.6%)

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	7
1	B	0	5
All	All	0	12

There are no bond length outliers.

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	269	ARG	NE-CZ-NH2	-16.94	111.83	120.30
1	A	224	ARG	NE-CZ-NH2	-16.08	112.26	120.30
1	A	262	ARG	NE-CZ-NH2	-15.06	112.77	120.30
1	B	199	ARG	NE-CZ-NH2	-14.87	112.86	120.30
1	A	224	ARG	NE-CZ-NH1	14.44	127.52	120.30
1	A	262	ARG	NE-CZ-NH1	14.14	127.37	120.30
1	B	199	ARG	NE-CZ-NH1	13.98	127.29	120.30
1	B	228	ARG	NE-CZ-NH2	-11.77	114.42	120.30
1	B	228	ARG	NE-CZ-NH1	11.28	125.94	120.30
1	A	107	ARG	NE-CZ-NH2	-10.88	114.86	120.30
1	A	269	ARG	NE-CZ-NH1	10.60	125.60	120.30
1	A	107	ARG	NE-CZ-NH1	10.38	125.49	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	262	ARG	NE-CZ-NH2	-10.02	115.29	120.30
1	B	224	ARG	NE-CZ-NH2	-9.43	115.59	120.30
1	B	262	ARG	NE-CZ-NH1	9.00	124.80	120.30
1	B	231	ARG	NE-CZ-NH2	-8.77	115.92	120.30
1	B	224	ARG	NE-CZ-NH1	8.25	124.42	120.30
1	B	231	ARG	NE-CZ-NH1	8.13	124.36	120.30
1	B	199	ARG	CG-CD-NE	6.45	125.35	111.80
1	A	224	ARG	CG-CD-NE	-6.22	98.73	111.80
1	A	78	HIS	N-CA-C	-6.15	94.38	111.00
1	B	78	HIS	N-CA-C	-6.07	94.60	111.00
1	A	262	ARG	CG-CD-NE	5.74	123.86	111.80
1	A	231	ARG	NE-CZ-NH2	5.45	123.03	120.30
1	B	228	ARG	CG-CD-NE	5.38	123.11	111.80
1	A	231	ARG	NE-CZ-NH1	-5.18	117.71	120.30
1	A	190	GLY	N-CA-C	-5.12	100.30	113.10
1	B	253	ASP	N-CA-C	-5.06	97.33	111.00

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	107	ARG	Sidechain
1	A	166	ARG	Sidechain
1	A	224	ARG	Sidechain
1	A	231	ARG	Sidechain
1	A	262	ARG	Sidechain
1	A	263	ARG	Sidechain
1	A	269	ARG	Sidechain
1	B	199	ARG	Sidechain
1	B	224	ARG	Sidechain
1	B	228	ARG	Sidechain
1	B	231	ARG	Sidechain
1	B	262	ARG	Sidechain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1693	407	1733	158	1
1	B	1702	410	1742	134	0
2	A	60	52	52	7	0
All	All	3455	869	3527	272	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 39.

All (272) 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:73:ILE:HA	1:A:89:ILE:HG13	1.44	0.98
1:A:95:GLN:HA	1:A:125:THR:HG21	1.44	0.98
1:A:250:VAL:HG13	1:A:259:VAL:HG22	1.55	0.89
1:A:187:ARG:HD2	1:A:191:ILE:HB	1.57	0.86
1:A:77:VAL:HG22	1:A:84:ILE:HG23	1.62	0.81
1:A:72:VAL:HG21	1:A:92:GLU:HB2	1.63	0.79
1:B:165:VAL:HG23	1:B:175:ALA:HB1	1.66	0.77
1:B:225:VAL:HG22	1:B:267:ILE:HG23	1.67	0.77
1:A:73:ILE:HB	1:A:87:GLU:O	1.84	0.76
1:B:104:LEU:HD21	1:B:110:VAL:HG21	1.68	0.76
1:B:98:ALA:HA	1:B:101:LEU:HD12	1.68	0.76
1:A:252:GLN:HB2	1:A:257:ILE:HD12	1.68	0.76
1:B:73:ILE:HG12	1:B:88:VAL:HG22	1.69	0.75
2:A:302:LF0:H2	1:B:129:ALA:HB2	1.68	0.74
1:B:213:LEU:O	1:B:217:ILE:HD12	1.85	0.74
1:A:271:TYR:OH	1:A:273:LYS:HD3	1.87	0.74
1:A:243:TRP:HE3	1:A:250:VAL:HG23	1.52	0.73
1:A:151:ILE:HA	1:A:154:MET:HG2	1.72	0.71
1:B:65:CYS:SG	1:B:74:LEU:HA	2.31	0.71
1:A:81:SER:HB3	1:A:200:ILE:HG12	1.74	0.69
1:B:213:LEU:HA	1:B:216:GLN:HG2	1.73	0.69
1:A:200:ILE:HA	1:A:203:ILE:HD13	1.74	0.69
1:A:178:MET:O	1:A:182:ILE:HD12	1.93	0.69
1:B:260:VAL:HB	1:B:261:PRO:HD2	1.74	0.69
1:A:58:PRO:HA	1:A:78:HIS:HE2	1.58	0.69
1:A:162:ILE:HD13	1:A:176:VAL:HG22	1.76	0.68
1:B:242:LEU:HD11	1:B:252:GLN:HB2	1.75	0.68
1:B:179:ALA:HA	1:B:182:ILE:HD12	1.75	0.67
1:A:204:ILE:HG22	1:B:201:VAL:HG21	1.77	0.67
1:A:155:ASN:HA	1:A:158:LEU:HD23	1.77	0.66
1:A:121:PHE:CD1	1:A:137:GLN:HG3	2.30	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:ASP:O	1:A:206:THR:HG23	1.96	0.66
1:B:133:ALA:HB1	1:B:135:ILE:HG12	1.76	0.66
1:A:200:ILE:HB	1:A:203:ILE:HB	1.78	0.66
1:B:148:GLN:HA	1:B:151:ILE:HD12	1.79	0.65
1:A:72:VAL:CG2	1:A:92:GLU:HB2	2.26	0.65
1:A:68:LEU:HD21	1:A:172:LEU:HD23	1.79	0.65
1:A:184:ASN:HB3	1:A:199:ARG:HH12	1.62	0.65
1:A:76:ALA:O	1:A:84:ILE:HA	1.97	0.64
1:A:242:LEU:HD21	1:A:252:GLN:HB3	1.79	0.64
1:B:253:ASP:HB3	1:B:256:ASP:H	1.62	0.64
1:A:81:SER:CB	1:A:200:ILE:HG12	2.28	0.63
1:A:271:TYR:CZ	1:A:273:LYS:HD3	2.33	0.63
1:B:180:VAL:HG12	1:B:184:ASN:HD21	1.63	0.63
1:A:73:ILE:HB	1:A:88:VAL:HA	1.82	0.62
1:B:250:VAL:HA	1:B:259:VAL:HG12	1.82	0.62
1:A:243:TRP:CE3	1:A:250:VAL:HG23	2.34	0.61
1:A:269:ARG:HG3	1:A:270:ASP:N	2.14	0.61
1:A:83:TYR:HB2	1:A:199:ARG:HD3	1.82	0.61
1:A:178:MET:HG3	1:B:102:LEU:HD21	1.82	0.61
1:A:182:ILE:O	1:A:186:LYS:HB2	2.01	0.61
1:A:187:ARG:CD	1:A:191:ILE:HB	2.30	0.61
1:A:244:LYS:HA	1:A:249:VAL:HG22	1.83	0.61
1:A:57:SER:N	1:A:58:PRO:HD2	2.16	0.60
1:A:204:ILE:O	1:A:208:ILE:HG12	2.01	0.60
1:B:212:GLU:HA	1:B:215:LYS:CE	2.32	0.60
1:A:63:LEU:HD23	1:A:75:VAL:O	2.02	0.60
1:A:269:ARG:NH1	1:A:270:ASP:HB2	2.16	0.60
1:B:212:GLU:HA	1:B:215:LYS:HE2	1.82	0.60
1:A:118:GLY:O	1:A:122:THR:HG23	2.01	0.60
1:B:242:LEU:HD21	1:B:252:GLN:HB2	1.82	0.60
1:A:81:SER:HA	1:A:200:ILE:HG23	1.82	0.60
1:A:85:GLU:CD	1:A:107:ARG:HE	2.06	0.60
1:A:177:GLN:HB3	1:B:102:LEU:CD2	2.32	0.60
1:A:181:PHE:CE1	1:B:105:ALA:HB1	2.37	0.60
1:A:155:ASN:O	1:A:159:LYS:HG3	2.02	0.59
1:A:216:GLN:O	1:A:220:ILE:HG12	2.02	0.59
1:A:67:HIS:HA	1:A:72:VAL:HG12	1.83	0.59
1:A:89:ILE:HG22	1:A:91:ALA:O	2.02	0.59
1:B:212:GLU:HG3	1:B:213:LEU:HD13	1.85	0.58
1:B:222:LYS:O	1:B:270:ASP:HB2	2.04	0.58
1:B:195:SER:HB3	1:B:198:GLU:HB2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:VAL:HG13	1:A:83:TYR:O	2.03	0.58
1:A:224:ARG:O	1:A:268:ILE:HG22	2.03	0.58
1:B:261:PRO:HG2	1:B:264:LYS:HB2	1.85	0.58
1:A:63:LEU:HD22	1:A:74:LEU:HD22	1.87	0.57
1:A:127:LYS:HA	1:A:130:CYS:SG	2.45	0.57
1:B:230:SER:HB3	1:B:233:PRO:CG	2.35	0.57
1:B:118:GLY:HA3	1:B:121:PHE:CD1	2.38	0.57
1:B:158:LEU:HD21	1:B:180:VAL:HG22	1.86	0.57
1:A:228:ARG:HA	1:A:235:TRP:HA	1.87	0.57
1:B:172:LEU:O	1:B:176:VAL:HG23	2.03	0.57
1:B:234:VAL:HG12	1:B:235:TRP:N	2.19	0.57
1:A:97:THR:HG22	1:A:101:LEU:HD11	1.87	0.56
1:B:65:CYS:SG	1:B:74:LEU:HG	2.45	0.56
1:B:135:ILE:N	1:B:135:ILE:HD13	2.21	0.56
1:A:69:GLU:OE1	1:A:172:LEU:HD22	2.05	0.56
1:A:153:SER:HA	1:A:156:LYS:HB3	1.88	0.56
1:A:271:TYR:OH	1:A:273:LYS:CD	2.52	0.56
1:B:61:TRP:CD2	1:B:78:HIS:HA	2.41	0.56
1:B:83:TYR:HB3	1:B:200:ILE:HD12	1.88	0.56
1:A:77:VAL:CG2	1:A:84:ILE:HG23	2.34	0.55
1:A:242:LEU:HD12	1:A:250:VAL:HG12	1.89	0.55
1:A:121:PHE:HA	1:A:126:VAL:HG11	1.87	0.55
1:A:68:LEU:HG	1:A:69:GLU:O	2.06	0.55
1:A:174:THR:HG22	1:A:178:MET:SD	2.47	0.55
1:B:263:ARG:NH1	1:B:264:LYS:HA	2.20	0.55
1:A:191:ILE:HG13	1:A:192:GLY:N	2.21	0.55
1:A:73:ILE:CG2	1:A:88:VAL:HA	2.36	0.54
1:A:208:ILE:O	1:A:211:LYS:HG2	2.07	0.54
1:B:112:THR:HG22	1:B:136:LYS:HB2	1.88	0.54
1:B:267:ILE:HD12	1:B:267:ILE:N	2.22	0.54
1:B:160:LYS:HD2	1:B:161:ILE:N	2.23	0.54
1:A:138:GLU:O	1:A:139:PHE:C	2.46	0.54
1:A:241:LEU:HA	1:A:251:ILE:HA	1.90	0.54
1:B:197:GLY:O	1:B:200:ILE:HG22	2.08	0.54
1:B:230:SER:HB3	1:B:233:PRO:HG2	1.89	0.54
1:A:155:ASN:CA	1:A:158:LEU:HD23	2.39	0.53
1:A:214:GLN:HA	1:A:217:ILE:HB	1.91	0.53
2:A:301:LF0:O21	1:B:170:GLU:HB3	2.09	0.53
1:A:162:ILE:HA	1:A:165:VAL:HG22	1.91	0.53
1:B:57:SER:N	1:B:58:PRO:HD2	2.23	0.53
1:B:67:HIS:CB	1:B:72:VAL:HG22	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:110:VAL:O	1:B:135:ILE:HG23	2.08	0.53
1:B:243:TRP:HE3	1:B:250:VAL:HG21	1.72	0.53
1:A:64:ASP:HB3	1:A:75:VAL:HG22	1.91	0.53
1:B:269:ARG:HG2	1:B:269:ARG:HH11	1.72	0.52
1:A:77:VAL:HG12	1:A:78:HIS:O	2.10	0.52
1:B:250:VAL:HG13	1:B:259:VAL:HG12	1.91	0.52
1:A:83:TYR:OH	1:B:107:ARG:HA	2.09	0.52
1:A:243:TRP:HB3	1:A:250:VAL:HB	1.91	0.52
1:A:172:LEU:O	1:A:176:VAL:HG23	2.09	0.52
1:B:133:ALA:CB	1:B:135:ILE:HG12	2.39	0.52
1:A:130:CYS:HB3	1:A:135:ILE:O	2.09	0.52
1:B:224:ARG:O	1:B:268:ILE:HG13	2.10	0.52
1:A:126:VAL:HG12	1:A:127:LYS:N	2.25	0.51
2:A:301:LF0:C12	2:A:301:LF0:H11	2.39	0.51
1:A:242:LEU:HD11	1:A:257:ILE:CG2	2.40	0.51
1:A:78:HIS:HB3	1:A:81:SER:CB	2.40	0.51
1:A:217:ILE:O	1:A:221:GLN:HG3	2.11	0.51
1:B:228:ARG:NH1	1:B:235:TRP:NE1	2.59	0.51
1:A:85:GLU:CD	1:A:107:ARG:NE	2.63	0.51
1:B:173:LYS:HZ2	1:B:173:LYS:HB2	1.76	0.50
1:A:239:ALA:HB1	1:A:252:GLN:O	2.11	0.50
1:B:228:ARG:HB3	1:B:264:LYS:HG2	1.93	0.50
1:A:83:TYR:HE1	1:B:106:GLY:O	1.94	0.50
1:A:98:ALA:HA	1:A:101:LEU:HD12	1.93	0.50
1:B:156:LYS:HA	1:B:159:LYS:HD3	1.93	0.50
1:B:196:ALA:HA	1:B:199:ARG:CZ	2.42	0.50
1:B:228:ARG:CZ	1:B:235:TRP:HE1	2.25	0.50
1:A:195:SER:HB3	1:A:198:GLU:CG	2.42	0.50
1:B:76:ALA:HB3	1:B:85:GLU:O	2.11	0.50
1:A:68:LEU:HD11	1:A:172:LEU:HD21	1.94	0.50
1:A:132:TRP:HH2	1:B:182:ILE:HG13	1.77	0.49
1:B:89:ILE:HG21	1:B:96:GLU:HB3	1.94	0.49
1:A:73:ILE:HD11	1:A:86:ALA:HB1	1.95	0.49
1:A:200:ILE:O	1:A:203:ILE:N	2.46	0.49
1:A:170:GLU:OE1	2:A:302:LF0:H9	2.13	0.49
1:B:269:ARG:HB3	1:B:271:TYR:HD1	1.78	0.49
1:B:67:HIS:HA	1:B:72:VAL:HG22	1.95	0.49
1:B:180:VAL:HG12	1:B:184:ASN:ND2	2.28	0.49
1:A:147:SER:O	1:A:151:ILE:HG13	2.13	0.49
1:B:66:THR:C	1:B:72:VAL:HG13	2.33	0.48
1:B:173:LYS:HB2	1:B:173:LYS:NZ	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:ILE:CB	1:A:88:VAL:HA	2.42	0.48
1:B:205:ALA:HA	1:B:208:ILE:HD12	1.94	0.48
1:B:234:VAL:HG12	1:B:235:TRP:H	1.77	0.48
1:B:200:ILE:CG2	1:B:201:VAL:N	2.77	0.48
1:A:83:TYR:CZ	1:B:107:ARG:HA	2.49	0.48
1:A:162:ILE:HD11	1:A:176:VAL:HA	1.95	0.48
1:B:74:LEU:HD23	1:B:75:VAL:N	2.28	0.48
1:B:165:VAL:HB	1:B:178:MET:CE	2.43	0.48
1:B:224:ARG:HB2	1:B:268:ILE:HG13	1.94	0.48
1:A:181:PHE:HE1	1:B:105:ALA:O	1.97	0.48
1:B:228:ARG:HA	1:B:235:TRP:CD1	2.49	0.48
1:A:98:ALA:HB3	2:A:301:LF0:H19	1.95	0.48
1:B:61:TRP:CD1	1:B:110:VAL:HG22	2.49	0.48
1:A:64:ASP:O	1:A:74:LEU:HD23	2.15	0.47
1:A:173:LYS:HE2	1:B:99:TYR:CE2	2.49	0.47
1:A:162:ILE:HG13	1:A:179:ALA:HB2	1.96	0.47
1:B:60:ILE:HG12	1:B:112:THR:OG1	2.15	0.47
1:A:224:ARG:HD3	1:A:224:ARG:HA	1.54	0.47
1:A:95:GLN:HG2	2:A:301:LF0:H21	1.97	0.47
1:A:162:ILE:CD1	1:A:176:VAL:HG22	2.43	0.47
1:B:110:VAL:O	1:B:135:ILE:HD12	2.14	0.47
1:B:228:ARG:NH1	1:B:235:TRP:HE1	2.13	0.47
1:A:252:GLN:CB	1:A:257:ILE:HG23	2.45	0.47
1:B:165:VAL:CG2	1:B:175:ALA:HB1	2.43	0.47
1:A:177:GLN:CG	1:B:103:LYS:HG2	2.45	0.46
1:A:224:ARG:HB3	1:A:238:PRO:HB2	1.97	0.46
1:B:190:GLY:HA2	1:B:193:GLY:O	2.14	0.46
1:B:204:ILE:O	1:B:208:ILE:HG13	2.14	0.46
1:A:81:SER:O	1:A:199:ARG:HA	2.16	0.46
1:A:160:LYS:O	1:A:164:GLN:HG3	2.15	0.46
1:A:201:VAL:HA	1:A:204:ILE:HD12	1.97	0.46
1:B:174:THR:O	1:B:178:MET:HG3	2.15	0.46
1:A:78:HIS:HB3	1:A:81:SER:OG	2.15	0.46
1:A:83:TYR:HB2	1:A:199:ARG:CD	2.46	0.46
1:A:225:VAL:HG13	1:A:266:LYS:O	2.15	0.46
1:A:225:VAL:HG13	1:A:267:ILE:HG13	1.96	0.46
1:A:226:TYR:O	1:A:266:LYS:HB2	2.16	0.46
1:B:250:VAL:HG13	1:B:259:VAL:CG1	2.46	0.46
1:A:61:TRP:CD1	1:A:110:VAL:HG22	2.50	0.46
1:A:204:ILE:HG21	1:B:201:VAL:HG11	1.98	0.46
1:A:68:LEU:HG	1:A:69:GLU:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:THR:HG22	1:A:101:LEU:CD1	2.47	0.45
1:A:102:LEU:CD2	1:B:177:GLN:HB3	2.47	0.45
1:A:103:LYS:HA	1:B:177:GLN:CD	2.36	0.45
1:B:72:VAL:O	1:B:89:ILE:HD12	2.16	0.45
1:B:146:GLN:O	1:B:150:VAL:HG23	2.15	0.45
1:A:68:LEU:HD23	1:A:71:LYS:O	2.16	0.45
1:A:73:ILE:HD13	1:A:176:VAL:HG11	1.98	0.45
1:A:199:ARG:HB2	1:A:201:VAL:HG23	1.97	0.45
1:B:273:LYS:O	1:B:273:LYS:HG3	2.16	0.45
1:A:224:ARG:HB3	1:A:238:PRO:CB	2.47	0.45
1:B:67:HIS:CA	1:B:72:VAL:HG22	2.46	0.44
1:B:161:ILE:O	1:B:165:VAL:HG13	2.17	0.44
1:B:181:PHE:CD1	1:B:181:PHE:C	2.89	0.44
1:A:62:GLN:HE21	1:A:148:GLN:CD	2.21	0.44
1:B:253:ASP:O	1:B:254:ASN:C	2.56	0.44
1:A:225:VAL:HG22	1:A:267:ILE:HG23	1.99	0.44
1:A:271:TYR:HH	1:A:273:LYS:HD3	1.80	0.44
1:B:103:LYS:O	1:B:107:ARG:HG2	2.17	0.44
1:B:162:ILE:O	1:B:165:VAL:HG22	2.17	0.44
1:B:225:VAL:HG13	1:B:266:LYS:O	2.17	0.44
1:B:242:LEU:CD1	1:B:252:GLN:HB2	2.45	0.44
1:B:67:HIS:HB2	1:B:72:VAL:HG22	1.98	0.44
1:B:162:ILE:HD13	1:B:176:VAL:HG22	1.99	0.44
1:A:58:PRO:HA	1:A:78:HIS:NE2	2.30	0.43
1:A:252:GLN:HB2	1:A:257:ILE:CD1	2.44	0.43
1:B:224:ARG:HG3	1:B:270:ASP:OD1	2.18	0.43
1:B:228:ARG:HA	1:B:235:TRP:HD1	1.82	0.43
1:A:78:HIS:HB3	1:A:81:SER:HB3	2.00	0.43
1:A:81:SER:CA	1:A:200:ILE:HG23	2.48	0.43
1:A:73:ILE:CD1	1:A:86:ALA:HB1	2.49	0.43
1:A:157:GLU:O	1:A:161:ILE:HG13	2.18	0.43
1:A:242:LEU:H	1:A:251:ILE:HA	1.84	0.43
1:B:114:HIS:HA	1:B:138:GLU:HB3	2.00	0.43
1:A:61:TRP:HA	1:A:78:HIS:HA	2.00	0.43
1:A:102:LEU:HD11	1:B:178:MET:HA	2.01	0.43
1:A:226:TYR:CD1	1:A:226:TYR:N	2.86	0.43
1:B:166:ARG:CD	1:B:172:LEU:HD13	2.49	0.43
1:A:73:ILE:HG22	1:A:88:VAL:HA	2.00	0.43
1:A:83:TYR:C	1:A:84:ILE:HD13	2.39	0.43
1:A:235:TRP:N	1:A:235:TRP:CD1	2.87	0.42
1:A:253:ASP:N	1:A:256:ASP:O	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:177:GLN:HB3	1:B:102:LEU:HG	2.00	0.42
1:A:94:GLY:HA3	1:A:123:SER:CB	2.49	0.42
1:B:89:ILE:HD12	1:B:89:ILE:H	1.83	0.42
1:A:83:TYR:HE2	1:A:85:GLU:HB2	1.85	0.42
1:A:184:ASN:O	1:A:185:HIS:C	2.57	0.42
1:B:235:TRP:N	1:B:235:TRP:CD2	2.83	0.42
1:A:95:GLN:HG2	2:A:301:LF0:H17	2.01	0.42
1:A:83:TYR:O	1:A:84:ILE:HD13	2.19	0.42
1:A:181:PHE:CE1	1:B:105:ALA:O	2.72	0.42
1:A:203:ILE:N	1:A:203:ILE:HD12	2.35	0.42
1:B:166:ARG:NE	1:B:172:LEU:HB2	2.35	0.42
1:B:212:GLU:HA	1:B:215:LYS:HE3	2.02	0.41
1:A:102:LEU:HG	1:B:177:GLN:HB3	2.02	0.41
1:A:103:LYS:HA	1:B:177:GLN:NE2	2.35	0.41
1:A:250:VAL:HG22	1:A:259:VAL:HG13	2.00	0.41
1:A:154:MET:HA	1:A:157:GLU:OE2	2.20	0.41
1:A:253:ASP:HB3	1:A:258:LYS:CE	2.50	0.41
1:B:254:ASN:ND2	1:B:255:SER:N	2.68	0.41
1:B:263:ARG:HH12	1:B:264:LYS:HA	1.84	0.41
1:A:111:LYS:O	1:A:135:ILE:HA	2.21	0.41
1:B:269:ARG:HG2	1:B:269:ARG:NH1	2.34	0.41
1:B:83:TYR:HB3	1:B:200:ILE:CD1	2.50	0.41
1:B:241:LEU:O	1:B:241:LEU:HD23	2.20	0.41
1:A:177:GLN:HG2	1:B:103:LYS:HG2	2.02	0.41
1:B:213:LEU:O	1:B:216:GLN:HB2	2.20	0.41
1:B:253:ASP:N	1:B:256:ASP:O	2.53	0.41
1:A:132:TRP:HH2	1:B:182:ILE:CG1	2.34	0.41
1:B:249:VAL:HG21	1:B:265:ALA:HB3	2.02	0.41
1:B:225:VAL:O	1:B:239:ALA:HB3	2.21	0.40
1:A:178:MET:O	1:A:181:PHE:N	2.54	0.40
1:B:152:GLU:O	1:B:156:LYS:HG3	2.21	0.40
1:B:61:TRP:CZ2	1:B:78:HIS:HB2	2.56	0.40
1:B:94:GLY:HA2	1:B:120:ASN:HB3	2.04	0.40
1:B:228:ARG:HG3	1:B:231:ARG:HA	2.03	0.40
1:B:253:ASP:O	1:B:256:ASP:O	2.39	0.40
1:B:263:ARG:HG3	1:B:264:LYS:N	2.36	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:GLN:OE1	1:A:274:GLN:OE1[12_565]	1.94	0.26

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	210/293 (72%)	205 (98%)	5 (2%)	0	100	100
1	B	212/293 (72%)	210 (99%)	2 (1%)	0	100	100
All	All	422/586 (72%)	415 (98%)	7 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	179/244 (73%)	132 (74%)	47 (26%)	0	3
1	B	180/244 (74%)	138 (77%)	42 (23%)	0	4
All	All	359/488 (74%)	270 (75%)	89 (25%)	0	3

All (89) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	SER
1	A	63	LEU
1	A	69	GLU

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Mol	Chain	Res	Type
1	A	73	ILE
1	A	84	ILE
1	A	93	THR
1	A	95	GLN
1	A	96	GLU
1	A	107	ARG
1	A	108	TRP
1	A	111	LYS
1	A	123	SER
1	A	125	THR
1	A	126	VAL
1	A	130	CYS
1	A	137	GLN
1	A	146	GLN
1	A	148	GLN
1	A	153	SER
1	A	154	MET
1	A	158	LEU
1	A	160	LYS
1	A	170	GLU
1	A	173	LYS
1	A	177	GLN
1	A	182	ILE
1	A	188	LYS
1	A	202	ASP
1	A	213	LEU
1	A	217	ILE
1	A	224	ARG
1	A	228	ARG
1	A	230	SER
1	A	231	ARG
1	A	236	LYS
1	A	240	LYS
1	A	244	LYS
1	A	246	GLU
1	A	249	VAL
1	A	253	ASP
1	A	255	SER
1	A	258	LYS
1	A	262	ARG
1	A	263	ARG
1	A	264	LYS

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Mol	Chain	Res	Type
1	A	274	GLN
1	A	275	MET
1	B	57	SER
1	B	67	HIS
1	B	78	HIS
1	B	87	GLU
1	B	89	ILE
1	B	92	GLU
1	B	93	THR
1	B	96	GLU
1	B	104	LEU
1	B	107	ARG
1	B	108	TRP
1	B	122	THR
1	B	123	SER
1	B	135	ILE
1	B	148	GLN
1	B	152	GLU
1	B	159	LYS
1	B	160	LYS
1	B	165	VAL
1	B	168	GLN
1	B	173	LYS
1	B	177	GLN
1	B	187	ARG
1	B	188	LYS
1	B	198	GLU
1	B	201	VAL
1	B	202	ASP
1	B	209	GLN
1	B	213	LEU
1	B	215	LYS
1	B	219	LYS
1	B	228	ARG
1	B	232	ASP
1	B	235	TRP
1	B	241	LEU
1	B	244	LYS
1	B	254	ASN
1	B	256	ASP
1	B	263	ARG
1	B	269	ARG

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Mol	Chain	Res	Type
1	B	273	LYS
1	B	275	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	120	ASN
1	A	137	GLN
1	A	146	GLN
1	A	148	GLN
1	A	164	GLN
1	A	168	GLN
1	B	62	GLN
1	B	114	HIS
1	B	168	GLN
1	B	171	HIS
1	B	184	ASN
1	B	254	ASN

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](#)

2 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	LF0	A	302	-	31,33,33	2.81	6 (19%)	41,49,49	1.70	10 (24%)
2	LF0	A	301	-	31,33,33	2.79	6 (19%)	41,49,49	1.75	10 (24%)

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	LF0	A	302	-	-	2/17/24/24	0/4/4/4
2	LF0	A	301	-	-	4/17/24/24	0/4/4/4

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	LF0	C1-C7	-8.12	1.40	1.49
2	A	302	LF0	C1-C7	-8.12	1.40	1.49
2	A	302	LF0	C2-C18	-7.31	1.39	1.53
2	A	301	LF0	C2-C18	-7.18	1.39	1.53
2	A	302	LF0	C21-C11	-6.85	1.39	1.51
2	A	301	LF0	C21-C11	-6.79	1.39	1.51
2	A	302	LF0	C17-C3	-6.53	1.40	1.50
2	A	301	LF0	C17-C3	-6.48	1.40	1.50
2	A	302	LF0	C5-N1	-2.51	1.33	1.37
2	A	301	LF0	C5-N1	-2.50	1.33	1.37
2	A	301	LF0	C3-N1	2.09	1.34	1.32
2	A	302	LF0	C3-N1	2.02	1.34	1.32

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	302	LF0	C3-N1-C5	5.52	123.49	118.42
2	A	301	LF0	C3-N1-C5	5.23	123.22	118.42
2	A	302	LF0	C6-C5-N1	-3.84	118.73	122.80
2	A	301	LF0	C6-C5-N1	-3.59	119.00	122.80
2	A	301	LF0	C12-C7-C1	3.16	125.78	119.91
2	A	302	LF0	C12-C7-C1	3.15	125.76	119.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	LF0	C16-C5-C6	2.93	122.29	119.13
2	A	302	LF0	C4-O27-C10	2.85	118.68	113.67
2	A	301	LF0	C13-C6-C5	-2.69	115.36	118.36
2	A	301	LF0	C8-C7-C12	-2.55	114.73	118.23
2	A	302	LF0	C16-C5-C6	2.45	121.77	119.13
2	A	302	LF0	C8-C7-C12	-2.43	114.89	118.23
2	A	301	LF0	O27-C4-C20	-2.38	107.85	112.11
2	A	302	LF0	C7-C12-C11	2.24	125.16	121.88
2	A	301	LF0	O27-C10-C11	-2.21	120.56	122.41
2	A	301	LF0	C4-O27-C10	2.09	117.34	113.67
2	A	302	LF0	C13-C6-C5	-2.06	116.06	118.36
2	A	302	LF0	O27-C4-C20	-2.05	108.45	112.11
2	A	302	LF0	C1-C6-C5	2.02	120.55	118.07
2	A	301	LF0	C7-C12-C11	2.02	124.84	121.88

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	LF0	C2-C18-C19-O20
2	A	301	LF0	C2-C18-C19-O21
2	A	301	LF0	O22-C18-C19-O20
2	A	302	LF0	C2-C18-C19-O20
2	A	302	LF0	C2-C18-C19-O21
2	A	301	LF0	O22-C18-C19-O21

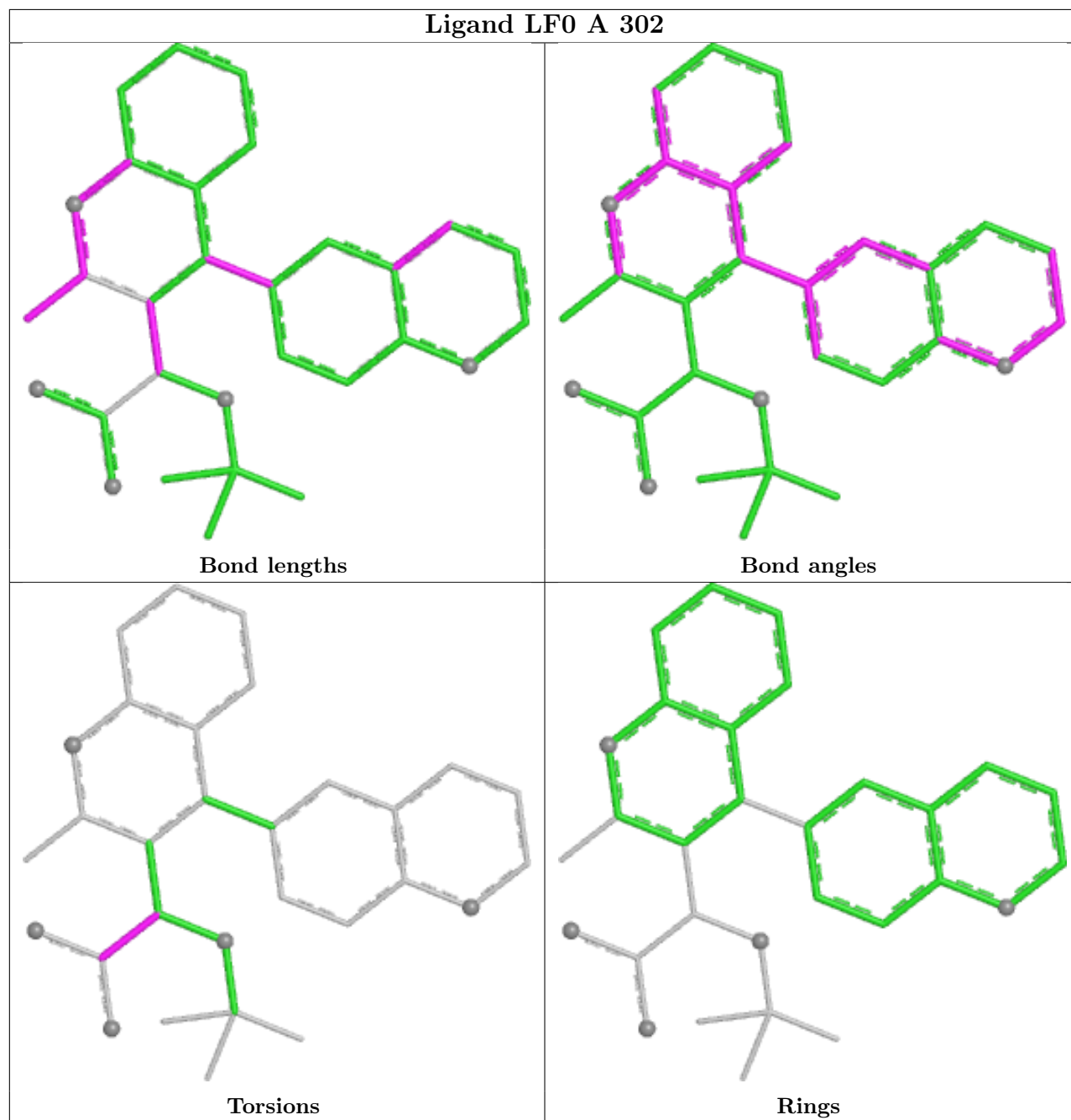
There are no ring outliers.

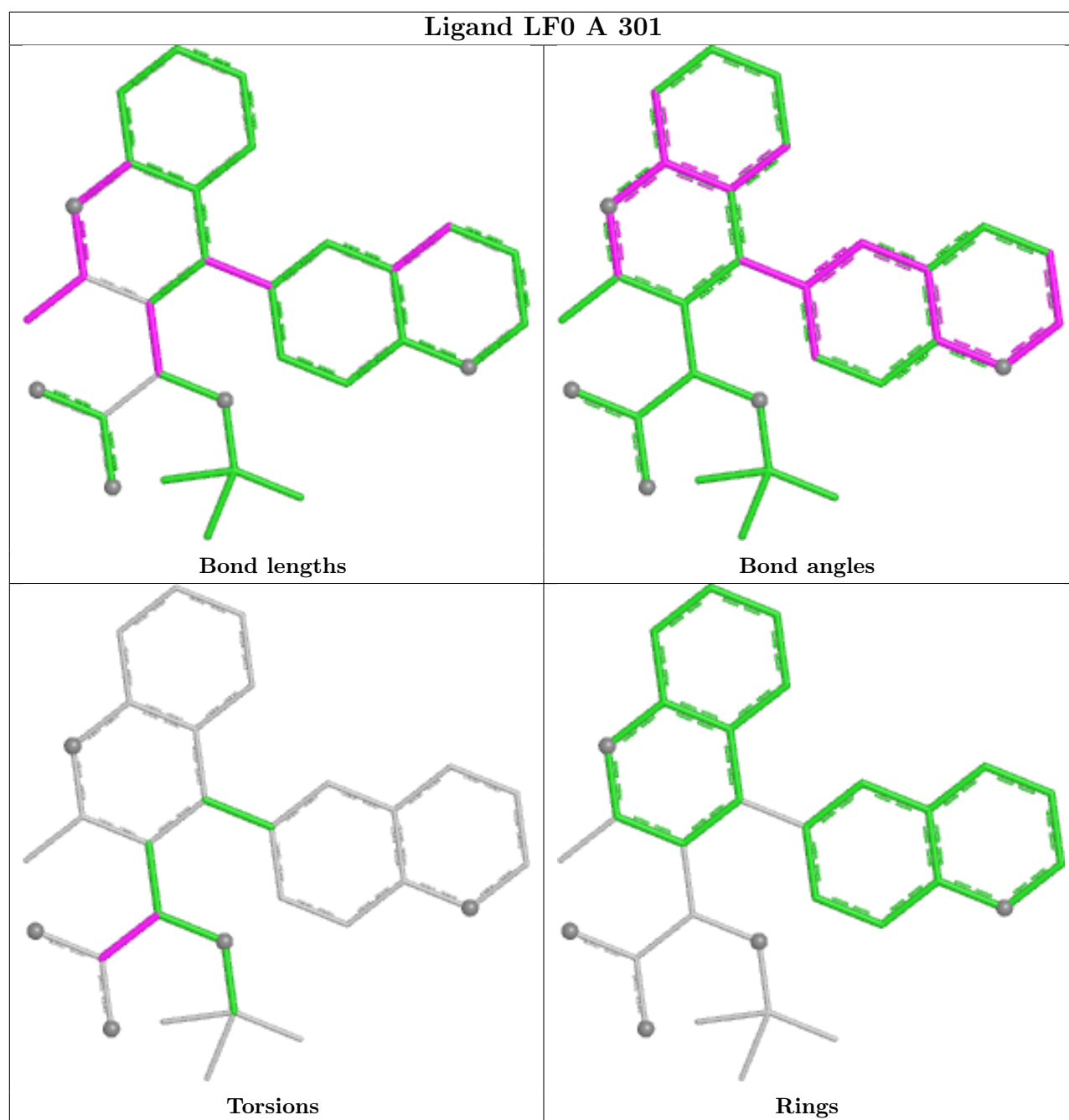
2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	302	LF0	2	0
2	A	301	LF0	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	214/293 (73%)	0.03	2 (0%) 81 67	175, 273, 300, 300	0
1	B	216/293 (73%)	0.00	1 (0%) 87 76	179, 261, 300, 300	0
All	All	430/586 (73%)	0.02	3 (0%) 84 71	175, 268, 300, 300	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	239	ALA	4.1
1	B	192	GLY	3.6
1	A	147	SER	2.6

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 monosaccharides in this entry.

6.4 Ligands [i](#)

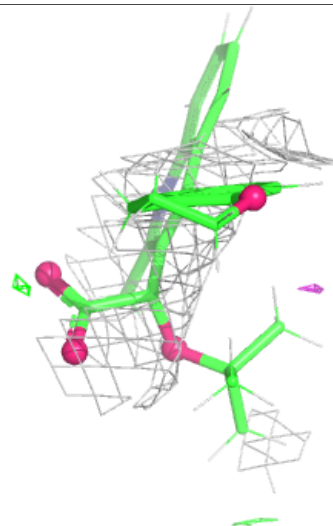
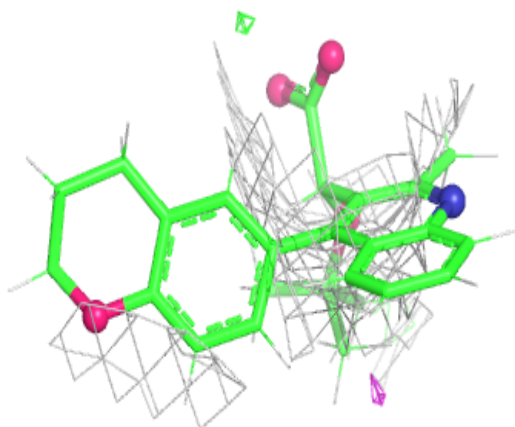
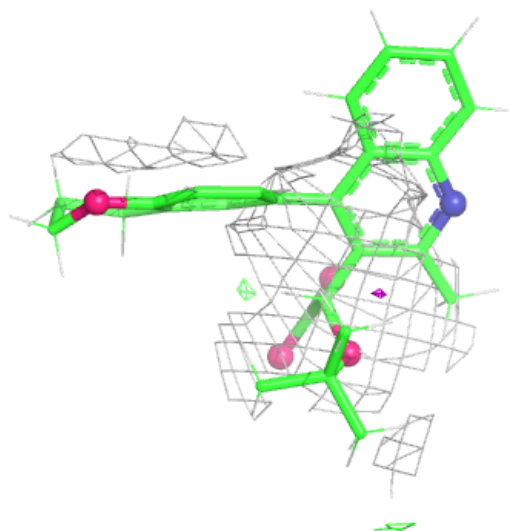
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists 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	LF0	A	301	30/30	0.82	0.17	300,300,300,300	0
2	LF0	A	302	30/30	0.88	0.23	283,283,283,283	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.

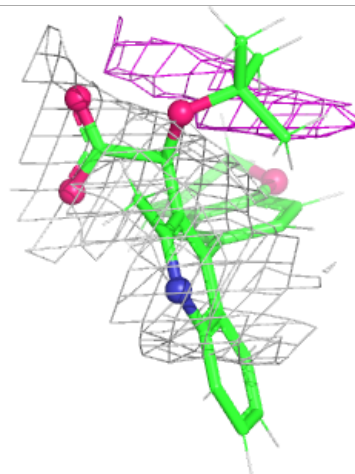
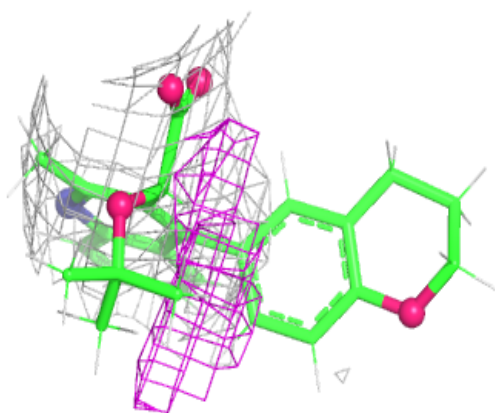
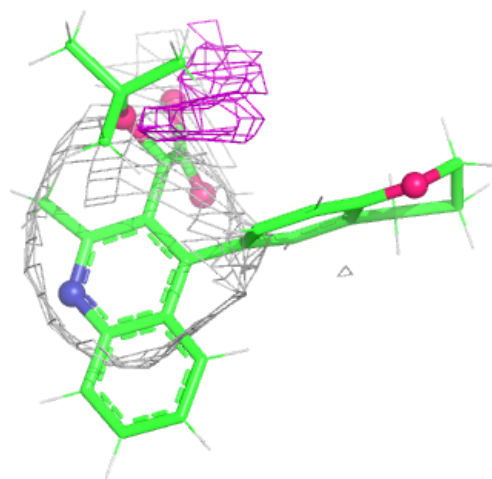
Electron density around LF0 A 301:

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



Electron density around LF0 A 302:

$2mF_o-DF_c$ (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.