



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 07:00 PM UTC

PDB ID : 4NQD / pdb_00004nqd
Title : Crystal structure of TCR-MR1 ternary complex and non-covalently bound 5-(2-oxopropylideneamino)-6-D-ribitylaminouracil
Authors : Birkinshaw, R.W.; Rossjohn, J.
Deposited on : 2013-11-25
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

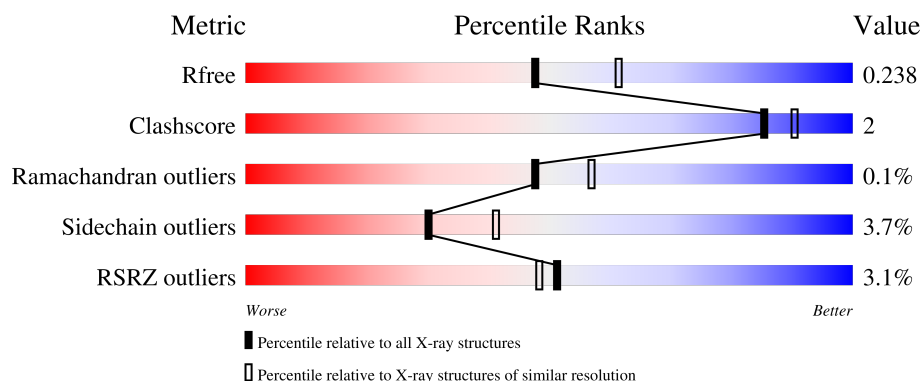
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

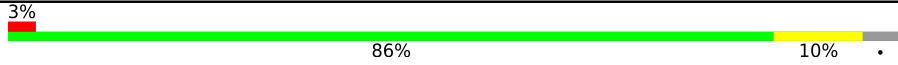
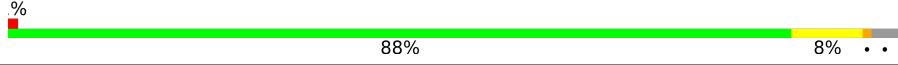
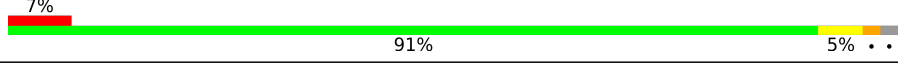
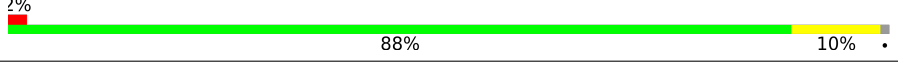
The reported resolution of this entry is 2.20 Å.

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	271	
1	C	271	
2	B	99	
2	F	99	
3	D	203	

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Mol	Chain	Length	Quality of chain
3	G	203	5% 81% 12% 6%
4	E	245	2% 92% 7%
4	H	245	2% 94% 5%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 13111 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 Major histocompatibility complex class I-related gene protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	260	Total	C	N	O	S	0	1	0
			2120	1359	365	386	10			
1	C	248	Total	C	N	O	S	0	2	0
			2043	1310	350	372	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP Q95460
A	261	SER	CYS	engineered mutation	UNP Q95460
C	0	MET	-	expression tag	UNP Q95460
C	261	SER	CYS	engineered mutation	UNP Q95460

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	96	Total	C	N	O	S	0	0	0
			785	502	131	150	2			
2	F	97	Total	C	N	O	S	0	0	0
			769	494	127	146	2			

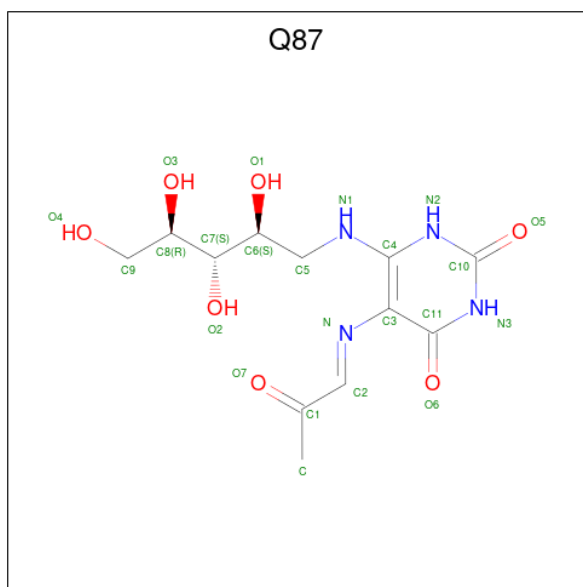
- Molecule 3 is a protein called TCR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	200	Total	C	N	O	S	0	0	0
			1548	978	248	313	9			
3	G	190	Total	C	N	O	S	0	1	0
			1460	929	230	292	9			

- Molecule 4 is a protein called TCR beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	243	Total	C	N	O	S	0	2	0
			1907	1202	333	363	9			
4	H	242	Total	C	N	O	S	0	0	0
			1882	1186	325	362	9			

- Molecule 5 is 1-deoxy-1-({2,6-dioxo-5-[(E)-(2-oxopropylidene)amino]-1,2,3,6-tetrahydropyrimidin-4-yl}amino)-D-ribose (CCD ID: Q87) (formula: C₁₂H₁₈N₄O₇).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			23	12	4	7		
5	C	1	Total	C	N	O	0	0
			23	12	4	7		

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	D	1	Total	C	O	0	0
			6	3	3		

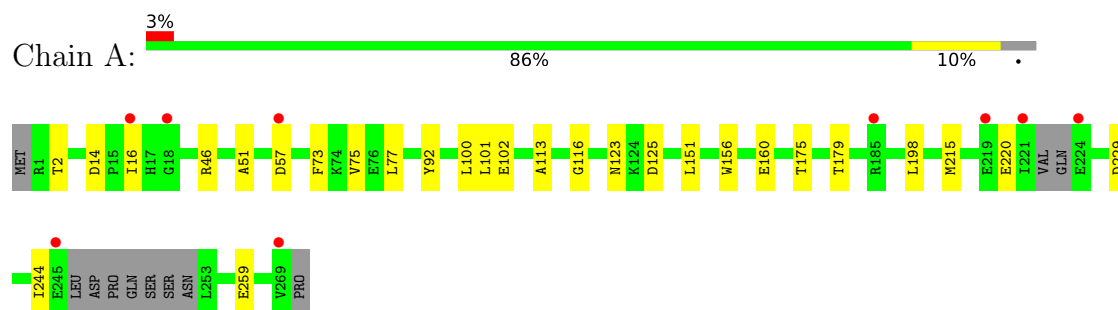
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	113	Total	O	0	0
			113	113		
7	B	38	Total	O	0	0
			38	38		
7	C	83	Total	O	0	0
			83	83		
7	D	84	Total	O	0	0
			84	84		
7	E	99	Total	O	0	0
			99	99		
7	F	23	Total	O	0	0
			23	23		
7	G	57	Total	O	0	0
			57	57		
7	H	48	Total	O	0	0
			48	48		

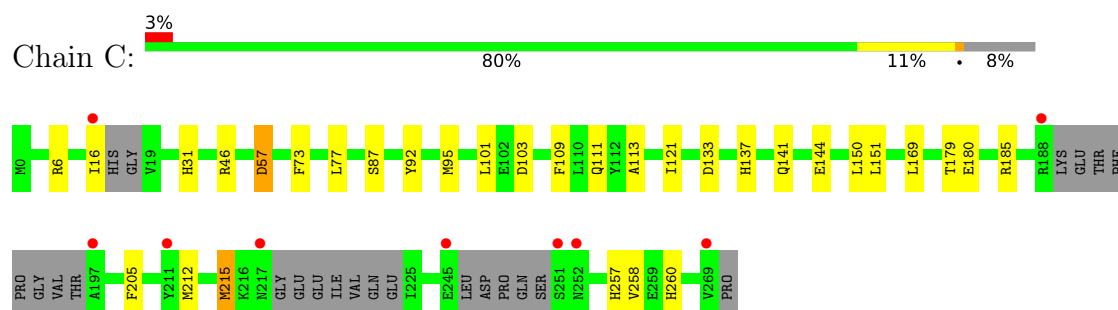
3 Residue-property plots [i](#)

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.

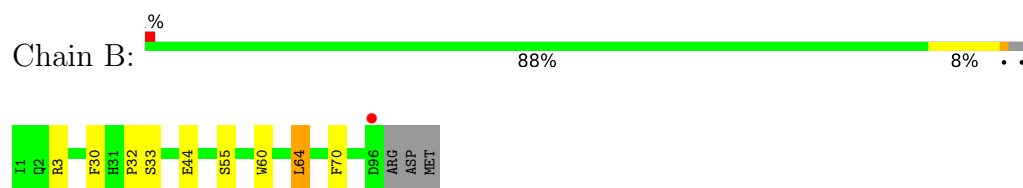
- Molecule 1: Major histocompatibility complex class I-related gene protein



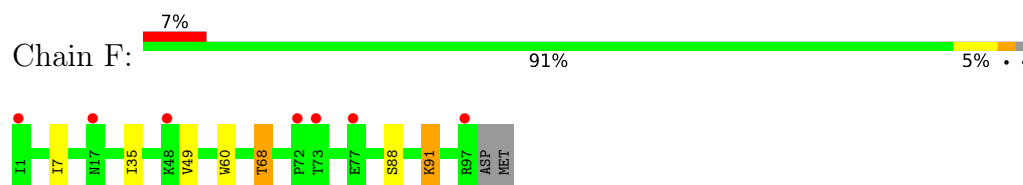
- Molecule 1: Major histocompatibility complex class I-related gene protein



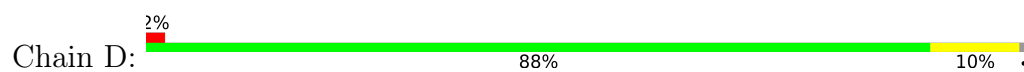
- Molecule 2: Beta-2-microglobulin



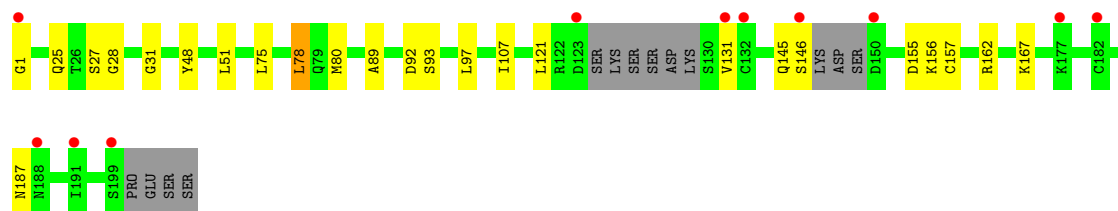
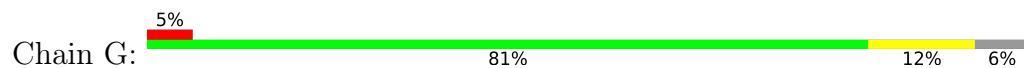
- Molecule 2: Beta-2-microglobulin



- Molecule 3: TCR alpha chain



• Molecule 3: TCR alpha chain



• Molecule 4: TCR beta chain



• Molecule 4: TCR beta chain



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	215.58Å 68.87Å 142.98Å 90.00° 104.21° 90.00°	Depositor
Resolution (Å)	49.51 – 2.20 49.51 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.7 (49.51-2.20) 97.6 (49.51-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.52 (at 2.20Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.181 , 0.227 0.191 , 0.238	Depositor DCC
R_{free} test set	5109 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	32.0	Xtriage
Anisotropy	0.465	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13111	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.71% 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: GOL, Q87

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	0.87	0/2187	1.16	5/2975 (0.2%)
1	C	0.86	0/2109	1.17	8/2865 (0.3%)
2	B	0.80	0/808	1.10	4/1100 (0.4%)
2	F	0.84	0/792	1.13	0/1082
3	D	0.84	0/1583	1.17	10/2148 (0.5%)
3	G	0.84	0/1495	1.16	3/2030 (0.1%)
4	E	0.81	0/1966	1.12	1/2679 (0.0%)
4	H	0.79	0/1933	1.13	1/2635 (0.0%)
All	All	0.83	0/12873	1.15	32/17514 (0.2%)

There are no bond length outliers.

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	155	ASP	CA-C-N	7.61	131.93	121.05
3	D	155	ASP	C-N-CA	7.61	131.93	121.05
3	D	92	ASP	CA-CB-CG	7.40	120.00	112.60
4	H	100	GLY	N-CA-C	6.92	120.53	112.50
1	C	133	ASP	CA-CB-CG	6.42	119.03	112.60
1	A	229	ASP	CA-CB-CG	5.99	118.59	112.60
2	B	33	SER	N-CA-C	5.64	118.36	111.82
1	A	175	THR	CA-C-N	5.58	128.21	120.29
1	A	175	THR	C-N-CA	5.58	128.21	120.29
3	G	92	ASP	CA-CB-CG	5.56	118.16	112.60
1	C	57	ASP	CA-CB-CG	5.53	118.13	112.60
2	B	70	PHE	CA-CB-CG	5.47	119.28	113.80
4	E	12	VAL	N-CA-CB	5.43	119.56	110.86
3	D	53	GLY	N-CA-C	5.28	118.45	111.70
1	C	260	HIS	CA-C-N	5.19	130.19	122.82
1	C	260	HIS	C-N-CA	5.19	130.19	122.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	162	ARG	CA-C-N	5.18	127.54	120.54
3	G	162	ARG	C-N-CA	5.18	127.54	120.54
1	A	51	ALA	CA-C-N	5.15	128.14	120.31
1	A	51	ALA	C-N-CA	5.15	128.14	120.31
3	D	147	LYS	CA-C-N	5.15	128.65	121.24
3	D	147	LYS	C-N-CA	5.15	128.65	121.24
1	C	103	ASP	CA-CB-CG	5.12	117.72	112.60
2	B	32	PRO	CA-C-N	5.10	128.07	120.31
2	B	32	PRO	C-N-CA	5.10	128.07	120.31
3	D	135	THR	CA-C-N	5.10	129.79	122.40
3	D	135	THR	C-N-CA	5.10	129.79	122.40
3	D	111	ILE	CA-C-N	5.08	127.04	120.44
3	D	111	ILE	C-N-CA	5.08	127.04	120.44
1	C	101	LEU	CA-C-N	5.05	127.30	120.38
1	C	101	LEU	C-N-CA	5.05	127.30	120.38
1	C	31	HIS	N-CA-C	5.05	116.25	109.24

There are no chirality outliers.

There are no planarity outliers.

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	2120	0	1989	10	0
1	C	2043	0	1919	13	0
2	B	785	0	731	3	0
2	F	769	0	699	4	0
3	D	1548	0	1456	7	0
3	G	1460	0	1360	8	0
4	E	1907	0	1788	11	0
4	H	1882	0	1754	4	0
5	A	23	0	0	0	0
5	C	23	0	0	0	0
6	D	6	0	8	0	0
7	A	113	0	0	0	0
7	B	38	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	C	83	0	0	1	0
7	D	84	0	0	0	0
7	E	99	0	0	0	0
7	F	23	0	0	0	0
7	G	57	0	0	0	0
7	H	48	0	0	0	0
All	All	13111	0	11704	53	0

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 2.

All (53) 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)
4:E:210:ARG:HE	4:E:212:GLN:HE21	1.16	0.93
3:D:1:GLY:HA2	3:D:27:SER:H	1.36	0.91
3:G:1:GLY:HA2	3:G:27:SER:H	1.53	0.73
4:E:210:ARG:HE	4:E:212:GLN:NE2	1.87	0.70
4:E:210:ARG:HH21	4:E:212:GLN:HE22	1.42	0.65
1:C:215:MET:HG3	1:C:257:HIS:CD2	2.40	0.56
3:D:1:GLY:HA2	3:D:27:SER:N	2.14	0.55
4:H:155:HIS:HB3	4:H:216:TYR:HB2	1.88	0.55
1:C:95:MET:HE3	1:C:109:PHE:CD1	2.43	0.53
1:C:113:ALA:HB2	2:F:60:TRP:CE2	2.44	0.53
1:A:2[A]:THR:HG22	1:A:102:GLU:H	1.75	0.51
1:A:116:GLY:O	2:B:3:ARG:NH2	2.44	0.51
3:D:78:LEU:HG	3:D:107:ILE:HD12	1.92	0.51
4:E:210:ARG:HH21	4:E:212:GLN:NE2	2.08	0.50
1:C:151:LEU:HD22	3:D:51:LEU:HD12	1.94	0.50
3:G:78:LEU:HG	3:G:107:ILE:HD12	1.94	0.49
1:A:113:ALA:HB2	2:B:60:TRP:CE2	2.48	0.49
3:D:28:GLY:HA3	3:D:93:SER:OG	2.13	0.49
4:E:208[A]:HIS:HB3	4:E:241:TRP:CE3	2.47	0.49
1:C:77:LEU:HD13	1:C:92:TYR:HB2	1.94	0.48
1:C:212:MET:HG2	1:C:258:VAL:HG22	1.95	0.48
4:E:128:VAL:HG23	4:E:238:ALA:HB3	1.94	0.48
1:A:77:LEU:HD13	1:A:92:TYR:HB2	1.96	0.48
1:A:123:ASN:HD22	1:A:125:ASP:H	1.61	0.47
2:B:30:PHE:HZ	2:B:64:LEU:HD12	1.80	0.47
1:A:2[A]:THR:HG22	1:A:102:GLU:N	2.31	0.46
1:A:151:LEU:HD22	3:G:51:LEU:HD12	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:144:GLU:HA	1:C:150:LEU:HD11	1.98	0.45
1:C:185:ARG:NH1	7:C:482:HOH:O	2.34	0.45
4:E:27:MET:HE1	4:E:105:PHE:CD1	2.51	0.45
2:F:7:ILE:HD12	2:F:91:LYS:HD2	1.99	0.45
1:C:46:ARG:HA	1:C:46:ARG:HD3	1.74	0.45
2:F:49:VAL:HA	2:F:68:THR:HG23	1.98	0.45
3:G:28:GLY:HA3	3:G:93[A]:SER:HB3	1.99	0.44
1:C:111:GLN:HG2	1:C:121:ILE:HG12	2.00	0.43
4:H:148:ALA:O	4:H:190:ALA:HA	2.18	0.43
3:G:121:LEU:HB3	4:H:129:PHE:HB3	2.00	0.43
3:D:89:ALA:HB1	3:D:97:LEU:HD22	2.00	0.43
4:E:86:THR:HG23	4:E:113:THR:HA	2.01	0.43
3:G:31:GLY:HA3	3:G:48:TYR:CE1	2.54	0.42
1:A:198:LEU:HB2	1:A:244:ILE:HG13	2.01	0.42
1:C:180:GLU:O	1:C:205:PHE:HA	2.19	0.42
4:E:131:PRO:HD3	4:E:144:LEU:HG	2.01	0.41
3:G:89:ALA:HB1	3:G:97:LEU:HD22	2.03	0.41
4:E:21:LEU:N	4:E:21:LEU:HD12	2.35	0.41
1:A:156:TRP:HA	1:A:160:GLU:HB2	2.02	0.41
3:G:80:MET:HG2	3:G:167:LYS:HE2	2.02	0.41
1:A:46:ARG:HD3	1:A:46:ARG:HA	1.81	0.40
4:E:29:HIS:HE1	4:E:105:PHE:CD2	2.39	0.40
4:H:154:ASP:CG	4:H:177:PRO:HG3	2.46	0.40
1:C:113:ALA:HB2	2:F:60:TRP:CD2	2.57	0.40
1:C:137:HIS:O	1:C:141:GLN:HG2	2.21	0.40
3:D:152:TYR:O	3:D:173:ALA:HA	2.22	0.40

There are no symmetry-related clashes.

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	255/271 (94%)	248 (97%)	6 (2%)	1 (0%)	30	34
1	C	240/271 (89%)	234 (98%)	6 (2%)	0	100	100
2	B	94/99 (95%)	94 (100%)	0	0	100	100
2	F	95/99 (96%)	92 (97%)	3 (3%)	0	100	100
3	D	198/203 (98%)	195 (98%)	3 (2%)	0	100	100
3	G	185/203 (91%)	180 (97%)	5 (3%)	0	100	100
4	E	243/245 (99%)	241 (99%)	2 (1%)	0	100	100
4	H	240/245 (98%)	233 (97%)	7 (3%)	0	100	100
All	All	1550/1636 (95%)	1517 (98%)	32 (2%)	1 (0%)	48	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	220	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	221/241 (92%)	211 (96%)	10 (4%)	24	33
1	C	216/241 (90%)	208 (96%)	8 (4%)	30	41
2	B	87/94 (93%)	84 (97%)	3 (3%)	32	44
2	F	82/94 (87%)	78 (95%)	4 (5%)	22	29
3	D	172/180 (96%)	166 (96%)	6 (4%)	32	43
3	G	159/180 (88%)	149 (94%)	10 (6%)	16	19
4	E	204/211 (97%)	200 (98%)	4 (2%)	48	64
4	H	200/211 (95%)	196 (98%)	4 (2%)	48	64
All	All	1341/1452 (92%)	1292 (96%)	49 (4%)	30	41

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	ASP
1	A	16	ILE
1	A	57	ASP
1	A	73	PHE
1	A	75	VAL
1	A	100	LEU
1	A	101	LEU
1	A	179	THR
1	A	215	MET
1	A	259	GLU
2	B	44	GLU
2	B	55	SER
2	B	64	LEU
1	C	6	ARG
1	C	16	ILE
1	C	57	ASP
1	C	73	PHE
1	C	87	SER
1	C	169	LEU
1	C	179	THR
1	C	215	MET
3	D	25	GLN
3	D	60	PHE
3	D	68	LYS
3	D	78	LEU
3	D	98	ILE
3	D	199	SER
4	E	12	VAL
4	E	181	GLN
4	E	185	ASN
4	E	237	SER
2	F	35	ILE
2	F	68	THR
2	F	88	SER
2	F	91	LYS
3	G	25	GLN
3	G	75	LEU
3	G	78	LEU
3	G	131	VAL
3	G	145	GLN
3	G	146	SER
3	G	155	ASP
3	G	156	LYS

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Mol	Chain	Res	Type
3	G	157	CYS
3	G	187	ASN
4	H	79	GLU
4	H	97	THR
4	H	147	LEU
4	H	184	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	GLN
1	A	93	GLN
1	A	123	ASN
1	A	137	HIS
1	A	146	ASN
1	A	147	GLN
1	A	153	GLN
1	A	239	GLN
1	C	111	GLN
1	C	117	GLN
1	C	153	GLN
1	C	239	GLN
1	C	264	HIS
3	D	19	GLN
3	D	21	ASN
4	E	22	GLN
4	E	120	ASN
4	E	212	GLN
2	F	8	GLN
2	F	13	HIS
3	G	3	ASN
3	G	19	GLN
3	G	21	ASN
3	G	25	GLN
3	G	37	GLN
4	H	37	GLN
4	H	168	HIS
4	H	204	ASN
4	H	234	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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$
5	Q87	A	301	-	22,23,23	1.15	1 (4%)	25,31,31	2.01	7 (28%)
6	GOL	D	301	-	5,5,5	0.09	0	5,5,5	0.17	0
5	Q87	C	301	-	22,23,23	1.34	3 (13%)	25,31,31	1.94	6 (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
5	Q87	A	301	-	-	3/19/20/20	0/1/1/1
6	GOL	D	301	-	-	2/4/4/4	-
5	Q87	C	301	-	-	2/19/20/20	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	301	Q87	C3-C4	3.32	1.48	1.43
5	C	301	Q87	C2-N	-2.79	1.25	1.29
5	A	301	Q87	C3-C4	2.60	1.47	1.43
5	C	301	Q87	C4-N1	2.41	1.36	1.32

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	301	Q87	C2-N-C3	4.78	125.73	120.42
5	A	301	Q87	C2-N-C3	4.31	125.21	120.42
5	C	301	Q87	N2-C10-N3	4.25	122.42	115.74
5	A	301	Q87	N2-C10-N3	4.22	122.37	115.74
5	A	301	Q87	C11-N3-C10	-3.90	120.99	126.37
5	C	301	Q87	N2-C4-N1	3.36	123.56	118.66
5	C	301	Q87	C11-N3-C10	-3.21	121.95	126.37
5	A	301	Q87	N2-C4-N1	3.06	123.12	118.66
5	A	301	Q87	O7-C1-C	2.42	123.11	119.32
5	C	301	Q87	O7-C1-C	2.39	123.07	119.32
5	A	301	Q87	C3-C11-N3	2.36	119.25	113.25
5	A	301	Q87	O6-C11-C3	-2.25	120.60	126.53
5	C	301	Q87	C3-C11-N3	2.03	118.43	113.25

There are no chirality outliers.

All (7) torsion outliers are listed below:

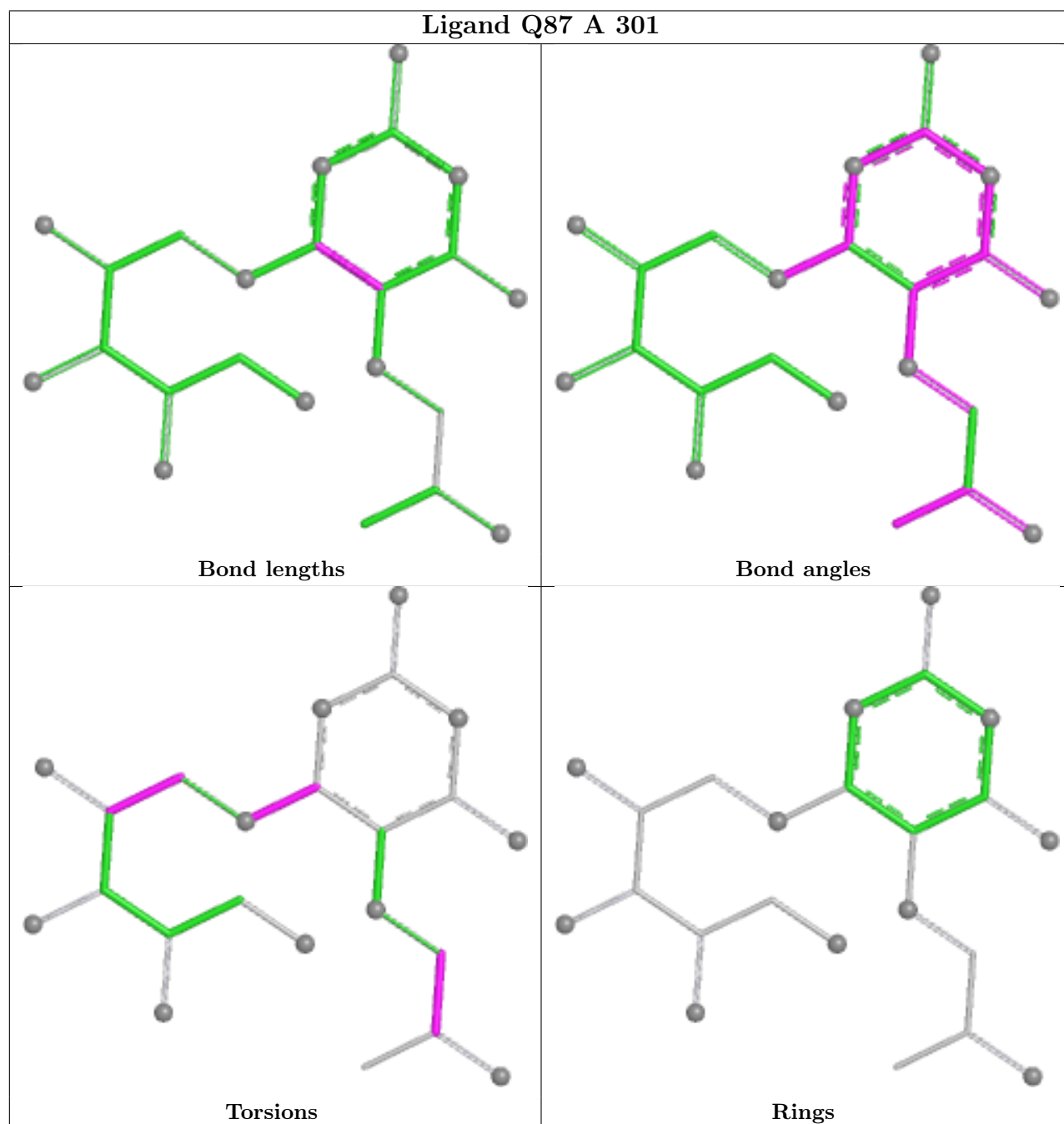
Mol	Chain	Res	Type	Atoms
5	A	301	Q87	N2-C4-N1-C5
5	C	301	Q87	N2-C4-N1-C5
6	D	301	GOL	O1-C1-C2-O2
6	D	301	GOL	O1-C1-C2-C3
5	A	301	Q87	N1-C5-C6-C7
5	A	301	Q87	O7-C1-C2-N
5	C	301	Q87	N1-C5-C6-C7

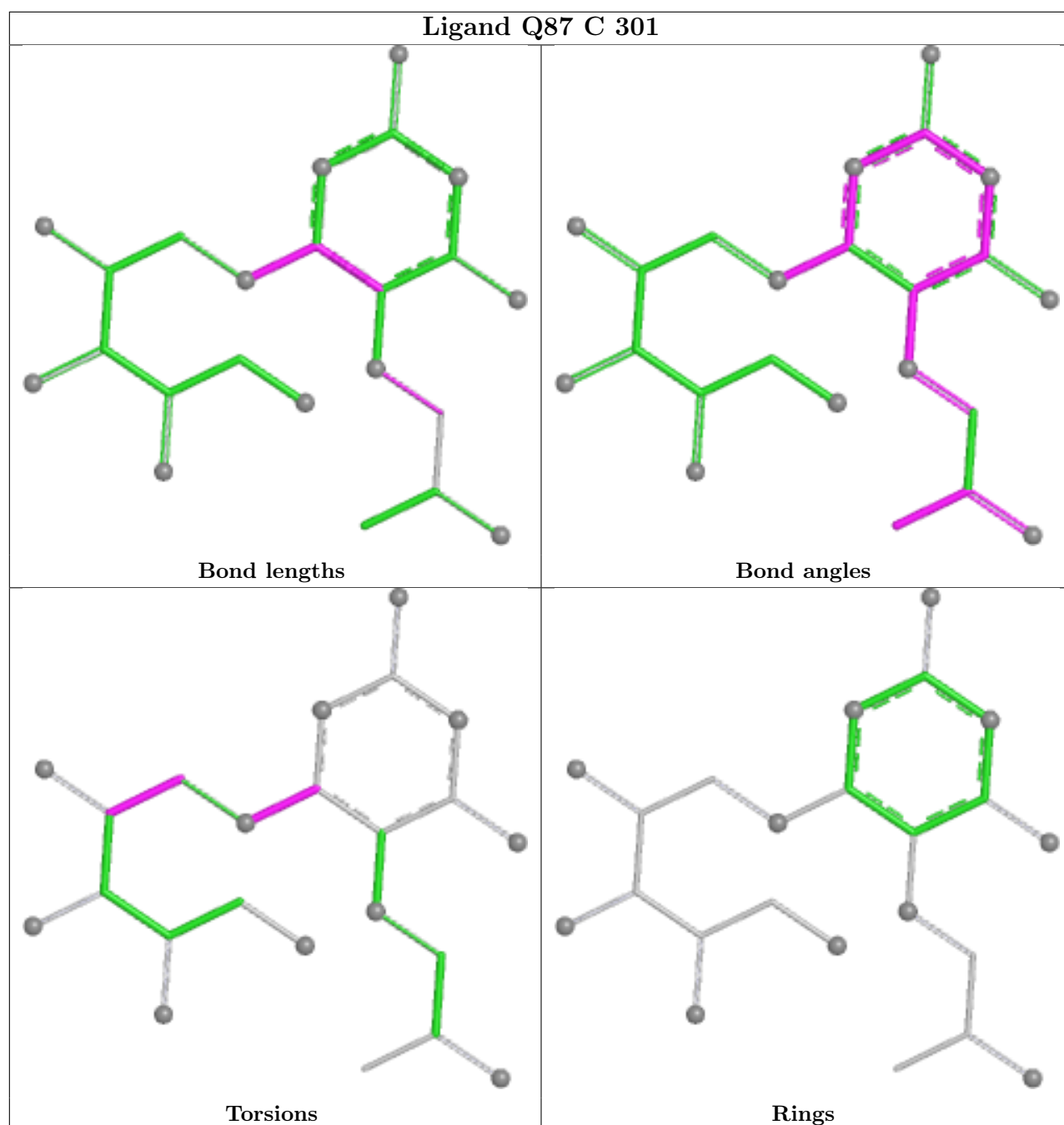
There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

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	260/271 (95%)	-0.19	9 (3%)	47	44	18, 31, 56, 79	1 (0%)
1	C	248/271 (91%)	-0.00	9 (3%)	46	43	17, 34, 59, 75	2 (0%)
2	B	96/99 (96%)	-0.09	1 (1%)	79	77	24, 35, 61, 74	0
2	F	97/99 (97%)	0.63	7 (7%)	21	18	27, 50, 72, 84	0
3	D	200/203 (98%)	-0.13	4 (2%)	65	62	19, 32, 58, 70	0
3	G	190/203 (93%)	0.25	11 (5%)	29	25	17, 39, 71, 94	1 (0%)
4	E	243/245 (99%)	-0.18	4 (1%)	70	67	20, 31, 49, 75	3 (1%)
4	H	242/245 (98%)	0.23	4 (1%)	69	66	23, 40, 59, 82	0
All	All	1576/1636 (96%)	0.02	49 (3%)	51	48	17, 35, 64, 94	7 (0%)

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	221	ILE	7.0
3	G	146	SER	5.6
1	C	16	ILE	4.8
4	E	244	ALA	4.6
4	H	244	ALA	4.5
2	B	96	ASP	4.2
2	F	97	ARG	4.0
1	C	251	SER	4.0
1	C	245	GLU	3.9
1	A	269	VAL	3.7
4	E	2	ALA	3.6
3	G	1	GLY	3.6
1	C	269	VAL	3.4
1	C	188	ARG	3.4
1	C	252	ASN	3.2
3	D	200	PRO	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	217	ASN	3.0
3	G	150	ASP	2.9
4	H	236	VAL	2.7
1	C	211	TYR	2.6
3	G	191	ILE	2.6
3	G	199	SER	2.6
4	H	221	ASN	2.6
2	F	72	PRO	2.6
3	G	188	ASN	2.6
3	G	182	CYS	2.5
4	E	184	LEU	2.5
1	A	245	GLU	2.5
3	G	131	VAL	2.4
2	F	73	THR	2.4
1	A	16	ILE	2.4
1	A	219	GLU	2.4
3	D	1	GLY	2.4
3	D	177	LYS	2.3
1	A	18	GLY	2.3
2	F	77	GLU	2.3
3	G	123	ASP	2.2
2	F	48	LYS	2.2
1	A	57	ASP	2.2
4	E	183	ALA	2.2
1	A	185	ARG	2.1
3	G	177	LYS	2.1
3	G	132	CYS	2.1
1	C	197	ALA	2.1
3	D	164	MET	2.1
1	A	224	GLU	2.1
2	F	17	ASN	2.1
4	H	227	ASP	2.0
2	F	1	ILE	2.0

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](#)

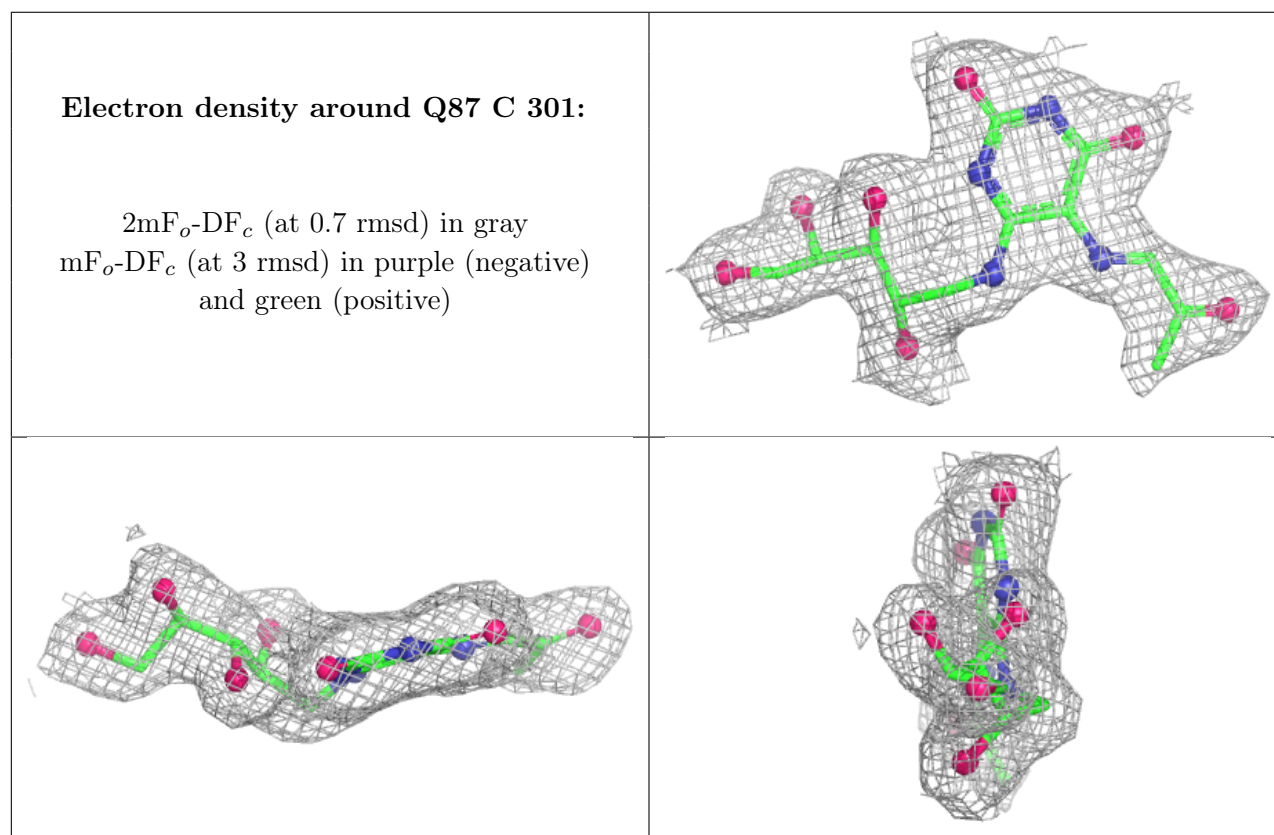
There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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.

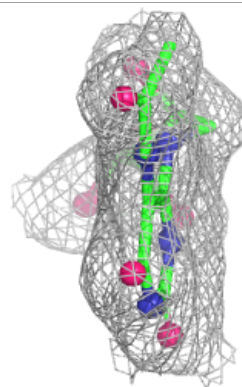
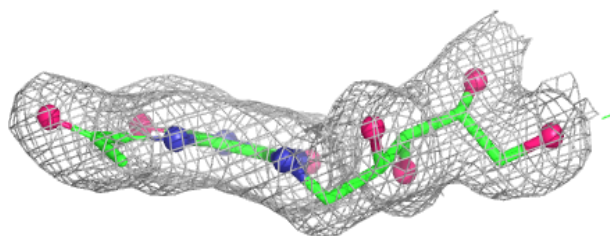
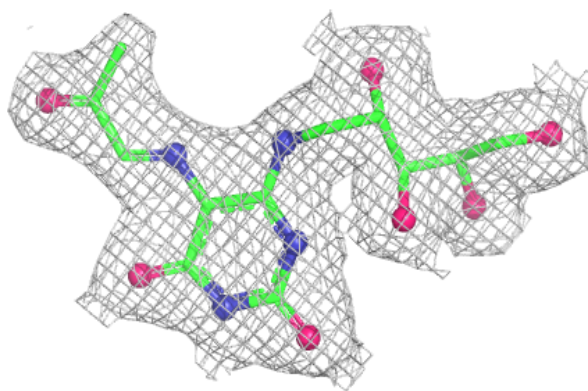
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	GOL	D	301	6/6	0.84	0.15	52,55,56,56	0
5	Q87	C	301	23/23	0.97	0.06	21,25,28,30	0
5	Q87	A	301	23/23	0.97	0.06	23,27,30,30	0

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 Q87 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.