



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 02:32 PM UTC

PDB ID : 2FM0 / pdb_00002fm0
Title : Crystal structure of PDE4D in complex with L-869298
Authors : Huai, Q.; Sun, Y.; Wang, H.; Macdonald, D.; Aspiotis, R.; Robinson, H.;
Huang, Z.; Ke, H.
Deposited on : 2006-01-06
Resolution : 2.00 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

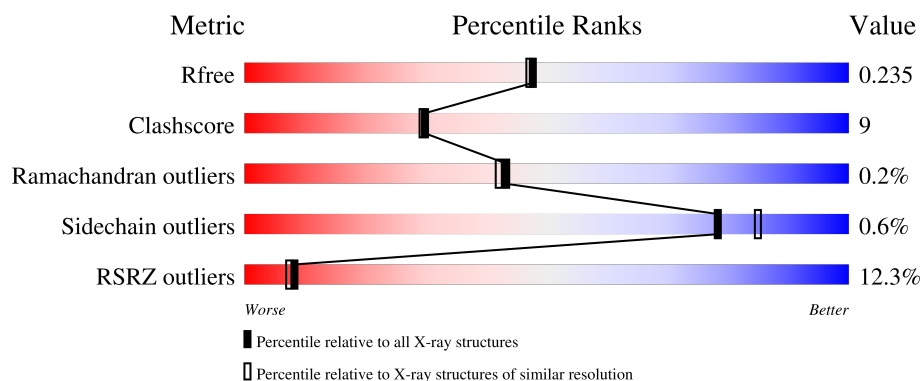
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	361	9% 75% 17% 7%
1	B	361	18% 70% 20% 9%
1	C	361	11% 72% 19% 9%
1	D	361	7% 75% 18% 7%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 11236 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 cAMP-specific 3',5'-cyclic phosphodiesterase 4D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	334	Total	C	N	O	S	0	0	0
			2704	1712	463	515	14			
1	B	327	Total	C	N	O	S	0	0	0
			2647	1673	452	508	14			
1	C	327	Total	C	N	O	S	0	0	0
			2647	1673	452	508	14			
1	D	334	Total	C	N	O	S	0	0	0
			2704	1712	463	515	14			

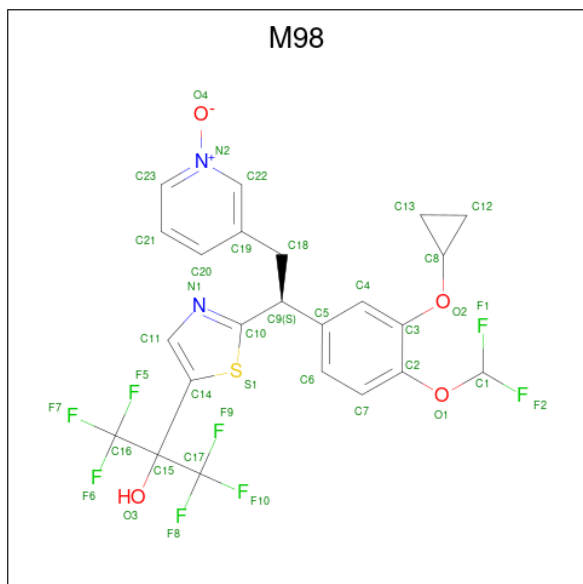
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		

- Molecule 4 is (S)-3-(2-(3-CYCLOPROPOXY-4-(DIFLUOROMETHOXY)PHENYL)-2-(5-(1,1,1,3,3,3-HEXAFLUORO-2-HYDROXYPROPAN-2-YL)THIAZOL-2-YL)ETHYL)PYRIDINE 1-OXIDE (CCD ID: M98) (formula: $C_{23}H_{18}F_8N_2O_4S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	F	N	O	S	0	0
			38	23	8	2	4	1		
4	B	1	Total	C	F	N	O	S	0	0
			38	23	8	2	4	1		
4	C	1	Total	C	F	N	O	S	0	0
			38	23	8	2	4	1		
4	D	1	Total	C	F	N	O	S	0	0
			38	23	8	2	4	1		

- Molecule 5 is water.

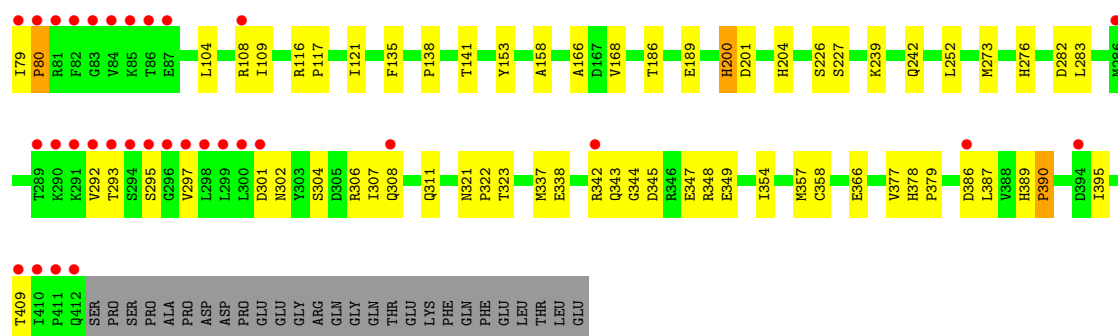
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	101	Total	O	0	0
			101	101		
5	B	81	Total	O	0	0
			81	81		
5	C	76	Total	O	0	0
			76	76		
5	D	116	Total	O	0	0
			116	116		

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.

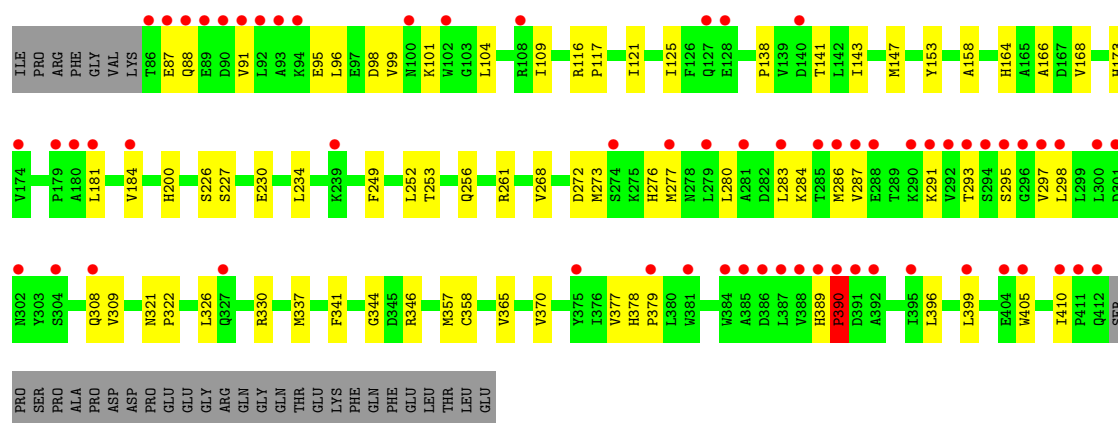
- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D

Chain A: 



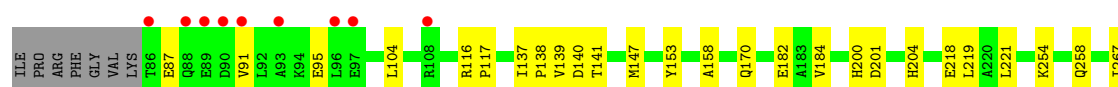
- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D

Chain B: 

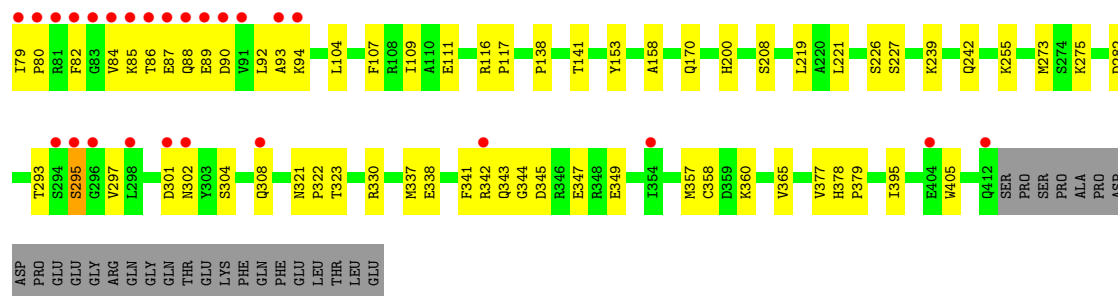
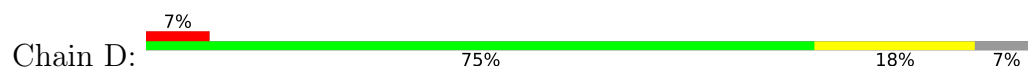


- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D

Chain C: 



- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	99.51Å 112.18Å 160.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.00 30.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-2.00) 96.1 (30.00-2.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.24 (at 2.00Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.223 , 0.245 0.213 , 0.235	Depositor DCC
R_{free} test set	12121 reflections (9.99%)	wwPDB-VP
Wilson B-factor (Å ²)	27.6	Xtriage
Anisotropy	0.089	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 33.6	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	0.94	EDS
Total number of atoms	11236	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.74% 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: ZN, M98, MG

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	0.39	0/2760	0.84	6/3749 (0.2%)
1	B	0.36	0/2701	0.84	4/3670 (0.1%)
1	C	0.35	0/2701	0.82	6/3670 (0.2%)
1	D	0.40	0/2760	0.86	9/3749 (0.2%)
All	All	0.38	0/10922	0.84	25/14838 (0.2%)

There are no bond length outliers.

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	301	ASP	N-CA-C	7.91	119.53	111.07
1	A	158	ALA	N-CA-C	7.15	118.72	111.07
1	D	200	HIS	N-CA-C	7.13	120.87	111.75
1	D	295	SER	N-CA-C	-7.01	101.50	110.19
1	D	153	TYR	N-CA-C	-6.55	98.95	109.96
1	A	377	VAL	N-CA-C	6.50	116.66	110.42
1	D	301	ASP	N-CA-C	6.48	119.31	111.40
1	D	158	ALA	N-CA-C	6.47	118.34	111.28
1	C	200	HIS	N-CA-C	6.41	120.67	112.34
1	C	158	ALA	N-CA-C	6.18	117.68	111.07
1	B	153	TYR	N-CA-C	-6.13	99.66	109.96
1	A	200	HIS	N-CA-C	6.09	120.26	112.34
1	A	153	TYR	N-CA-C	-6.02	99.84	109.96
1	B	200	HIS	N-CA-C	5.99	120.13	112.34
1	D	88	GLN	N-CA-C	-5.92	106.41	113.21
1	B	377	VAL	N-CA-C	5.84	116.02	110.53
1	D	297	VAL	N-CA-C	5.79	118.18	109.20
1	B	158	ALA	N-CA-C	5.72	117.19	111.07
1	C	153	TYR	N-CA-C	-5.62	100.52	109.96
1	D	377	VAL	N-CA-C	5.28	115.49	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	374	ASP	N-CA-C	5.25	117.00	111.28
1	D	208	SER	N-CA-C	5.09	116.67	110.41
1	C	184	VAL	N-CA-C	5.07	115.74	110.82
1	A	276	HIS	N-CA-C	5.01	117.14	111.02
1	C	302	ASN	N-CA-C	5.01	116.58	110.41

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	2704	0	2664	48	0
1	B	2647	0	2599	50	0
1	C	2647	0	2599	45	0
1	D	2704	0	2664	46	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	38	0	17	2	0
4	B	38	0	17	3	0
4	C	38	0	17	5	0
4	D	38	0	17	2	0
5	A	101	0	0	1	0
5	B	81	0	0	2	0
5	C	76	0	0	1	0
5	D	116	0	0	3	0
All	All	11236	0	10594	183	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 9.

All (183) 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:D:337:MET:HE2	1:D:365:VAL:HG22	1.36	1.08
1:B:337:MET:HE2	1:B:365:VAL:HG22	1.43	0.99
1:A:292:VAL:HG12	1:A:293:THR:H	1.34	0.91
1:D:282:ASP:HB3	1:D:308:GLN:NE2	1.95	0.81
1:A:282:ASP:HB3	1:A:308:GLN:NE2	1.97	0.79
1:C:293:THR:HG23	1:C:295:SER:H	1.48	0.78
1:B:104:LEU:HD11	1:B:109:ILE:HD11	1.70	0.73
1:B:96:LEU:O	1:B:99:VAL:HG23	1.89	0.72
1:C:292:VAL:HG22	1:C:293:THR:H	1.53	0.72
1:B:276:HIS:HD2	1:B:277:MET:HE2	1.55	0.71
1:C:273:MET:HE2	4:C:603:M98:H11	1.74	0.70
1:D:79:ILE:N	1:D:80:PRO:HD2	2.07	0.69
1:C:221:LEU:HD23	1:C:221:LEU:O	1.94	0.68
1:A:292:VAL:HG12	1:A:293:THR:N	2.08	0.68
1:D:86:THR:HG21	1:D:92:LEU:HD23	1.77	0.67
1:D:275:LYS:HE2	5:D:679:HOH:O	1.94	0.67
1:A:79:ILE:N	1:A:80:PRO:HD2	2.11	0.66
1:C:330:ARG:HD3	1:C:405:TRP:CH2	2.31	0.65
1:A:242:GLN:OE1	1:D:242:GLN:OE1	2.15	0.64
1:A:104:LEU:HD11	1:A:109:ILE:HD11	1.78	0.64
5:B:642:HOH:O	1:D:84:VAL:HG13	1.97	0.64
1:C:357:MET:SD	4:C:603:M98:H122	2.38	0.64
1:B:321:ASN:HB2	1:B:322:PRO:HD3	1.80	0.63
1:C:321:ASN:HB2	1:C:322:PRO:HD3	1.81	0.63
1:A:357:MET:SD	4:A:601:M98:H122	2.38	0.62
1:B:273:MET:HE2	4:B:602:M98:H11	1.81	0.62
1:C:293:THR:HG22	1:C:297:VAL:O	1.99	0.61
1:C:366:GLU:HG2	1:C:409:THR:HG22	1.81	0.61
1:C:291:LYS:O	1:C:299:LEU:HB3	2.00	0.61
1:D:282:ASP:HB3	1:D:308:GLN:HE22	1.62	0.61
1:A:239:LYS:HZ3	1:D:239:LYS:HZ3	1.49	0.60
1:D:345:ASP:O	1:D:349:GLU:HG3	2.01	0.60
1:A:321:ASN:HB2	1:A:322:PRO:HD3	1.83	0.60
1:B:184:VAL:HG22	1:B:297:VAL:CG1	2.32	0.59
1:D:321:ASN:HB2	1:D:322:PRO:HD3	1.84	0.59
1:A:295:SER:C	1:A:297:VAL:H	2.09	0.59
1:D:79:ILE:N	1:D:79:ILE:HD12	2.17	0.59
1:D:273:MET:HE2	4:D:604:M98:H11	1.84	0.59
1:D:337:MET:CE	1:D:365:VAL:HG22	2.24	0.59
1:C:292:VAL:HG22	1:C:293:THR:N	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:366:GLU:H	1:C:366:GLU:CD	2.10	0.58
1:A:389:HIS:CE1	1:A:390:PRO:HB3	2.40	0.57
1:C:393:GLN:HE21	1:C:397:ASP:CG	2.12	0.57
1:A:79:ILE:N	1:A:80:PRO:CD	2.67	0.57
1:D:86:THR:O	1:D:89:GLU:HB2	2.05	0.57
1:C:254:LYS:O	1:C:258:GLN:HG3	2.06	0.56
1:D:344:GLY:HA3	1:D:358:CYS:O	2.06	0.56
1:B:396:LEU:O	1:B:396:LEU:HD23	2.05	0.55
1:C:338:GLU:OE2	1:C:342:ARG:NH2	2.40	0.55
1:D:87:GLU:C	1:D:89:GLU:H	2.15	0.54
1:A:273:MET:HE2	4:A:601:M98:H11	1.88	0.54
1:D:79:ILE:N	1:D:80:PRO:CD	2.71	0.53
1:A:121:ILE:HD12	1:A:166:ALA:HB1	1.90	0.53
1:B:125:ILE:HD13	1:B:173:HIS:HB2	1.91	0.53
5:A:684:HOH:O	1:B:261:ARG:HD3	2.08	0.53
1:B:291:LYS:O	1:B:298:LEU:HD12	2.09	0.53
1:C:344:GLY:HA3	1:C:358:CYS:O	2.08	0.53
1:D:221:LEU:C	1:D:221:LEU:HD23	2.33	0.53
1:B:147:MET:HE1	1:D:349:GLU:HB3	1.91	0.52
1:B:357:MET:SD	4:B:602:M98:H122	2.48	0.52
1:B:87:GLU:HG3	1:B:88:GLN:N	2.25	0.52
1:D:330:ARG:HD3	1:D:405:TRP:CH2	2.45	0.52
1:A:345:ASP:O	1:A:349:GLU:HG3	2.08	0.52
1:A:239:LYS:HE3	1:C:218:GLU:HB2	1.92	0.52
1:C:378:HIS:HB3	1:C:379:PRO:HD3	1.92	0.52
1:A:337:MET:HE3	1:A:337:MET:HA	1.92	0.52
1:B:138:PRO:HG2	1:B:141:THR:OG1	2.10	0.52
1:B:276:HIS:CD2	1:B:277:MET:HE2	2.41	0.51
1:B:138:PRO:HG2	1:B:141:THR:CB	2.41	0.51
1:A:292:VAL:CG1	1:A:293:THR:H	2.16	0.51
1:A:344:GLY:HA3	1:A:358:CYS:O	2.10	0.51
1:D:338:GLU:OE2	1:D:342:ARG:NH2	2.44	0.51
1:D:107:PHE:O	1:D:111:GLU:HG3	2.10	0.51
1:A:104:LEU:HD11	1:A:109:ILE:CD1	2.40	0.51
1:C:116:ARG:N	1:C:117:PRO:CD	2.74	0.51
1:C:297:VAL:HG12	1:C:298:LEU:N	2.26	0.51
1:C:324:LYS:HE2	5:C:655:HOH:O	2.11	0.51
1:B:91:VAL:O	1:B:95:GLU:HG2	2.11	0.50
1:A:186:THR:OG1	1:A:189:GLU:HG3	2.11	0.50
1:D:357:MET:SD	4:D:604:M98:H122	2.52	0.50
1:C:104:LEU:HD22	1:C:170:GLN:HG3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:116:ARG:N	1:D:117:PRO:CD	2.75	0.49
1:A:239:LYS:NZ	1:D:239:LYS:NZ	2.60	0.49
1:C:182:GLU:O	1:C:297:VAL:HG11	2.12	0.49
1:B:181:LEU:C	1:B:184:VAL:HG23	2.37	0.49
1:B:249:PHE:HA	1:B:252:LEU:HD13	1.94	0.49
5:B:659:HOH:O	1:D:85:LYS:HD2	2.13	0.49
1:D:221:LEU:HD23	1:D:221:LEU:O	2.12	0.49
1:B:121:ILE:HD12	1:B:166:ALA:HB1	1.95	0.49
1:C:221:LEU:HD23	1:C:221:LEU:C	2.37	0.49
1:B:346:ARG:HD2	5:D:624:HOH:O	2.13	0.49
1:B:138:PRO:HG2	1:B:141:THR:HB	1.95	0.48
1:A:239:LYS:HZ3	1:D:239:LYS:NZ	2.11	0.48
1:B:87:GLU:HG3	1:B:88:GLN:HG3	1.95	0.48
1:C:138:PRO:HG2	1:C:141:THR:OG1	2.12	0.48
1:A:138:PRO:HG2	1:A:141:THR:OG1	2.13	0.48
1:B:283:LEU:O	1:B:287:VAL:HG23	2.14	0.48
1:D:104:LEU:HD22	1:D:170:GLN:HG3	1.96	0.48
1:B:389:HIS:CD2	1:B:390:PRO:HB3	2.49	0.47
1:D:226:SER:O	1:D:227:SER:C	2.56	0.47
1:D:255:LYS:HD2	1:D:255:LYS:HA	1.70	0.47
1:B:280:LEU:HG	1:B:284:LYS:HE3	1.95	0.47
1:B:378:HIS:HB3	1:B:379:PRO:HD3	1.95	0.47
1:A:282:ASP:HB3	1:A:308:GLN:CD	2.40	0.47
1:B:116:ARG:N	1:B:117:PRO:CD	2.78	0.47
1:A:302:ASN:O	1:A:306:ARG:HG3	2.13	0.47
1:A:307:ILE:O	1:A:311:GLN:HG3	2.15	0.47
1:A:338:GLU:OE2	1:A:342:ARG:NH2	2.48	0.47
1:B:181:LEU:HA	1:B:184:VAL:HG21	1.97	0.46
1:C:283:LEU:O	1:C:287:VAL:HG23	2.15	0.46
1:A:295:SER:C	1:A:297:VAL:N	2.74	0.46
1:D:104:LEU:HD11	1:D:109:ILE:HD11	1.97	0.46
1:A:116:ARG:N	1:A:117:PRO:CD	2.79	0.46
1:A:348:ARG:HD3	1:A:354:ILE:HD11	1.97	0.45
1:C:364:SER:HB3	1:C:367:LYS:HB3	1.97	0.45
1:D:293:THR:O	1:D:295:SER:O	2.34	0.45
1:D:138:PRO:HG2	1:D:141:THR:OG1	2.16	0.45
1:A:302:ASN:OD1	1:A:304:SER:HB3	2.17	0.45
1:C:372:PHE:HB2	4:C:603:M98:H132	1.98	0.45
1:C:87:GLU:O	1:C:91:VAL:HG23	2.17	0.45
1:B:293:THR:C	1:B:295:SER:H	2.24	0.45
1:C:287:VAL:HG11	1:C:386:ASP:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:349:GLU:HB3	1:C:147:MET:HE1	1.98	0.45
1:B:330:ARG:HH11	1:B:405:TRP:HH2	1.65	0.45
1:C:406:TYR:O	1:C:409:THR:HB	2.17	0.45
1:B:184:VAL:CG2	1:B:297:VAL:CG1	2.94	0.44
1:D:337:MET:HE3	1:D:341:PHE:CZ	2.52	0.44
1:A:226:SER:O	1:A:227:SER:C	2.59	0.44
1:D:378:HIS:HB3	1:D:379:PRO:HD3	1.98	0.44
1:A:135:PHE:HB3	1:A:252:LEU:HD11	1.99	0.44
1:B:184:VAL:HG22	1:B:297:VAL:HG11	1.99	0.44
1:C:293:THR:HG22	1:C:297:VAL:N	2.32	0.44
1:D:302:ASN:OD1	1:D:304:SER:HB3	2.17	0.44
1:A:378:HIS:HB3	1:A:379:PRO:HD3	2.00	0.43
1:A:283:LEU:HD11	1:A:387:LEU:HD22	1.99	0.43
1:B:87:GLU:HG3	1:B:88:GLN:H	1.83	0.43
1:D:85:LYS:HG3	5:D:714:HOH:O	2.18	0.43
1:B:230:GLU:HG2	1:B:272:ASP:HB2	2.00	0.43
1:B:253:THR:OG1	1:B:256:GLN:HG3	2.18	0.43
1:B:147:MET:CE	1:D:349:GLU:HB3	2.49	0.43
1:B:234:LEU:HG	1:B:268:VAL:HG11	2.01	0.43
1:C:201:ASP:O	1:C:204:HIS:HB2	2.19	0.43
1:C:293:THR:HG23	1:C:295:SER:N	2.26	0.43
1:D:90:ASP:O	1:D:94:LYS:HG3	2.19	0.43
1:A:108:ARG:HH11	1:A:108:ARG:HG2	1.84	0.43
1:B:226:SER:O	1:B:227:SER:C	2.62	0.43
1:B:143:ILE:O	1:B:147:MET:HG3	2.20	0.42
1:A:409:THR:O	1:A:409:THR:HG22	2.17	0.42
1:C:267:ILE:HG21	1:C:314:VAL:HG21	2.01	0.42
1:D:219:LEU:HD23	1:D:219:LEU:HA	1.89	0.42
1:A:366:GLU:HG2	1:A:409:THR:HG22	2.01	0.42
1:D:323:THR:HB	1:D:395:ILE:HG23	2.00	0.42
1:C:373:ILE:HA	1:C:377:VAL:HB	2.01	0.42
1:C:139:VAL:HG13	1:C:140:ASP:N	2.35	0.42
4:B:602:M98:H4	4:B:602:M98:S1	2.60	0.42
1:C:91:VAL:O	1:C:95:GLU:HG2	2.20	0.42
4:C:603:M98:H4	4:C:603:M98:S1	2.60	0.42
1:A:168:VAL:HG21	1:A:200:HIS:CE1	2.55	0.42
1:A:345:ASP:OD1	1:A:348:ARG:NH2	2.52	0.42
1:B:234:LEU:HD21	1:B:268:VAL:HB	2.01	0.42
1:B:286:MET:HE1	1:B:309:VAL:CG2	2.49	0.42
1:C:372:PHE:CG	4:C:603:M98:H132	2.55	0.41
1:B:344:GLY:HA3	1:B:358:CYS:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:337:MET:HE3	1:B:341:PHE:CZ	2.55	0.41
1:A:323:THR:HB	1:A:395:ILE:HG23	2.01	0.41
1:A:293:THR:C	1:A:295:SER:N	2.78	0.41
1:C:389:HIS:CE1	1:C:390:PRO:HB3	2.55	0.41
1:C:219:LEU:HD12	1:C:219:LEU:HA	1.94	0.41
1:B:181:LEU:HA	1:B:184:VAL:CG2	2.50	0.41
1:B:370:VAL:HG21	1:B:410:ILE:HD11	2.02	0.41
1:B:378:HIS:HA	1:B:399:LEU:HD21	2.02	0.41
1:D:345:ASP:OD1	1:D:360:LYS:HE2	2.21	0.41
1:A:295:SER:O	1:A:297:VAL:N	2.54	0.41
1:B:98:ASP:OD1	1:B:101:LYS:HD2	2.20	0.41
1:C:297:VAL:HG12	1:C:298:LEU:H	1.85	0.41
1:C:270:ALA:HB1	1:C:279:LEU:HD11	2.02	0.41
1:A:282:ASP:HB3	1:A:308:GLN:HE22	1.82	0.40
1:A:343:GLN:O	1:A:347:GLU:HG3	2.21	0.40
1:C:137:ILE:O	1:C:138:PRO:C	2.64	0.40
1:D:343:GLN:O	1:D:347:GLU:HG3	2.21	0.40
1:A:201:ASP:O	1:A:204:HIS:HB2	2.21	0.40
1:B:164:HIS:O	1:B:168:VAL:HG23	2.21	0.40
1:D:82:PHE:CZ	1:D:93:ALA:HA	2.56	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	332/361 (92%)	321 (97%)	10 (3%)	1 (0%)	36	35
1	B	325/361 (90%)	310 (95%)	13 (4%)	2 (1%)	21	17
1	C	325/361 (90%)	309 (95%)	16 (5%)	0	100	100
1	D	332/361 (92%)	322 (97%)	10 (3%)	0	100	100
All	All	1314/1444 (91%)	1262 (96%)	49 (4%)	3 (0%)	43	42

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	326	LEU
1	A	80	PRO
1	B	390	PRO

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	305/329 (93%)	303 (99%)	2 (1%)	76	82
1	B	299/329 (91%)	297 (99%)	2 (1%)	76	82
1	C	299/329 (91%)	296 (99%)	3 (1%)	68	75
1	D	305/329 (93%)	305 (100%)	0	100	100
All	All	1208/1316 (92%)	1201 (99%)	7 (1%)	78	85

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	386	ASP
1	A	390	PRO
1	B	308	GLN
1	B	390	PRO
1	C	306	ARG
1	C	390	PRO
1	C	401	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	123	HIS
1	A	210	GLN
1	A	245	ASN
1	A	250	GLN
1	A	308	GLN

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Mol	Chain	Res	Type
1	B	123	HIS
1	B	245	ASN
1	B	250	GLN
1	B	258	GLN
1	B	321	ASN
1	B	369	GLN
1	B	407	GLN
1	C	242	GLN
1	C	245	ASN
1	C	250	GLN
1	C	308	GLN
1	C	321	ASN
1	C	393	GLN
1	C	407	GLN
1	D	123	HIS
1	D	127	GLN
1	D	210	GLN
1	D	245	ASN
1	D	308	GLN
1	D	407	GLN

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](#)

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 for Mogul analysis.

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	$\# Z > 2$
4	M98	C	603	-	39,41,41	1.62	8 (20%)	51,63,63	1.77	3 (5%)
4	M98	D	604	-	39,41,41	1.59	8 (20%)	51,63,63	1.72	3 (5%)
4	M98	B	602	-	39,41,41	1.65	9 (23%)	51,63,63	1.80	3 (5%)
4	M98	A	601	-	39,41,41	1.65	8 (20%)	51,63,63	1.78	3 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	M98	C	603	-	-	4/42/46/46	0/4/4/4
4	M98	D	604	-	-	4/42/46/46	0/4/4/4
4	M98	B	602	-	-	3/42/46/46	0/4/4/4
4	M98	A	601	-	-	5/42/46/46	0/4/4/4

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	604	M98	C11-N1	3.96	1.45	1.37
4	C	603	M98	C11-C14	3.90	1.41	1.34
4	C	603	M98	C11-N1	3.88	1.44	1.37
4	D	604	M98	C11-C14	3.86	1.41	1.34
4	B	602	M98	C11-C14	3.85	1.41	1.34
4	B	602	M98	C10-S1	-3.83	1.66	1.75
4	A	601	M98	C11-N1	3.71	1.44	1.37
4	A	601	M98	C10-S1	-3.69	1.67	1.75
4	A	601	M98	C11-C14	3.62	1.40	1.34
4	B	602	M98	C11-N1	3.41	1.44	1.37
4	A	601	M98	C13-C8	3.41	1.54	1.48
4	D	604	M98	C13-C8	3.37	1.54	1.48
4	C	603	M98	C10-S1	-3.36	1.67	1.75
4	C	603	M98	C13-C8	3.27	1.54	1.48
4	D	604	M98	C10-S1	-3.12	1.68	1.75
4	D	604	M98	C12-C8	3.10	1.53	1.48
4	C	603	M98	C17-C15	3.08	1.57	1.53
4	A	601	M98	C12-C8	3.08	1.53	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	602	M98	C13-C8	3.05	1.53	1.48
4	C	603	M98	C12-C8	3.01	1.53	1.48
4	B	602	M98	C17-C15	2.99	1.57	1.53
4	B	602	M98	C12-C8	2.92	1.53	1.48
4	A	601	M98	C17-C15	2.91	1.57	1.53
4	A	601	M98	C14-S1	-2.69	1.67	1.73
4	D	604	M98	C22-N2	2.61	1.40	1.35
4	B	602	M98	C14-S1	-2.59	1.67	1.73
4	D	604	M98	C17-C15	2.58	1.56	1.53
4	B	602	M98	C16-C15	2.51	1.56	1.53
4	A	601	M98	C22-N2	2.50	1.40	1.35
4	C	603	M98	C22-N2	2.50	1.40	1.35
4	B	602	M98	C22-N2	2.34	1.39	1.35
4	C	603	M98	C14-S1	-2.08	1.68	1.73
4	D	604	M98	C14-S1	-2.02	1.69	1.73

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	602	M98	C14-C11-N1	-9.93	106.96	117.10
4	C	603	M98	C14-C11-N1	-9.74	107.16	117.10
4	A	601	M98	C14-C11-N1	-9.73	107.16	117.10
4	D	604	M98	C14-C11-N1	-9.41	107.49	117.10
4	B	602	M98	C11-C14-S1	5.39	113.85	108.93
4	A	601	M98	C11-C14-S1	5.25	113.72	108.93
4	C	603	M98	C11-C14-S1	5.01	113.50	108.93
4	D	604	M98	C11-C14-S1	4.80	113.31	108.93
4	C	603	M98	S1-C10-N1	-3.61	111.05	115.98
4	D	604	M98	S1-C10-N1	-3.57	111.11	115.98
4	A	601	M98	S1-C10-N1	-3.52	111.17	115.98
4	B	602	M98	S1-C10-N1	-3.33	111.42	115.98

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	601	M98	C13-C8-O2-C3
4	B	602	M98	C13-C8-O2-C3
4	C	603	M98	C13-C8-O2-C3
4	D	604	M98	C13-C8-O2-C3
4	A	601	M98	C4-C5-C9-C10
4	B	602	M98	C4-C5-C9-C10

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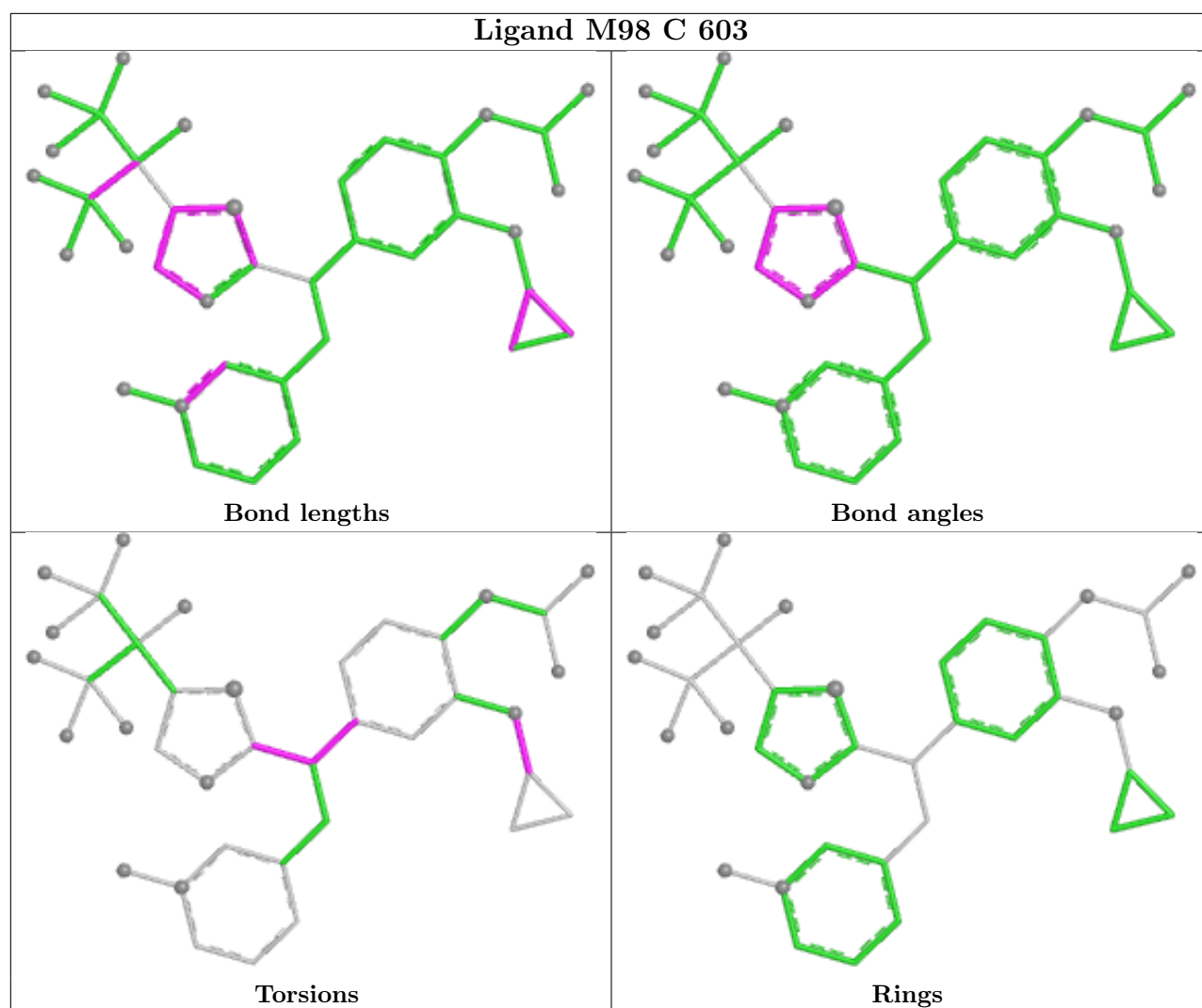
Mol	Chain	Res	Type	Atoms
4	C	603	M98	C4-C5-C9-C10
4	A	601	M98	S1-C14-C15-O3
4	A	601	M98	C6-C5-C9-C10
4	B	602	M98	C6-C5-C9-C10
4	C	603	M98	C6-C5-C9-C10
4	D	604	M98	C4-C5-C9-C10
4	D	604	M98	C6-C5-C9-C10
4	A	601	M98	N1-C10-C9-C18
4	C	603	M98	N1-C10-C9-C18
4	D	604	M98	N1-C10-C9-C18

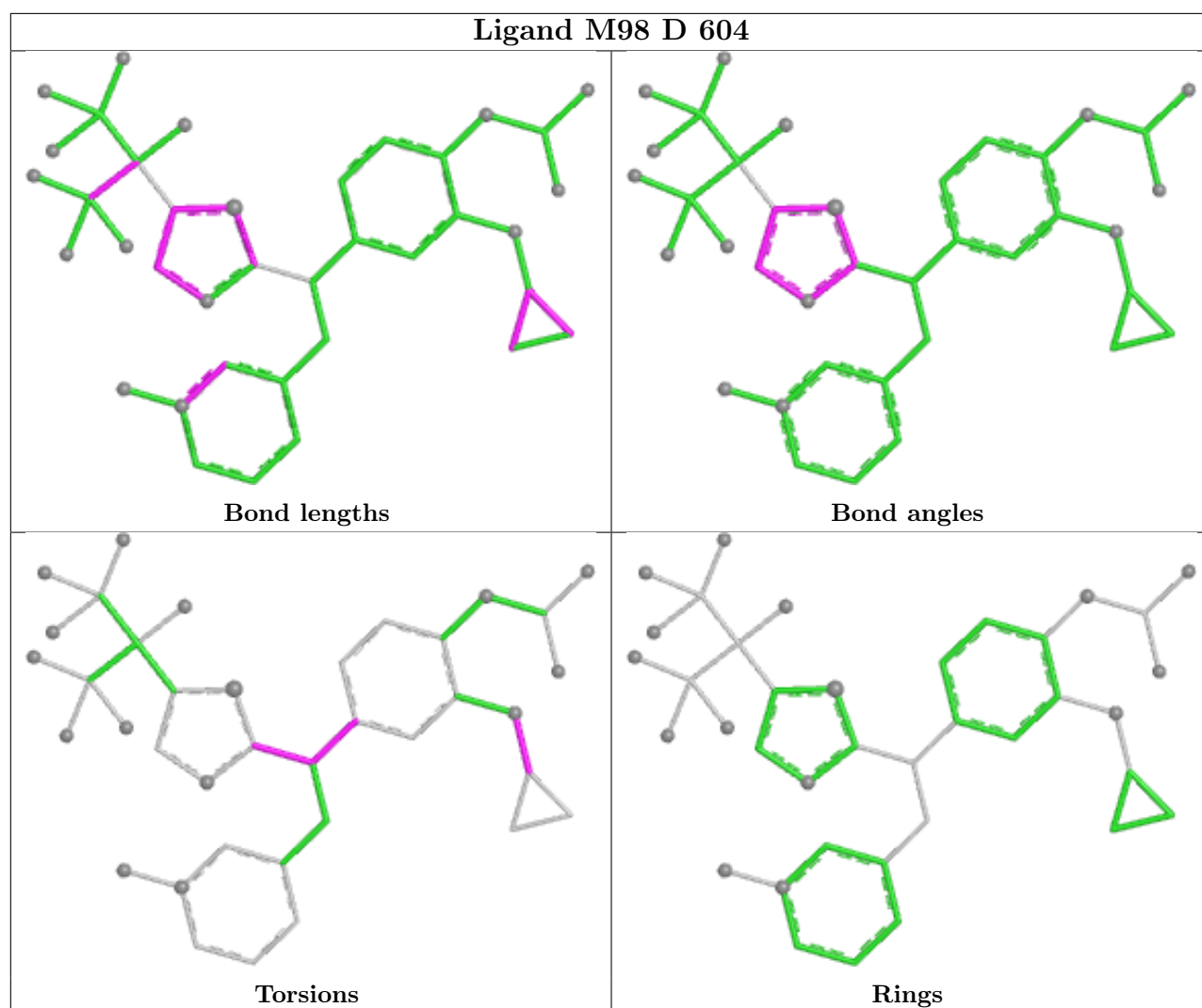
There are no ring outliers.

4 monomers are involved in 12 short contacts:

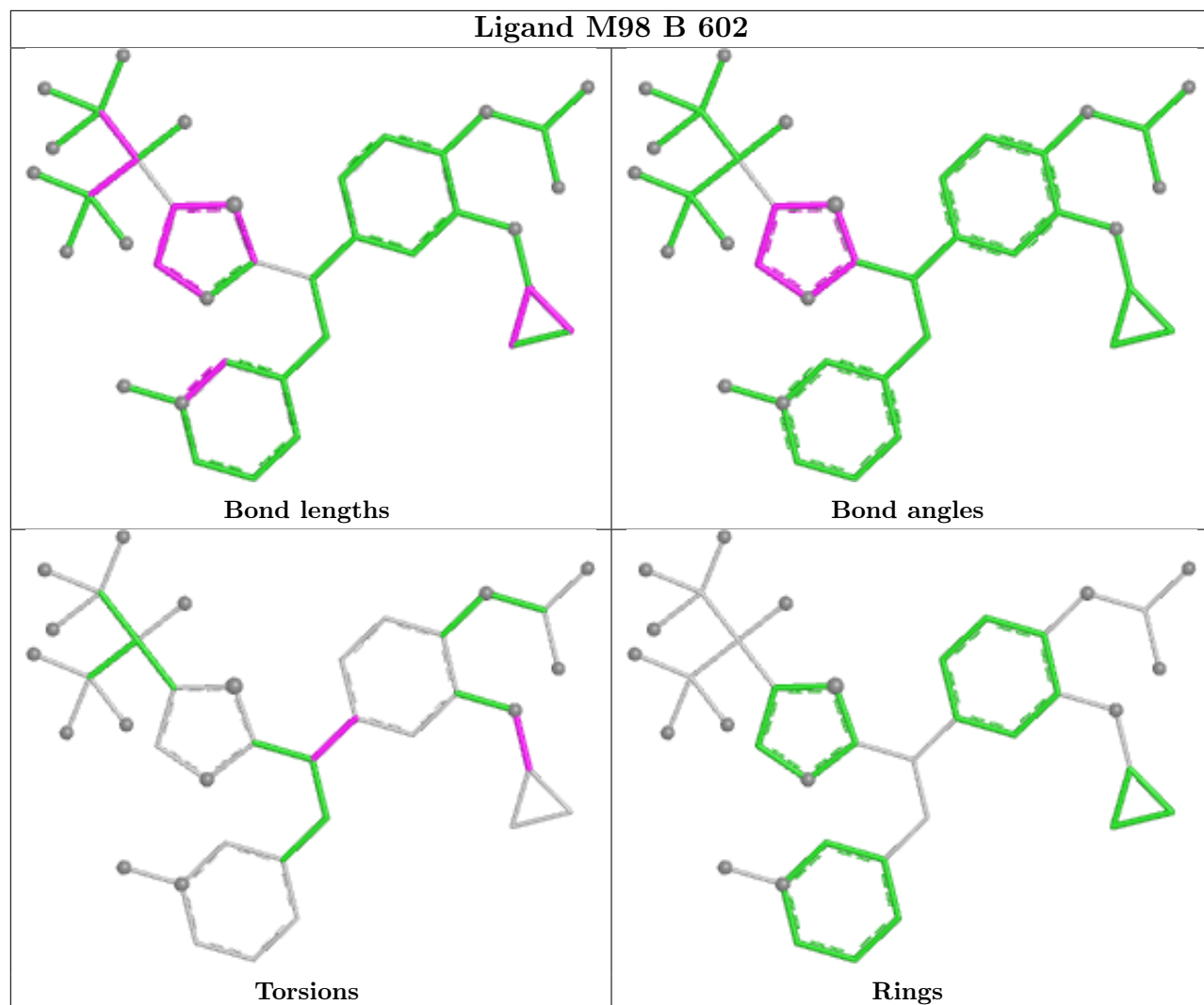
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	603	M98	5	0
4	D	604	M98	2	0
4	B	602	M98	3	0
4	A	601	M98	2	0

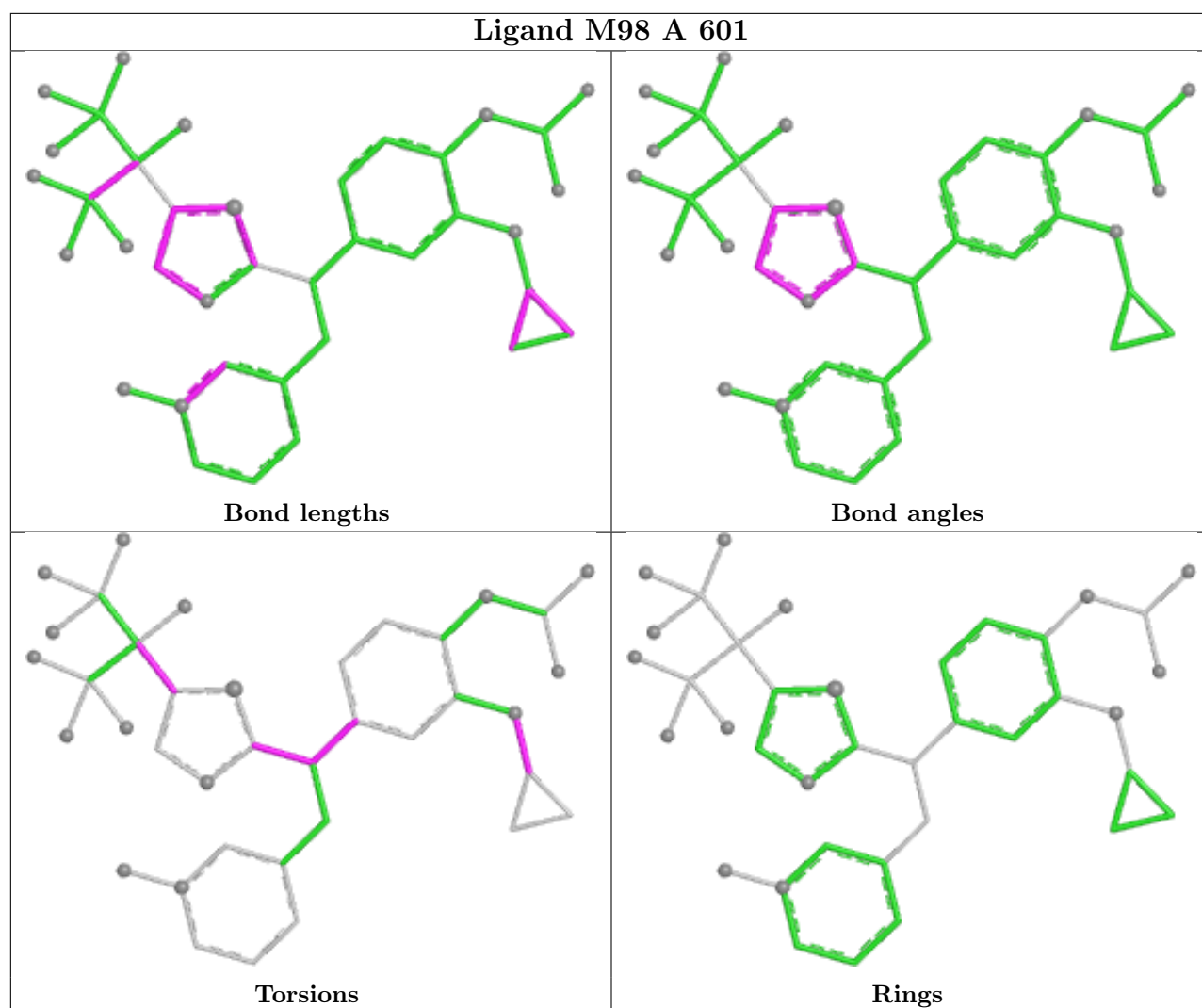
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 M98 B 602





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	334/361 (92%)	0.39	32 (9%) 13 12	17, 27, 62, 85	0
1	B	327/361 (90%)	0.97	64 (19%) 3 3	19, 35, 57, 91	0
1	C	327/361 (90%)	0.75	41 (12%) 8 7	19, 35, 69, 80	0
1	D	334/361 (92%)	0.32	26 (7%) 19 18	17, 27, 47, 83	0
All	All	1322/1444 (91%)	0.60	163 (12%) 8 7	17, 31, 61, 91	0

All (163) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	79	ILE	9.7
1	D	84	VAL	8.1
1	D	79	ILE	7.3
1	D	82	PHE	7.1
1	B	412	GLN	6.7
1	A	294	SER	6.5
1	A	82	PHE	6.3
1	A	296	GLY	5.8
1	D	80	PRO	5.8
1	A	80	PRO	5.7
1	A	293	THR	5.5
1	A	81	ARG	5.5
1	B	295	SER	5.3
1	D	296	GLY	5.0
1	B	391	ASP	4.9
1	C	327	GLN	4.8
1	D	86	THR	4.8
1	A	297	VAL	4.7
1	A	298	LEU	4.7
1	C	86	THR	4.6
1	D	83	GLY	4.6

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Mol	Chain	Res	Type	RSRZ
1	B	296	GLY	4.6
1	A	411	PRO	4.6
1	C	297	VAL	4.5
1	D	412	GLN	4.4
1	D	85	LYS	4.4
1	A	295	SER	4.4
1	C	292	VAL	4.4
1	A	299	LEU	4.3
1	C	298	LEU	4.2
1	B	281	ALA	4.0
1	C	293	THR	4.0
1	B	86	THR	3.9
1	D	89	GLU	3.9
1	A	301	ASP	3.9
1	B	390	PRO	3.9
1	C	289	THR	3.8
1	B	93	ALA	3.7
1	B	285	THR	3.6
1	B	180	ALA	3.6
1	C	411	PRO	3.6
1	B	301	ASP	3.6
1	B	293	THR	3.6
1	B	388	VAL	3.5
1	C	287	VAL	3.5
1	C	282	ASP	3.5
1	C	283	LEU	3.4
1	C	295	SER	3.3
1	B	385	ALA	3.3
1	D	404	GLU	3.3
1	B	294	SER	3.3
1	A	84	VAL	3.2
1	B	91	VAL	3.2
1	B	184	VAL	3.2
1	B	92	LEU	3.2
1	C	301	ASP	3.2
1	B	239	LYS	3.2
1	D	87	GLU	3.2
1	A	289	THR	3.1
1	C	91	VAL	3.1
1	B	298	LEU	3.0
1	A	409	THR	3.0
1	C	97	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	81	ARG	3.0
1	C	93	ALA	3.0
1	B	387	LEU	2.9
1	B	292	VAL	2.9
1	A	290	LYS	2.9
1	C	299	LEU	2.9
1	D	91	VAL	2.9
1	A	412	GLN	2.9
1	A	291	LYS	2.9
1	C	296	GLY	2.9
1	A	83	GLY	2.8
1	C	412	GLN	2.8
1	C	277	MET	2.8
1	C	302	ASN	2.7
1	C	279	LEU	2.7
1	B	386	ASP	2.7
1	D	342	ARG	2.7
1	B	288	GLU	2.7
1	B	381	TRP	2.7
1	B	283	LEU	2.7
1	C	300	LEU	2.7
1	B	277	MET	2.7
1	C	89	GLU	2.7
1	C	90	ASP	2.7
1	A	308	GLN	2.6
1	A	410	ILE	2.6
1	A	108	ARG	2.6
1	D	301	ASP	2.6
1	B	302	ASN	2.6
1	A	85	LYS	2.6
1	C	397	ASP	2.6
1	D	295	SER	2.6
1	B	140	ASP	2.5
1	B	88	GLN	2.5
1	C	392	ALA	2.5
1	B	411	PRO	2.5
1	C	385	ALA	2.5
1	C	294	SER	2.4
1	B	279	LEU	2.4
1	C	275	LYS	2.4
1	A	394	ASP	2.4
1	B	174	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	285	THR	2.4
1	B	286	MET	2.4
1	D	294	SER	2.4
1	B	379	PRO	2.4
1	B	395	ILE	2.4
1	B	87	GLU	2.3
1	C	281	ALA	2.3
1	C	288	GLU	2.3
1	A	292	VAL	2.3
1	B	287	VAL	2.3
1	B	102	TRP	2.3
1	B	392	ALA	2.3
1	B	300	LEU	2.3
1	C	96	LEU	2.3
1	B	94	LYS	2.3
1	D	308	GLN	2.3
1	D	90	ASP	2.3
1	B	389	HIS	2.3
1	B	410	ILE	2.3
1	B	179	PRO	2.3
1	B	108	ARG	2.3
1	A	300	LEU	2.3
1	B	181	LEU	2.3
1	B	375	TYR	2.3
1	D	94	LYS	2.2
1	D	298	LEU	2.2
1	B	404	GLU	2.2
1	D	88	GLN	2.2
1	B	399	LEU	2.2
1	B	327	GLN	2.2
1	C	88	GLN	2.2
1	B	405	TRP	2.2
1	A	86	THR	2.2
1	A	386	ASP	2.2
1	C	395	ILE	2.2
1	B	89	GLU	2.2
1	B	100	ASN	2.2
1	C	394	ASP	2.2
1	B	297	VAL	2.1
1	B	290	LYS	2.1
1	C	280	LEU	2.1
1	C	108	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	290	LYS	2.1
1	D	93	ALA	2.1
1	B	274	SER	2.1
1	B	308	GLN	2.1
1	A	342	ARG	2.1
1	D	354	ILE	2.1
1	B	384	TRP	2.1
1	D	302	ASN	2.0
1	B	90	ASP	2.0
1	B	127	GLN	2.0
1	A	87	GLU	2.0
1	B	128	GLU	2.0
1	A	286	MET	2.0
1	B	304	SER	2.0
1	B	291	LYS	2.0
1	C	409	THR	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 [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
4	M98	C	603	38/38	0.92	0.10	32,36,44,46	0
4	M98	D	604	38/38	0.93	0.09	25,31,42,44	0
4	M98	A	601	38/38	0.94	0.09	25,29,39,41	0
4	M98	B	602	38/38	0.94	0.09	29,32,41,43	0
3	MG	C	506	1/1	0.95	0.06	25,25,25,25	0
3	MG	B	504	1/1	0.96	0.05	26,26,26,26	0
3	MG	D	508	1/1	0.96	0.06	24,24,24,24	0

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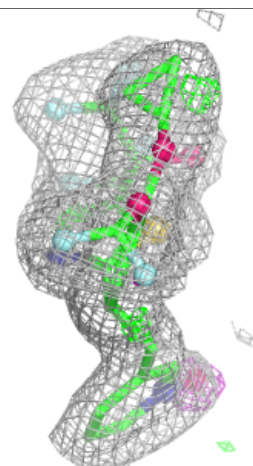
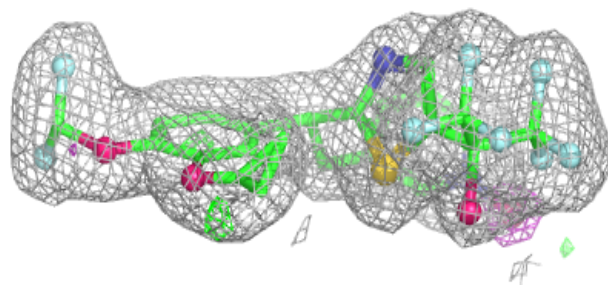
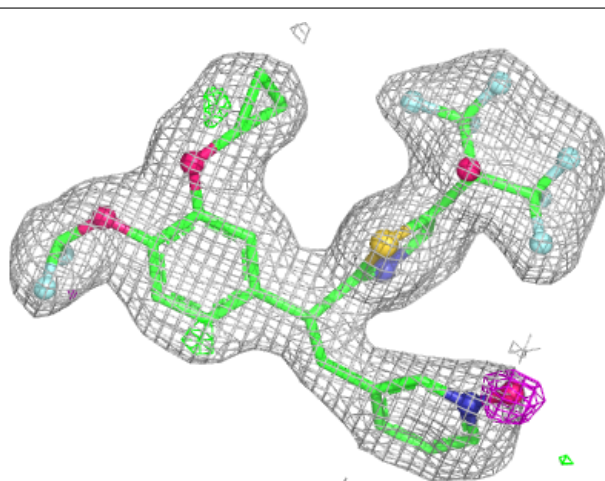
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MG	A	502	1/1	0.98	0.03	21,21,21,21	0
2	ZN	B	503	1/1	0.98	0.05	30,30,30,30	0
2	ZN	D	507	1/1	0.99	0.03	24,24,24,24	0
2	ZN	A	501	1/1	0.99	0.04	24,24,24,24	0
2	ZN	C	505	1/1	0.99	0.04	27,27,27,27	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.

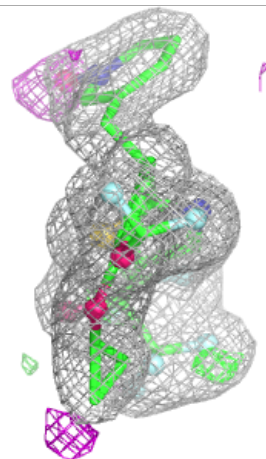
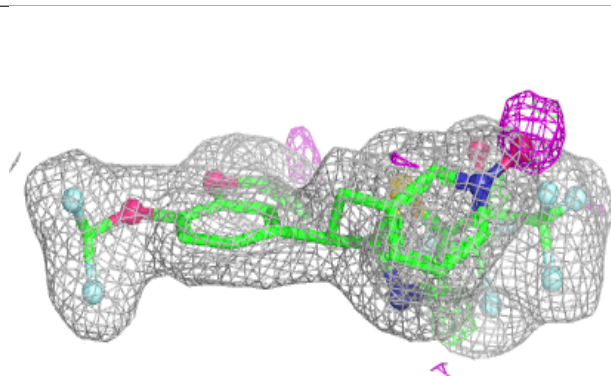
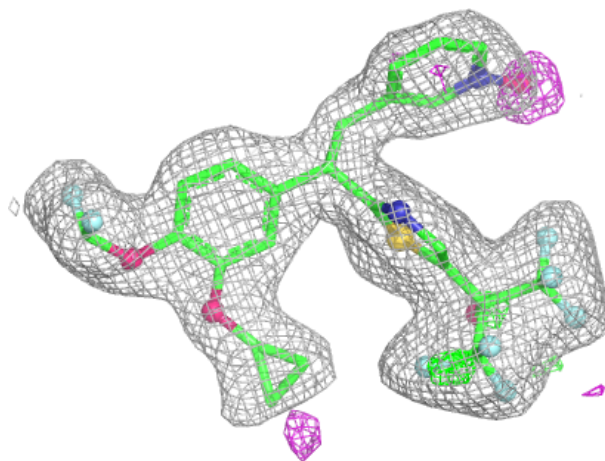
Electron density around M98 C 603:

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



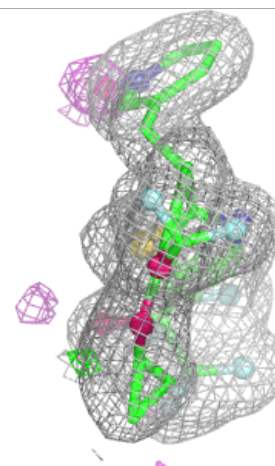
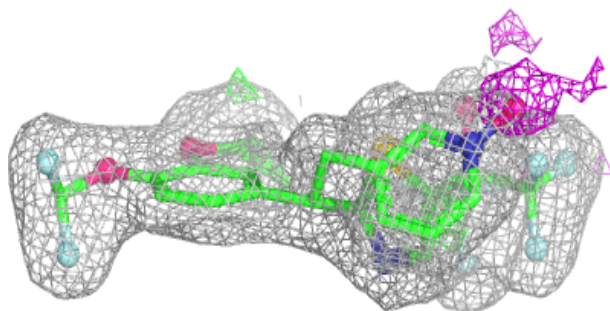
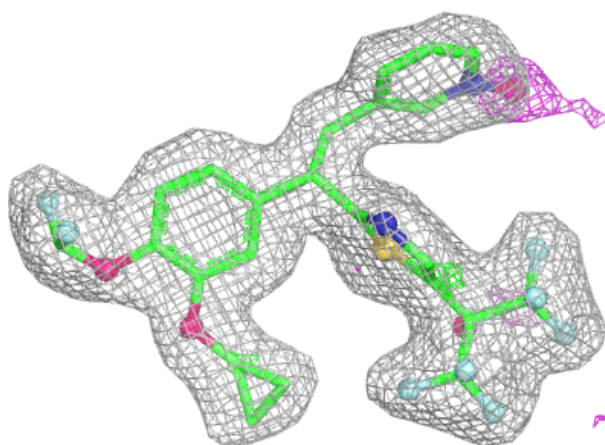
Electron density around M98 D 604:

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



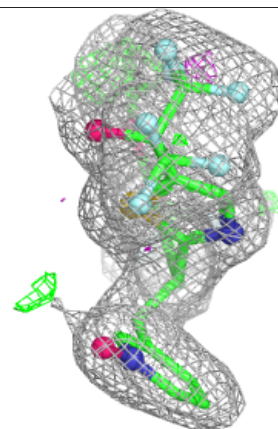
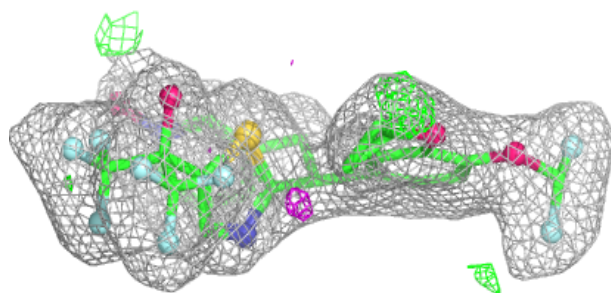
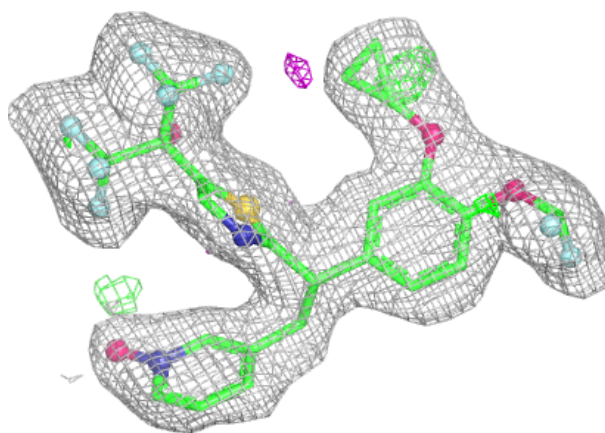
Electron density around M98 A 601:

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



Electron density around M98 B 602:

$2mF_o-DF_c$ (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.