



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 04:25 pm BST

PDB ID : 6G8N
Title : Yeast 20S proteasome in complex with Cystargolide B Derivative 2
Authors : Groll, M.; Tello-Aburto, R.
Deposited on : 2018-04-09
Resolution : 3.00 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

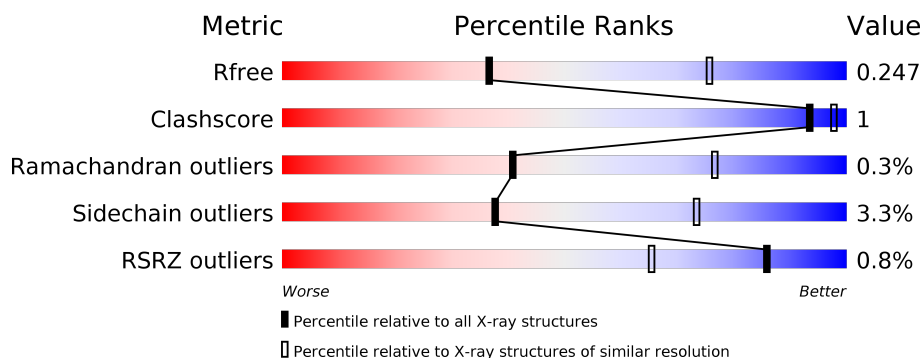
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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.





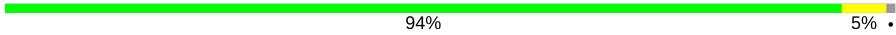
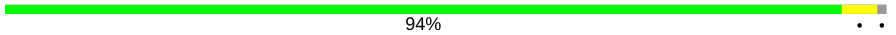






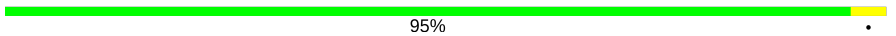
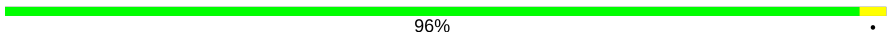
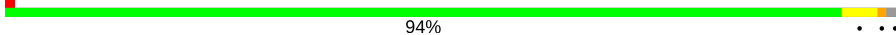



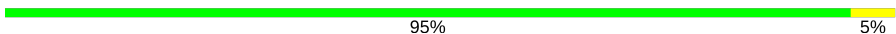




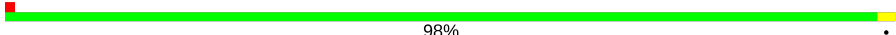
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 on 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	250	<div> <div>%</div> <div> <div></div> <div>97%</div> <div></div> </div> </div>
1	O	250	<div> <div></div> <div>96%</div> <div></div> </div>
2	B	258	<div> <div>2%</div> <div> <div></div> <div>88%</div> <div>6% 5%</div> </div> </div>
2	P	258	<div> <div>2%</div> <div> <div></div> <div>89%</div> <div>6% 5%</div> </div> </div>
3	C	254	<div> <div>%</div> <div> <div></div> <div>87%</div> <div>6% 6%</div> </div> </div>
3	Q	254	<div> <div>2%</div> <div> <div></div> <div>88%</div> <div>5% 6%</div> </div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	D	260	
4	R	260	
5	E	234	
5	S	234	
6	F	288	
6	T	288	
7	G	252	
7	U	252	
8	H	232	
8	V	232	
9	I	205	
9	W	205	
10	J	198	
10	X	198	
11	K	212	
11	Y	212	
12	L	222	
12	Z	222	
13	M	246	
13	a	246	
14	N	196	
14	b	196	

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 49531 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 Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			
1	O	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			

- Molecule 2 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			
2	P	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			

- Molecule 3 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	240	Total	C	N	O	S	0	0	0
			1881	1176	329	372	4			
3	Q	240	Total	C	N	O	S	0	0	0
			1881	1176	329	372	4			

- Molecule 4 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	235	Total	C	N	O	S	0	0	0
			1813	1136	304	366	7			
4	R	235	Total	C	N	O	S	0	0	0
			1813	1136	304	366	7			

- Molecule 5 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	231	Total	C	N	O	S	0	0	0
			1773	1114	307	348	4			
5	S	231	Total	C	N	O	S	0	0	0
			1773	1114	307	348	4			

- Molecule 6 is a protein called Probable proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	243	Total	C	N	O	S	0	0	0
			1892	1203	329	356	4			
6	T	243	Total	C	N	O	S	0	0	0
			1892	1203	329	356	4			

- Molecule 7 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	241	Total	C	N	O	S	0	0	0
			1907	1214	320	365	8			
7	U	241	Total	C	N	O	S	0	0	0
			1907	1214	320	365	8			

- Molecule 8 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	226	Total	C	N	O	S	0	0	0
			1719	1082	298	332	7			
8	V	226	Total	C	N	O	S	0	0	0
			1719	1082	298	332	7			

- Molecule 9 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			
9	W	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			

- Molecule 10 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	195	Total	C	N	O	S	0	0	0
			1561	992	264	299	6			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	X	195	Total	C	N	O	S	0	0	0
			1561	992	264	299	6			

- Molecule 11 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	212	Total	C	N	O	S	0	0	0
			1644	1045	280	312	7			
11	Y	212	Total	C	N	O	S	0	0	0
			1644	1045	280	312	7			

- Molecule 12 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			
12	Z	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			

- Molecule 13 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	229	Total	C	N	O	S	0	0	0
			1790	1133	306	344	7			
13	a	232	Total	C	N	O	S	0	0	0
			1815	1148	311	349	7			

- Molecule 14 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			
14	b	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			

- Molecule 15 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	G	1	Total	Mg	0	0
			1	1		
15	K	1	Total	Mg	0	0
			1	1		

Continued on next page...

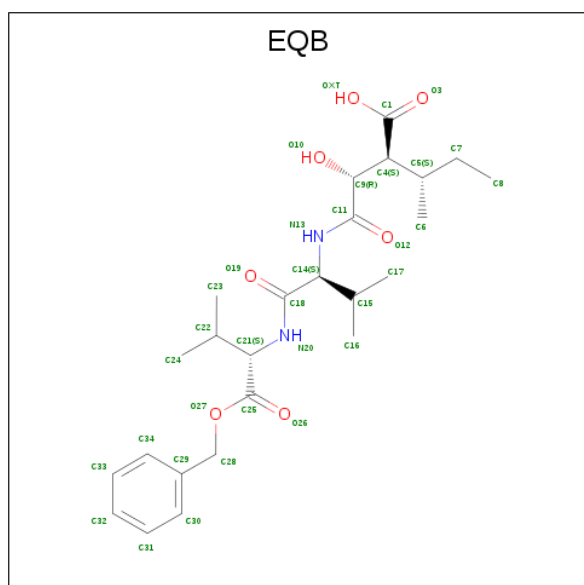
Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
15	I	1	Total Mg 1 1	0	0
15	V	1	Total Mg 1 1	0	0
15	W	1	Total Mg 1 1	0	0
15	Z	1	Total Mg 1 1	0	0
15	N	1	Total Mg 1 1	0	0
15	Y	1	Total Mg 1 1	0	0

- Molecule 16 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	G	1	Total Cl 1 1	0	0
16	U	1	Total Cl 1 1	0	0

- Molecule 17 is (2 {S},3 {S})-3-methyl-2-[(1 {R})-2-[(2 {S})-3-methyl-1-[(2 {S})-3-methyl-1-oxidanylidene-1-phenylmethoxy-butan-2-yl]amino]-1-oxidanylidene-butan-2-yl]amino]-1-oxidanyl-2-oxidanylidene-ethyl]pentanoic acid (three-letter code: EQB) (formula: C₂₅H₃₈N₂O₇).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
17	H	1	Total 33	C 25	N 2	O 6	0	0
17	K	1	Total 33	C 25	N 2	O 6	0	0
17	N	1	Total 33	C 25	N 2	O 6	0	0
17	V	1	Total 33	C 25	N 2	O 6	0	0
17	Y	1	Total 33	C 25	N 2	O 6	0	0
17	b	1	Total 33	C 25	N 2	O 6	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Proteasome subunit alpha type-2



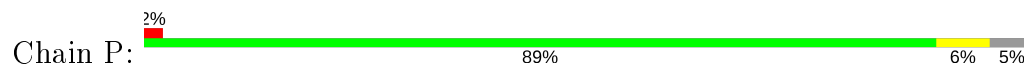
- Molecule 1: Proteasome subunit alpha type-2



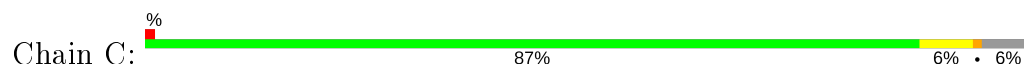
- Molecule 2: Proteasome subunit alpha type-3



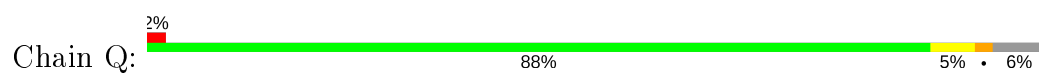
- Molecule 2: Proteasome subunit alpha type-3



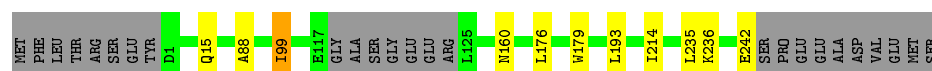
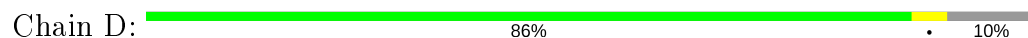
- Molecule 3: Proteasome subunit alpha type-4



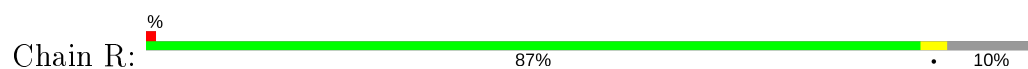
- Molecule 3: Proteasome subunit alpha type-4



- Molecule 4: Proteasome subunit alpha type-5



- Molecule 4: Proteasome subunit alpha type-5



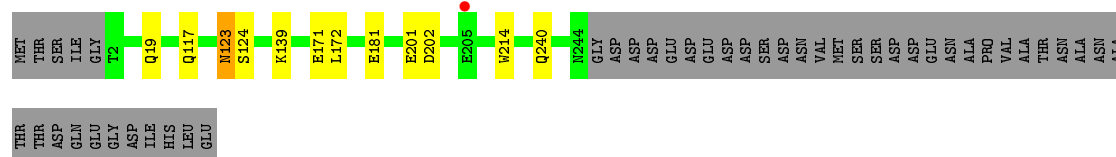
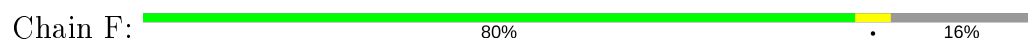
- Molecule 5: Proteasome subunit alpha type-6



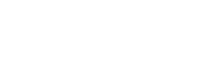
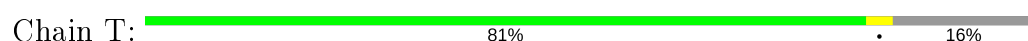
- Molecule 5: Proteasome subunit alpha type-6

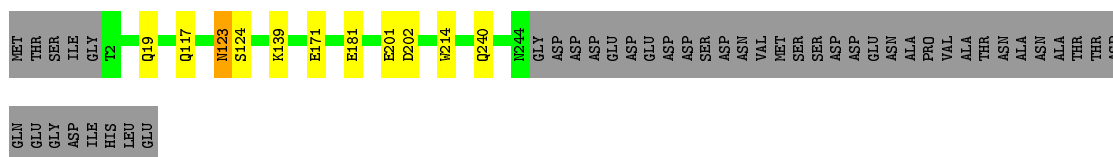


- Molecule 6: Probable proteasome subunit alpha type-7



- Molecule 6: Probable proteasome subunit alpha type-7





- Molecule 7: Proteasome subunit alpha type-1

Chain G: 90% 6% .



- Molecule 7: Proteasome subunit alpha type-1

Chain U: 90% 6% .



- Molecule 8: Proteasome subunit beta type-2

Chain H: 3% 91% 6% .



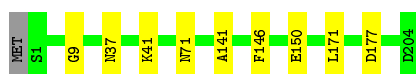
- Molecule 8: Proteasome subunit beta type-2

Chain V: 3% 89% 7% .



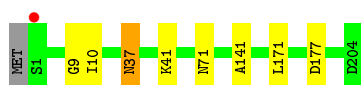
- Molecule 9: Proteasome subunit beta type-3

Chain I: 95% .

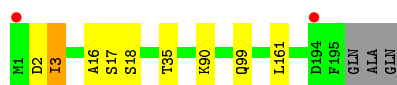


- Molecule 9: Proteasome subunit beta type-3

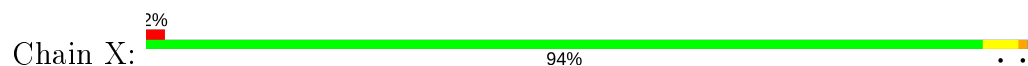
Chain W: 96% .



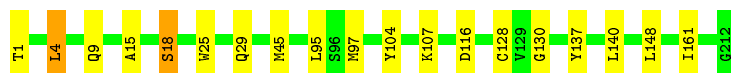
- Molecule 10: Proteasome subunit beta type-4



- Molecule 10: Proteasome subunit beta type-4



- Molecule 11: Proteasome subunit beta type-5



- Molecule 11: Proteasome subunit beta type-5



- Molecule 12: Proteasome subunit beta type-6



- Molecule 12: Proteasome subunit beta type-6



- Molecule 13: Proteasome subunit beta type-7

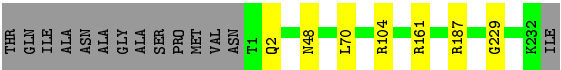


- Molecule 13: Proteasome subunit beta type-7

Chain a:

91%

• 6%



● Molecule 14: Proteasome subunit beta type-1

Chain N:

94%

6% •



● Molecule 14: Proteasome subunit beta type-1

Chain b:

%

98%

•



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	136.22Å 302.72Å 143.97Å 90.00° 112.82° 90.00°	Depositor
Resolution (Å)	15.00 – 3.00 15.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	94.2 (15.00-3.00) 95.0 (15.00-3.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.182 , 0.238 0.196 , 0.247	Depositor DCC
R_{free} test set	10072 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	71.6	Xtriage
Anisotropy	0.264	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 42.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	49531	wwPDB-VP
Average B, all atoms (Å ²)	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.75% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, EQB, CL

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	0/1952	0.58	0/2642
1	O	0.38	0/1952	0.58	0/2642
2	B	0.39	0/1934	0.62	0/2618
2	P	0.39	0/1934	0.62	0/2618
3	C	0.38	0/1910	0.64	0/2586
3	Q	0.38	0/1910	0.64	0/2586
4	D	0.38	0/1837	0.60	0/2475
4	R	0.37	0/1837	0.60	0/2475
5	E	0.38	0/1800	0.59	0/2433
5	S	0.37	0/1800	0.58	0/2433
6	F	0.38	0/1932	0.57	0/2609
6	T	0.37	0/1932	0.57	0/2609
7	G	0.39	0/1945	0.59	0/2634
7	U	0.38	0/1945	0.59	0/2634
8	H	0.39	0/1750	0.71	3/2373 (0.1%)
8	V	0.40	0/1750	0.72	2/2373 (0.1%)
9	I	0.39	0/1611	0.60	0/2174
9	W	0.39	0/1611	0.61	0/2174
10	J	0.39	0/1589	0.63	0/2142
10	X	0.39	0/1589	0.63	0/2142
11	K	0.41	0/1681	0.65	0/2274
11	Y	0.39	0/1681	0.65	1/2274 (0.0%)
12	L	0.40	0/1795	0.61	0/2420
12	Z	0.40	0/1795	0.60	0/2420
13	M	0.40	0/1821	0.64	0/2470
13	a	0.40	0/1846	0.65	0/2503
14	N	0.38	0/1541	0.61	0/2087
14	b	0.38	0/1541	0.62	0/2087
All	All	0.39	0/50221	0.62	6/67907 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	V	55	VAL	CG1-CB-CG2	-13.18	89.81	110.90
8	H	55	VAL	CG1-CB-CG2	-12.17	91.42	110.90
8	V	55	VAL	CA-CB-CG1	10.27	126.30	110.90
8	H	55	VAL	CA-CB-CG2	8.15	123.12	110.90
11	Y	4	LEU	CA-CB-CG	5.37	127.66	115.30
8	H	196	ARG	NE-CZ-NH1	5.18	122.89	120.30

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	1915	0	1929	2	0
1	O	1915	0	1929	3	0
2	B	1904	0	1904	7	0
2	P	1904	0	1904	5	0
3	C	1881	0	1895	7	0
3	Q	1881	0	1895	6	0
4	D	1813	0	1797	3	0
4	R	1813	0	1797	1	0
5	E	1773	0	1775	4	0
5	S	1773	0	1775	3	0
6	F	1892	0	1883	3	0
6	T	1892	0	1883	3	0
7	G	1907	0	1901	3	0
7	U	1907	0	1901	3	0
8	H	1719	0	1718	9	0
8	V	1719	0	1718	15	0
9	I	1581	0	1574	5	0
9	W	1581	0	1574	6	0
10	J	1561	0	1569	2	0
10	X	1561	0	1569	2	0
11	K	1644	0	1594	11	0
11	Y	1644	0	1594	5	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	L	1757	0	1711	5	0
12	Z	1757	0	1711	5	0
13	M	1790	0	1793	1	0
13	a	1815	0	1821	0	0
14	N	1512	0	1480	8	0
14	b	1512	0	1480	0	0
15	G	1	0	0	0	0
15	I	1	0	0	0	0
15	K	1	0	0	0	0
15	N	1	0	0	0	0
15	V	1	0	0	0	0
15	W	1	0	0	0	0
15	Y	1	0	0	0	0
15	Z	1	0	0	0	0
16	G	1	0	0	0	0
16	U	1	0	0	0	0
17	H	33	0	0	4	0
17	K	33	0	0	3	0
17	N	33	0	0	4	0
17	V	33	0	0	6	0
17	Y	33	0	0	2	0
17	b	33	0	0	0	0
All	All	49531	0	49074	118	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 1.

All (118) 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)
8:H:3:ILE:HG13	8:H:99:ILE:HD12	1.62	0.79
11:K:4:LEU:HD22	11:K:4:LEU:O	1.83	0.79
14:N:1:THR:O	14:N:128:GLY:HA3	1.88	0.74
8:V:3:ILE:HD11	8:V:127:LEU:HB3	1.74	0.70
12:L:31:THR:HG23	12:L:36:ASN:HD21	1.56	0.69
12:Z:31:THR:HG23	12:Z:36:ASN:HD21	1.57	0.69
3:Q:160:GLN:HE21	3:Q:160:GLN:HA	1.59	0.67
14:N:46:SER:HA	17:N:201:EQB:O3	1.95	0.65
8:V:46:ALA:HA	17:V:301:EQB:O3	1.97	0.65
3:C:160:GLN:HA	3:C:160:GLN:HE21	1.61	0.65
8:H:1:THR:OG1	17:H:301:EQB:O10	2.10	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:4:LEU:CD1	11:K:161:ILE:HD11	2.32	0.60
7:U:23:PHE:O	7:U:26:THR:HB	2.01	0.60
8:V:1:THR:OG1	17:V:301:EQB:O10	2.17	0.59
11:Y:1:THR:O	11:Y:130:GLY:HA3	2.01	0.59
7:G:23:PHE:O	7:G:26:THR:HB	2.01	0.59
1:O:12:PHE:H	2:P:20:GLN:HE22	1.51	0.58
6:F:123:ASN:HD22	6:F:124:SER:N	2.02	0.57
8:V:1:THR:HG21	17:V:301:EQB:O3	2.04	0.57
8:V:46:ALA:HA	17:V:301:EQB:C6	2.33	0.57
8:H:1:THR:HG21	17:H:301:EQB:O3	2.04	0.57
11:Y:1:THR:HG21	17:Y:301:EQB:O3	2.05	0.56
11:K:1:THR:HG21	17:K:301:EQB:O3	2.05	0.56
11:K:4:LEU:C	11:K:4:LEU:HD22	2.28	0.54
8:V:33:LYS:HG2	17:V:301:EQB:C8	2.37	0.54
6:T:123:ASN:HD22	6:T:124:SER:N	2.06	0.54
11:K:4:LEU:HD13	11:K:15:ALA:O	2.07	0.53
14:N:20:THR:CG2	17:N:201:EQB:C23	2.86	0.53
14:N:20:THR:HG22	17:N:201:EQB:C23	2.38	0.53
14:N:36:ARG:HG3	14:N:42:TRP:CE2	2.44	0.52
5:S:12:PHE:H	6:T:19:GLN:HE22	1.55	0.52
17:Y:301:EQB:N20	17:Y:301:EQB:C16	2.73	0.51
14:N:1:THR:HG21	17:N:201:EQB:O3	2.11	0.51
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.93	0.50
5:E:118:ASN:N	5:E:118:ASN:HD22	2.09	0.50
12:Z:31:THR:CG2	12:Z:36:ASN:HD21	2.26	0.49
9:I:9:GLY:HA3	9:I:41:LYS:HE2	1.95	0.48
1:A:12:PHE:H	2:B:20:GLN:HE22	1.61	0.48
2:B:95:GLN:HE22	9:I:71:ASN:HD22	1.61	0.48
9:W:9:GLY:HA3	9:W:41:LYS:HE2	1.95	0.48
2:P:124:HIS:HB3	3:Q:124:VAL:HG12	1.96	0.48
5:S:118:ASN:N	5:S:118:ASN:HD22	2.11	0.48
8:V:46:ALA:CA	17:V:301:EQB:O3	2.62	0.47
5:S:87:LEU:HD21	5:S:107:ALA:HB1	1.96	0.47
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.95	0.47
12:L:31:THR:CG2	12:L:36:ASN:HD21	2.26	0.47
8:V:3:ILE:HD11	8:V:127:LEU:CB	2.44	0.46
5:E:87:LEU:HD21	5:E:107:ALA:HB1	1.96	0.46
7:G:73:VAL:HG12	7:G:133:THR:HB	1.97	0.46
8:H:113:ILE:HB	8:H:119:THR:HG22	1.98	0.46
8:H:3:ILE:HD11	8:H:127:LEU:HB3	1.97	0.46
11:K:4:LEU:CD1	11:K:161:ILE:CD1	2.93	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:V:113:ILE:HB	8:V:119:THR:HG22	1.98	0.45
11:K:4:LEU:HD13	11:K:161:ILE:HD11	1.98	0.45
11:K:1:THR:O	11:K:130:GLY:HA3	2.16	0.45
11:K:4:LEU:C	11:K:4:LEU:CD2	2.85	0.45
7:U:73:VAL:HG12	7:U:133:THR:HB	1.98	0.45
9:W:37:ASN:HD22	9:W:37:ASN:C	2.20	0.45
2:B:12:PHE:H	3:C:17:GLN:HE22	1.64	0.44
4:D:160:ASN:HB3	4:D:179:TRP:CE2	2.52	0.44
5:E:12:PHE:H	6:F:19:GLN:HE22	1.63	0.44
8:V:51:ASP:O	8:V:55:VAL:HG12	2.17	0.44
2:P:95:GLN:HE22	9:W:71:ASN:HD22	1.66	0.44
1:A:64:VAL:HG11	1:A:212:ALA:HB3	2.00	0.44
2:B:95:GLN:NE2	9:I:71:ASN:HD22	2.15	0.44
2:B:124:HIS:HB3	3:C:124:VAL:HG12	2.00	0.44
12:Z:42:LYS:HD2	12:Z:55:ASN:HD22	1.83	0.44
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.53	0.43
8:V:80:LEU:HD13	8:V:119:THR:HG21	2.00	0.43
11:K:18:SER:OG	11:K:29:GLN:O	2.37	0.43
7:G:167:GLN:HE21	7:G:171:THR:HG23	1.83	0.43
8:H:19:ARG:NH1	8:H:169:SER:O	2.51	0.43
6:T:123:ASN:C	6:T:123:ASN:HD22	2.21	0.43
7:U:167:GLN:HE21	7:U:171:THR:HG23	1.84	0.43
17:H:301:EQB:C1	17:H:301:EQB:N13	2.82	0.43
9:I:141:ALA:HB2	9:I:177:ASP:HB2	2.00	0.43
1:O:64:VAL:HG11	1:O:212:ALA:HB3	2.01	0.43
9:W:141:ALA:HB2	9:W:177:ASP:HB2	2.01	0.43
2:B:95:GLN:HE22	2:B:98:LEU:HD23	1.83	0.42
6:F:123:ASN:C	6:F:123:ASN:HD22	2.21	0.42
12:L:42:LYS:HD2	12:L:55:ASN:HD22	1.84	0.42
8:V:19:ARG:NH1	8:V:169:SER:O	2.52	0.42
11:Y:18:SER:OG	11:Y:29:GLN:O	2.38	0.42
14:N:83:LYS:HG3	14:N:119:VAL:CG2	2.50	0.42
5:E:92:ASN:HD21	12:L:70:ASN:HD21	1.66	0.42
9:W:10:ILE:HG21	9:W:141:ALA:HB3	2.02	0.42
3:C:201:VAL:O	3:C:202:GLN:CB	2.68	0.42
3:C:38:ASN:C	3:C:38:ASN:HD22	2.23	0.42
11:K:128:CYS:HB2	11:K:137:TYR:CE2	2.54	0.42
14:N:3:ILE:HG22	14:N:16:ALA:CB	2.49	0.42
12:Z:141:ALA:HB1	12:Z:195:HIS:NE2	2.35	0.42
3:C:9:PHE:H	4:D:15:GLN:HE22	1.68	0.41
8:V:3:ILE:O	8:V:126:SER:HA	2.19	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:K:301:EQB:C11	17:K:301:EQB:C6	2.97	0.41
3:Q:38:ASN:C	3:Q:38:ASN:HD22	2.23	0.41
8:V:3:ILE:HG12	8:V:127:LEU:O	2.21	0.41
11:Y:128:CYS:HB2	11:Y:137:TYR:CE2	2.56	0.41
12:Z:3:ASN:HD22	12:Z:4:PRO:HD2	1.86	0.41
13:M:127:LEU:O	13:M:138:SER:OG	2.31	0.41
1:O:75:TYR:HB3	1:O:82:TYR:CD1	2.56	0.41
8:V:14:ILE:HG22	8:V:176:CYS:HB3	2.03	0.41
2:B:47:ALA:HB1	2:B:64:LYS:HD2	2.02	0.41
10:J:3:ILE:HG23	10:J:18:SER:HB3	2.02	0.41
2:P:47:ALA:HB1	2:P:64:LYS:HD2	2.03	0.41
2:P:95:GLN:NE2	9:W:71:ASN:HD22	2.18	0.41
3:Q:51:LYS:O	3:Q:52:LEU:HB2	2.20	0.41
8:H:46:ALA:HA	17:H:301:EQB:O3	2.21	0.41
9:I:146:PHE:O	9:I:150:GLU:HB2	2.22	0.40
17:K:301:EQB:N20	17:K:301:EQB:C16	2.83	0.40
3:Q:35:LYS:HG2	3:Q:158:SER:O	2.21	0.40
3:C:35:LYS:HG2	3:C:158:SER:O	2.21	0.40
8:H:55:VAL:HG12	8:H:56:THR:N	2.36	0.40
12:L:3:ASN:HD22	12:L:4:PRO:HD2	1.85	0.40
3:Q:169:VAL:HG23	3:Q:196:SER:HB2	2.03	0.40
4:D:88:ALA:HA	4:D:99:ILE:HG21	2.02	0.40
8:H:51:ASP:O	8:H:55:VAL:HB	2.21	0.40
10:X:3:ILE:HG23	10:X:18:SER:HB3	2.02	0.40
11:Y:35:ILE:HD13	11:Y:53:GLN:HA	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	248/250 (99%)	240 (97%)	7 (3%)	1 (0%)	34 72

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	O	248/250 (99%)	239 (96%)	8 (3%)	1 (0%)	34	72
2	B	242/258 (94%)	233 (96%)	5 (2%)	4 (2%)	9	39
2	P	242/258 (94%)	233 (96%)	5 (2%)	4 (2%)	9	39
3	C	238/254 (94%)	232 (98%)	3 (1%)	3 (1%)	12	45
3	Q	238/254 (94%)	233 (98%)	2 (1%)	3 (1%)	12	45
4	D	231/260 (89%)	226 (98%)	5 (2%)	0	100	100
4	R	231/260 (89%)	226 (98%)	5 (2%)	0	100	100
5	E	229/234 (98%)	220 (96%)	9 (4%)	0	100	100
5	S	229/234 (98%)	219 (96%)	10 (4%)	0	100	100
6	F	241/288 (84%)	238 (99%)	3 (1%)	0	100	100
6	T	241/288 (84%)	238 (99%)	3 (1%)	0	100	100
7	G	239/252 (95%)	237 (99%)	2 (1%)	0	100	100
7	U	239/252 (95%)	236 (99%)	3 (1%)	0	100	100
8	H	224/232 (97%)	218 (97%)	6 (3%)	0	100	100
8	V	224/232 (97%)	218 (97%)	6 (3%)	0	100	100
9	I	202/205 (98%)	193 (96%)	9 (4%)	0	100	100
9	W	202/205 (98%)	193 (96%)	9 (4%)	0	100	100
10	J	193/198 (98%)	187 (97%)	6 (3%)	0	100	100
10	X	193/198 (98%)	186 (96%)	7 (4%)	0	100	100
11	K	210/212 (99%)	208 (99%)	2 (1%)	0	100	100
11	Y	210/212 (99%)	207 (99%)	3 (1%)	0	100	100
12	L	220/222 (99%)	214 (97%)	6 (3%)	0	100	100
12	Z	220/222 (99%)	214 (97%)	6 (3%)	0	100	100
13	M	227/246 (92%)	219 (96%)	8 (4%)	0	100	100
13	a	230/246 (94%)	221 (96%)	8 (4%)	1 (0%)	34	72
14	N	194/196 (99%)	191 (98%)	3 (2%)	0	100	100
14	b	194/196 (99%)	190 (98%)	4 (2%)	0	100	100
All	All	6279/6614 (95%)	6109 (97%)	153 (2%)	17 (0%)	41	76

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	51	VAL
2	B	221	ASP
3	C	202	GLN
1	O	2	THR
2	P	51	VAL
2	P	221	ASP
3	Q	202	GLN
2	B	218	GLY
2	B	220	ASN
2	P	218	GLY
2	P	220	ASN
3	C	205	ALA
3	Q	205	ALA
3	C	183	PRO
3	Q	183	PRO
13	a	229	GLY

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	209/209 (100%)	206 (99%)	3 (1%)	67	88
1	O	209/209 (100%)	206 (99%)	3 (1%)	67	88
2	B	203/216 (94%)	198 (98%)	5 (2%)	47	79
2	P	203/216 (94%)	197 (97%)	6 (3%)	41	75
3	C	212/226 (94%)	203 (96%)	9 (4%)	30	66
3	Q	212/226 (94%)	203 (96%)	9 (4%)	30	66
4	D	194/215 (90%)	187 (96%)	7 (4%)	35	70
4	R	194/215 (90%)	187 (96%)	7 (4%)	35	70
5	E	190/193 (98%)	182 (96%)	8 (4%)	30	66
5	S	190/193 (98%)	183 (96%)	7 (4%)	34	70
6	F	201/239 (84%)	191 (95%)	10 (5%)	24	60

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	T	201/239 (84%)	192 (96%)	9 (4%)	27	64
7	G	206/210 (98%)	198 (96%)	8 (4%)	32	69
7	U	206/210 (98%)	198 (96%)	8 (4%)	32	69
8	H	185/190 (97%)	180 (97%)	5 (3%)	44	77
8	V	185/190 (97%)	179 (97%)	6 (3%)	39	74
9	I	172/173 (99%)	170 (99%)	2 (1%)	71	90
9	W	172/173 (99%)	170 (99%)	2 (1%)	71	90
10	J	173/175 (99%)	167 (96%)	6 (4%)	36	71
10	X	173/175 (99%)	168 (97%)	5 (3%)	42	76
11	K	169/169 (100%)	157 (93%)	12 (7%)	14	46
11	Y	169/169 (100%)	158 (94%)	11 (6%)	17	50
12	L	185/185 (100%)	181 (98%)	4 (2%)	52	81
12	Z	185/185 (100%)	180 (97%)	5 (3%)	44	77
13	M	195/208 (94%)	189 (97%)	6 (3%)	40	75
13	a	198/208 (95%)	192 (97%)	6 (3%)	41	75
14	N	162/162 (100%)	159 (98%)	3 (2%)	57	84
14	b	162/162 (100%)	158 (98%)	4 (2%)	47	79
All	All	5315/5540 (96%)	5139 (97%)	176 (3%)	38	73

All (176) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	122	THR
1	A	157	PHE
1	A	250	LEU
2	B	50	LYS
2	B	58	GLN
2	B	119	GLN
2	B	191	LEU
2	B	238	LEU
3	C	4	ARG
3	C	38	ASN
3	C	51	LYS
3	C	147	GLN
3	C	160	GLN
3	C	169	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	C	180	LYS
3	C	206	LYS
3	C	240	GLU
4	D	99	ILE
4	D	176	LEU
4	D	193	LEU
4	D	214	ILE
4	D	235	LEU
4	D	236	LYS
4	D	242	GLU
5	E	9	THR
5	E	29	LYS
5	E	71	LEU
5	E	116	GLN
5	E	118	ASN
5	E	184	ASN
5	E	188	LEU
5	E	202	ASP
6	F	117	GLN
6	F	123	ASN
6	F	139	LYS
6	F	171	GLU
6	F	172	LEU
6	F	181	GLU
6	F	201	GLU
6	F	202	ASP
6	F	214	TRP
6	F	240	GLN
7	G	83	ASN
7	G	115	LEU
7	G	117	GLN
7	G	122	ARG
7	G	125	MET
7	G	208	GLU
7	G	235	ARG
7	G	236	LEU
8	H	30	ASN
8	H	31	CYS
8	H	55	VAL
8	H	68	LEU
8	H	196	ARG
9	I	37	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	I	171	LEU
10	J	2	ASP
10	J	3	ILE
10	J	17	SER
10	J	35	THR
10	J	90	LYS
10	J	99	GLN
11	K	4	LEU
11	K	9	GLN
11	K	18	SER
11	K	25	TRP
11	K	45	MET
11	K	95	LEU
11	K	97	MET
11	K	104	TYR
11	K	107	LYS
11	K	116	ASP
11	K	140	LEU
11	K	148	LEU
12	L	23	LEU
12	L	49	ASN
12	L	136	CYS
12	L	150	LEU
13	M	2	GLN
13	M	48	ASN
13	M	70	LEU
13	M	104	ARG
13	M	161	ARG
13	M	187	ARG
14	N	83	LYS
14	N	104	ASP
14	N	107	LYS
1	O	122	THR
1	O	157	PHE
1	O	250	LEU
2	P	50	LYS
2	P	58	GLN
2	P	113	ARG
2	P	119	GLN
2	P	191	LEU
2	P	238	LEU
3	Q	4	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	Q	38	ASN
3	Q	51	LYS
3	Q	147	GLN
3	Q	160	GLN
3	Q	169	VAL
3	Q	180	LYS
3	Q	206	LYS
3	Q	240	GLU
4	R	99	ILE
4	R	176	LEU
4	R	193	LEU
4	R	214	ILE
4	R	235	LEU
4	R	236	LYS
4	R	242	GLU
5	S	9	THR
5	S	29	LYS
5	S	71	LEU
5	S	118	ASN
5	S	184	ASN
5	S	188	LEU
5	S	202	ASP
6	T	117	GLN
6	T	123	ASN
6	T	139	LYS
6	T	171	GLU
6	T	181	GLU
6	T	201	GLU
6	T	202	ASP
6	T	214	TRP
6	T	240	GLN
7	U	83	ASN
7	U	115	LEU
7	U	117	GLN
7	U	122	ARG
7	U	125	MET
7	U	208	GLU
7	U	235	ARG
7	U	236	LEU
8	V	30	ASN
8	V	31	CYS
8	V	55	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
8	V	68	LEU
8	V	80	LEU
8	V	196	ARG
9	W	37	ASN
9	W	171	LEU
10	X	2	ASP
10	X	3	ILE
10	X	17	SER
10	X	35	THR
10	X	99	GLN
11	Y	4	LEU
11	Y	9	GLN
11	Y	18	SER
11	Y	25	TRP
11	Y	45	MET
11	Y	97	MET
11	Y	104	TYR
11	Y	107	LYS
11	Y	116	ASP
11	Y	140	LEU
11	Y	148	LEU
12	Z	23	LEU
12	Z	49	ASN
12	Z	130	SER
12	Z	136	CYS
12	Z	150	LEU
13	a	2	GLN
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	161	ARG
13	a	187	ARG
14	b	36	ARG
14	b	83	LYS
14	b	104	ASP
14	b	107	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (131) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	20	GLN
2	B	58	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	95	GLN
2	B	119	GLN
2	B	123	GLN
2	B	155	ASN
2	B	176	GLN
3	C	17	GLN
3	C	38	ASN
3	C	77	ASN
3	C	147	GLN
3	C	160	GLN
4	D	15	GLN
4	D	91	HIS
4	D	100	ASN
4	D	225	ASN
5	E	68	HIS
5	E	99	ASN
5	E	116	GLN
5	E	118	ASN
5	E	120	GLN
5	E	151	ASN
5	E	184	ASN
6	F	19	GLN
6	F	86	ASN
6	F	117	GLN
6	F	123	ASN
6	F	191	GLN
6	F	203	ASN
6	F	240	GLN
7	G	6	HIS
7	G	83	ASN
7	G	114	ASN
7	G	117	GLN
7	G	121	GLN
7	G	166	GLN
7	G	167	GLN
7	G	175	ASN
8	H	9	ASN
8	H	22	GLN
8	H	30	ASN
8	H	165	ASN
8	H	172	ASN
8	H	189	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	I	37	ASN
9	I	88	GLN
10	J	55	GLN
11	K	9	GLN
11	K	85	ASN
11	K	176	ASN
11	K	208	ASN
12	L	3	ASN
12	L	36	ASN
12	L	49	ASN
12	L	55	ASN
12	L	70	ASN
12	L	152	ASN
12	L	153	GLN
12	L	158	ASN
13	M	18	ASN
13	M	26	ASN
13	M	48	ASN
13	M	102	GLN
13	M	179	ASN
13	M	194	ASN
13	M	213	GLN
14	N	161	GLN
2	P	20	GLN
2	P	58	GLN
2	P	95	GLN
2	P	119	GLN
2	P	123	GLN
2	P	155	ASN
2	P	176	GLN
3	Q	17	GLN
3	Q	38	ASN
3	Q	77	ASN
3	Q	147	GLN
3	Q	160	GLN
4	R	15	GLN
4	R	91	HIS
4	R	225	ASN
5	S	68	HIS
5	S	92	ASN
5	S	99	ASN
5	S	116	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	S	118	ASN
5	S	120	GLN
5	S	151	ASN
5	S	184	ASN
6	T	19	GLN
6	T	86	ASN
6	T	117	GLN
6	T	123	ASN
6	T	191	GLN
6	T	240	GLN
7	U	83	ASN
7	U	114	ASN
7	U	117	GLN
7	U	121	GLN
7	U	166	GLN
7	U	167	GLN
7	U	175	ASN
8	V	9	ASN
8	V	22	GLN
8	V	30	ASN
8	V	172	ASN
8	V	189	ASN
9	W	37	ASN
9	W	88	GLN
10	X	55	GLN
11	Y	9	GLN
11	Y	85	ASN
11	Y	176	ASN
11	Y	208	ASN
12	Z	3	ASN
12	Z	36	ASN
12	Z	49	ASN
12	Z	55	ASN
12	Z	70	ASN
12	Z	152	ASN
12	Z	153	GLN
12	Z	158	ASN
13	a	18	ASN
13	a	26	ASN
13	a	48	ASN
13	a	102	GLN
13	a	179	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	a	194	ASN
13	a	213	GLN
14	b	161	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 16 ligands modelled in this entry, 10 are monoatomic - leaving 6 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
17	EQB	H	301	8	33,33,34	1.56	3 (9%)	40,44,46	1.10	3 (7%)
17	EQB	N	201	14	33,33,34	1.16	2 (6%)	40,44,46	1.44	10 (25%)
17	EQB	Y	301	11	33,33,34	1.02	2 (6%)	40,44,46	1.18	5 (12%)
17	EQB	b	201	14	33,33,34	1.33	4 (12%)	40,44,46	1.48	7 (17%)
17	EQB	V	301	8	33,33,34	1.22	2 (6%)	40,44,46	1.28	4 (10%)
17	EQB	K	301	11	33,33,34	1.17	3 (9%)	40,44,46	1.04	3 (7%)

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
17	EQB	H	301	8	-	2/45/45/47	0/1/1/1
17	EQB	N	201	14	-	8/45/45/47	0/1/1/1
17	EQB	Y	301	11	-	3/45/45/47	0/1/1/1
17	EQB	b	201	14	-	6/45/45/47	0/1/1/1
17	EQB	V	301	8	-	6/45/45/47	0/1/1/1
17	EQB	K	301	11	-	7/45/45/47	0/1/1/1

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	V	301	EQB	C28-C29	-5.05	1.38	1.50
17	N	201	EQB	C28-C29	-4.83	1.39	1.50
17	b	201	EQB	C28-C29	-4.78	1.39	1.50
17	H	301	EQB	C28-C29	-4.65	1.39	1.50
17	K	301	EQB	C28-C29	-4.18	1.40	1.50
17	H	301	EQB	C4-C9	-4.17	1.50	1.54
17	H	301	EQB	C4-C5	-4.06	1.49	1.55
17	Y	301	EQB	C28-C29	-3.51	1.42	1.50
17	K	301	EQB	C4-C5	-3.14	1.50	1.55
17	b	201	EQB	C4-C5	-3.02	1.50	1.55
17	Y	301	EQB	C4-C5	-2.64	1.51	1.55
17	b	201	EQB	C4-C9	-2.45	1.52	1.54
17	K	301	EQB	C4-C9	-2.44	1.52	1.54
17	N	201	EQB	C4-C9	-2.35	1.52	1.54
17	V	301	EQB	O27-C28	-2.17	1.41	1.45
17	b	201	EQB	C9-C11	-2.12	1.48	1.52

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	V	301	EQB	O3-C1-C4	-3.94	115.28	125.23
17	N	201	EQB	C22-C21-N20	-3.29	103.30	111.43
17	b	201	EQB	C15-C14-N13	-3.21	103.49	111.43
17	K	301	EQB	O3-C1-C4	-2.89	117.91	125.23
17	V	301	EQB	C6-C5-C4	-2.89	107.68	112.67
17	V	301	EQB	C6-C5-C7	-2.85	104.57	111.78
17	N	201	EQB	C14-C18-N20	-2.80	110.43	116.48
17	H	301	EQB	C15-C14-C18	-2.74	104.52	111.38
17	b	201	EQB	C9-C4-C1	-2.59	105.27	110.65

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	N	201	EQB	C15-C14-C18	-2.52	105.07	111.38
17	Y	301	EQB	C15-C14-C18	-2.45	105.25	111.38
17	Y	301	EQB	O3-C1-C4	-2.43	119.08	125.23
17	N	201	EQB	C9-C4-C1	-2.39	105.70	110.65
17	K	301	EQB	C6-C5-C4	-2.37	108.57	112.67
17	b	201	EQB	O27-C25-C21	2.37	115.13	111.32
17	b	201	EQB	O3-C1-C4	-2.36	119.26	125.23
17	Y	301	EQB	C15-C14-N13	-2.36	105.59	111.43
17	N	201	EQB	O3-C1-C4	-2.35	119.29	125.23
17	N	201	EQB	O27-C25-C21	2.30	115.03	111.32
17	N	201	EQB	C21-N20-C18	2.27	127.67	121.89
17	N	201	EQB	O27-C28-C29	2.26	114.82	109.39
17	Y	301	EQB	O10-C9-C11	-2.23	105.84	110.63
17	N	201	EQB	C18-C14-N13	2.22	116.39	110.36
17	Y	301	EQB	C6-C5-C7	-2.13	106.39	111.78
17	b	201	EQB	C14-C18-N20	-2.09	111.97	116.48
17	H	301	EQB	C24-C22-C21	-2.08	105.28	111.16
17	H	301	EQB	C22-C21-C25	-2.08	105.81	111.56
17	b	201	EQB	C15-C14-C18	-2.07	106.20	111.38
17	V	301	EQB	C21-N20-C18	-2.07	116.62	121.89
17	b	201	EQB	C22-C21-N20	-2.06	106.34	111.43
17	K	301	EQB	C6-C5-C7	-2.05	106.59	111.78
17	N	201	EQB	C6-C5-C7	-2.02	106.66	111.78

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	N	201	EQB	O12-C11-C9-O10
17	N	201	EQB	N13-C11-C9-O10
17	Y	301	EQB	O12-C11-C9-O10
17	b	201	EQB	O12-C11-C9-C4
17	b	201	EQB	N13-C11-C9-C4
17	b	201	EQB	O12-C11-C9-O10
17	b	201	EQB	N13-C11-C9-O10
17	V	301	EQB	C5-C4-C9-O10
17	K	301	EQB	O3-C1-C4-C5
17	K	301	EQB	O12-C11-C9-O10
17	Y	301	EQB	N13-C11-C9-O10
17	K	301	EQB	N13-C11-C9-O10
17	b	201	EQB	C29-C28-O27-C25
17	V	301	EQB	C9-C4-C5-C7

Continued on next page...

Continued from previous page...

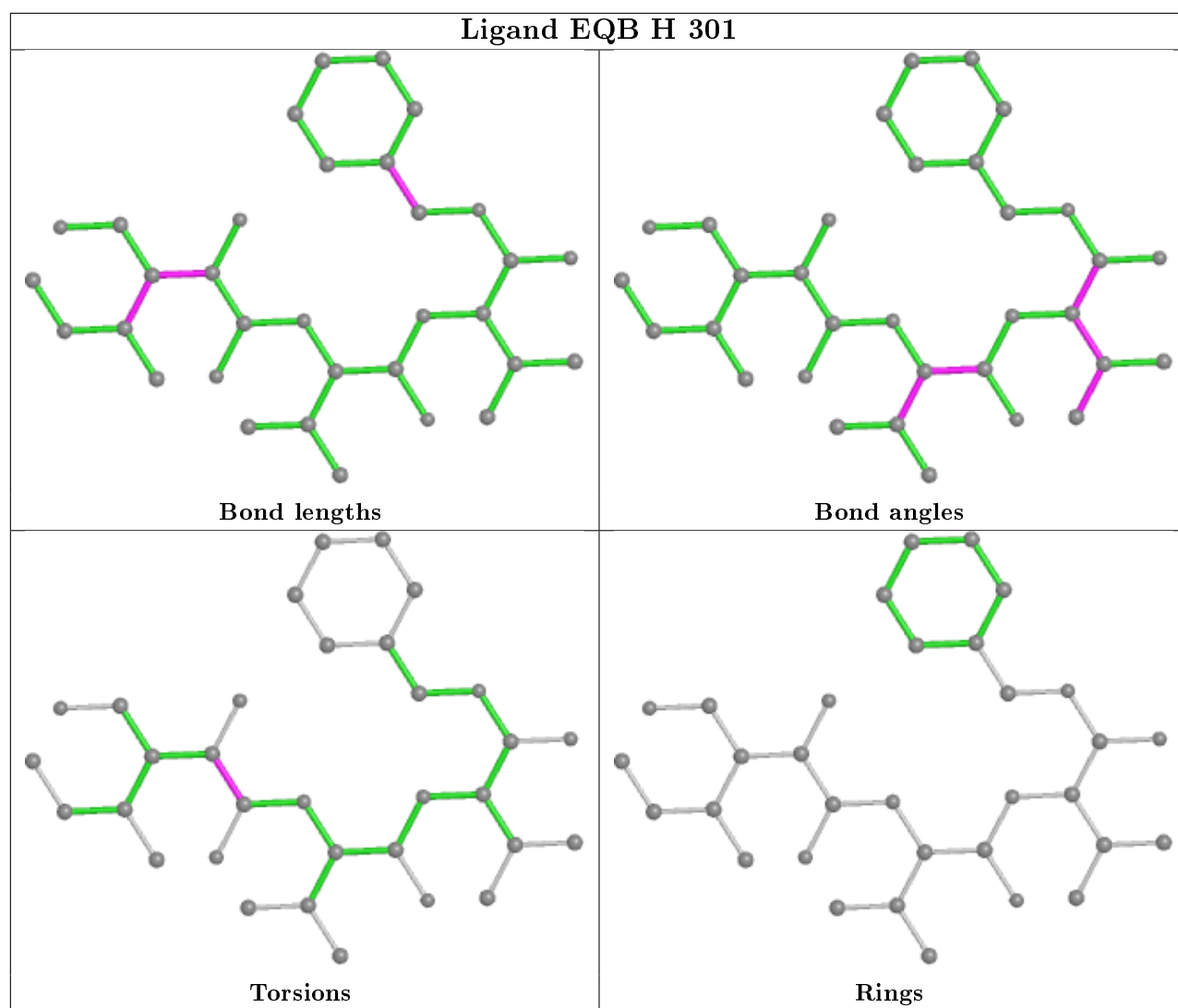
Mol	Chain	Res	Type	Atoms
17	V	301	EQB	O12-C11-C9-O10
17	H	301	EQB	N13-C11-C9-O10
17	K	301	EQB	C5-C4-C9-O10
17	V	301	EQB	O3-C1-C4-C5
17	K	301	EQB	O3-C1-C4-C9
17	N	201	EQB	O12-C11-C9-C4
17	Y	301	EQB	O12-C11-C9-C4
17	K	301	EQB	O12-C11-C9-C4
17	V	301	EQB	N13-C11-C9-O10
17	N	201	EQB	N13-C11-C9-C4
17	H	301	EQB	O12-C11-C9-O10
17	N	201	EQB	N20-C21-C25-O27
17	b	201	EQB	N20-C21-C25-O27
17	K	301	EQB	C22-C21-N20-C18
17	N	201	EQB	C22-C21-C25-O27
17	N	201	EQB	C22-C21-C25-O26
17	N	201	EQB	N20-C21-C25-O26
17	V	301	EQB	C1-C4-C5-C6

There are no ring outliers.

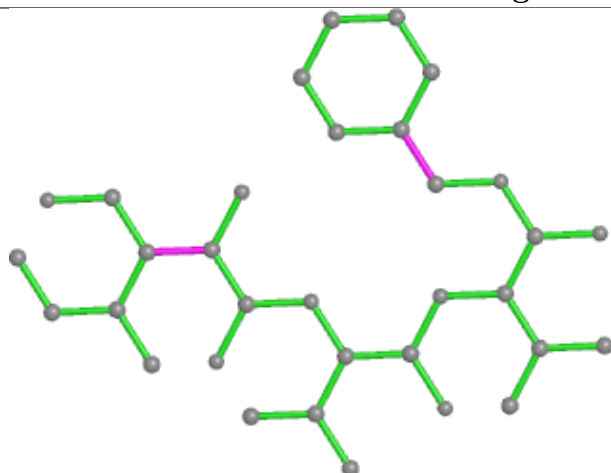
5 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	H	301	EQB	4	0
17	N	201	EQB	4	0
17	Y	301	EQB	2	0
17	V	301	EQB	6	0
17	K	301	EQB	3	0

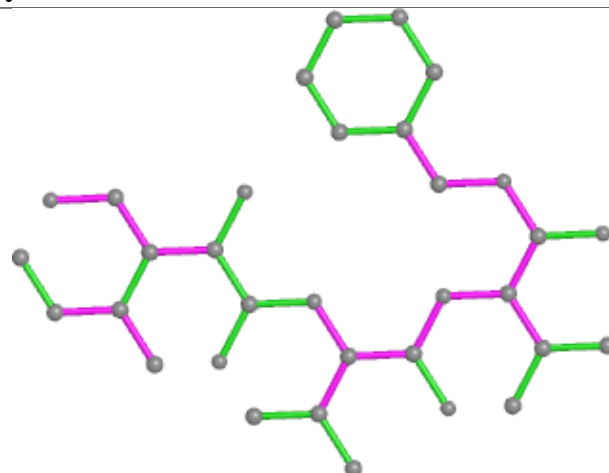
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



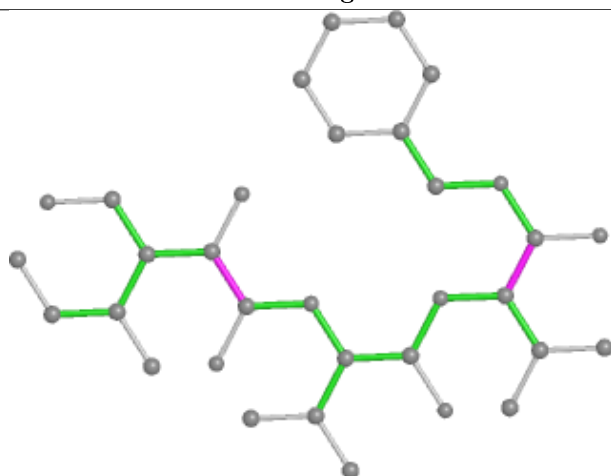
Ligand EQB N 201



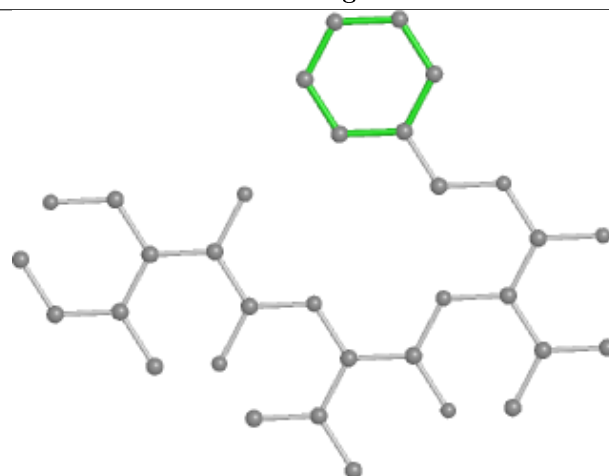
Bond lengths



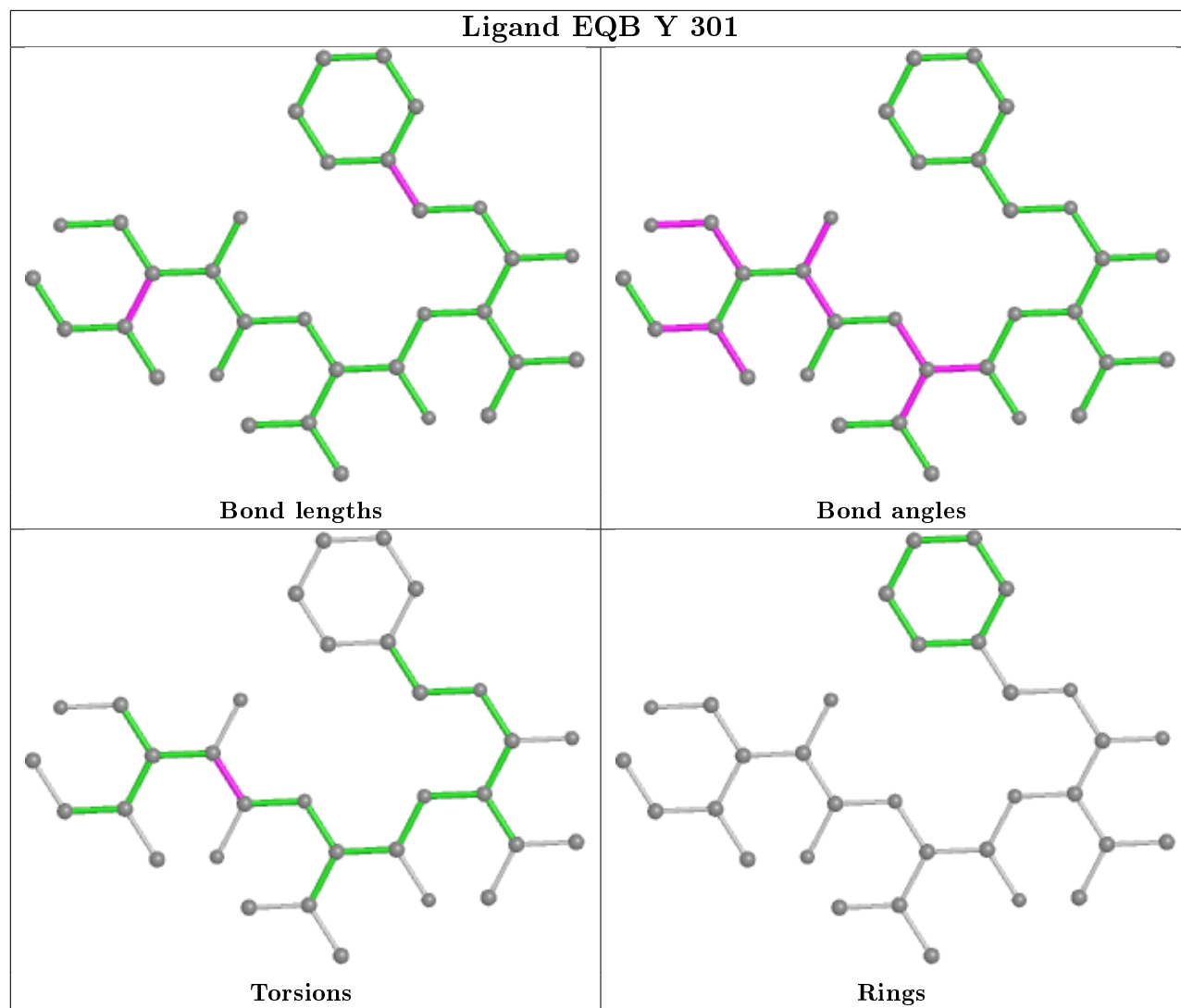
Bond angles



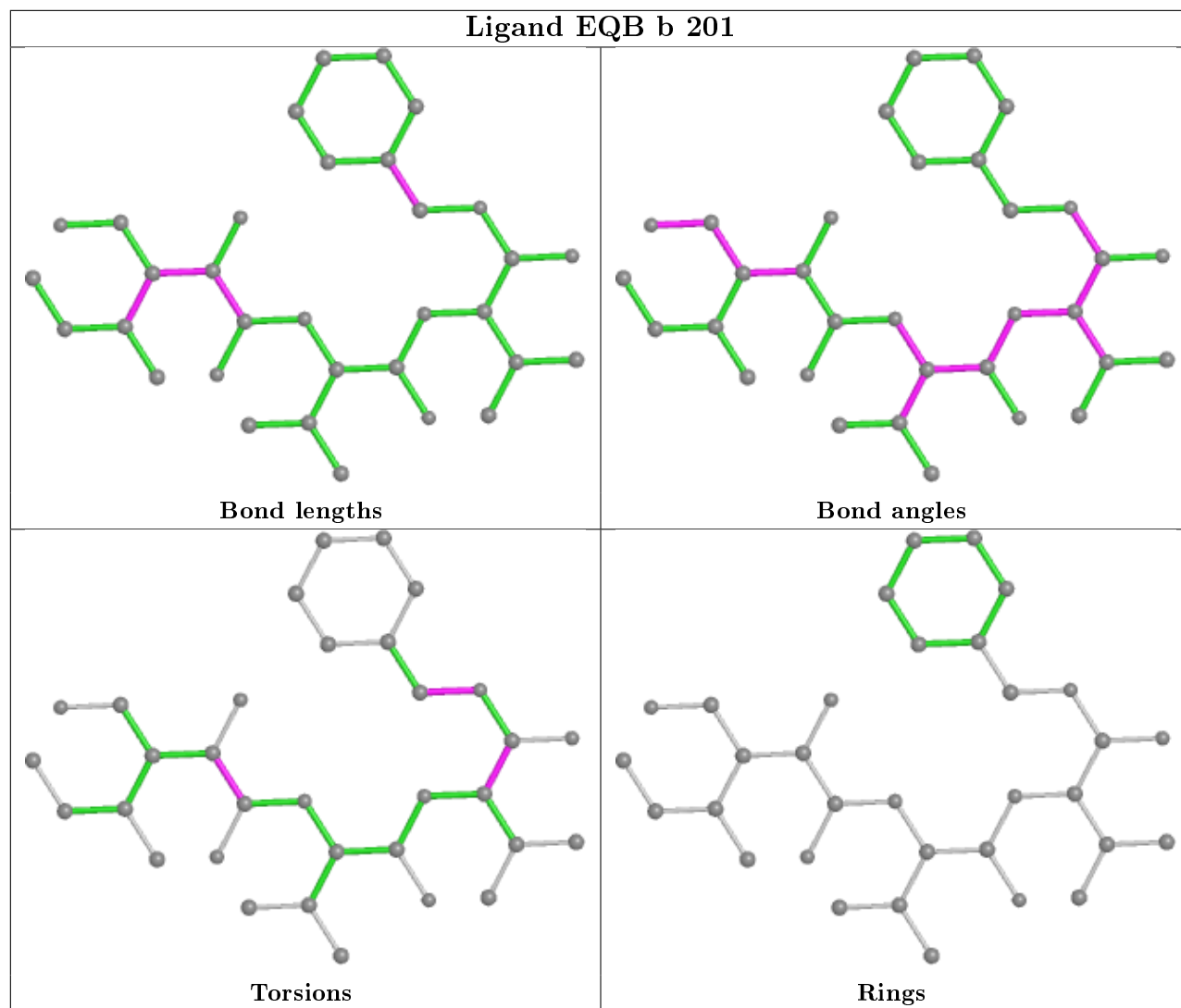
Torsions

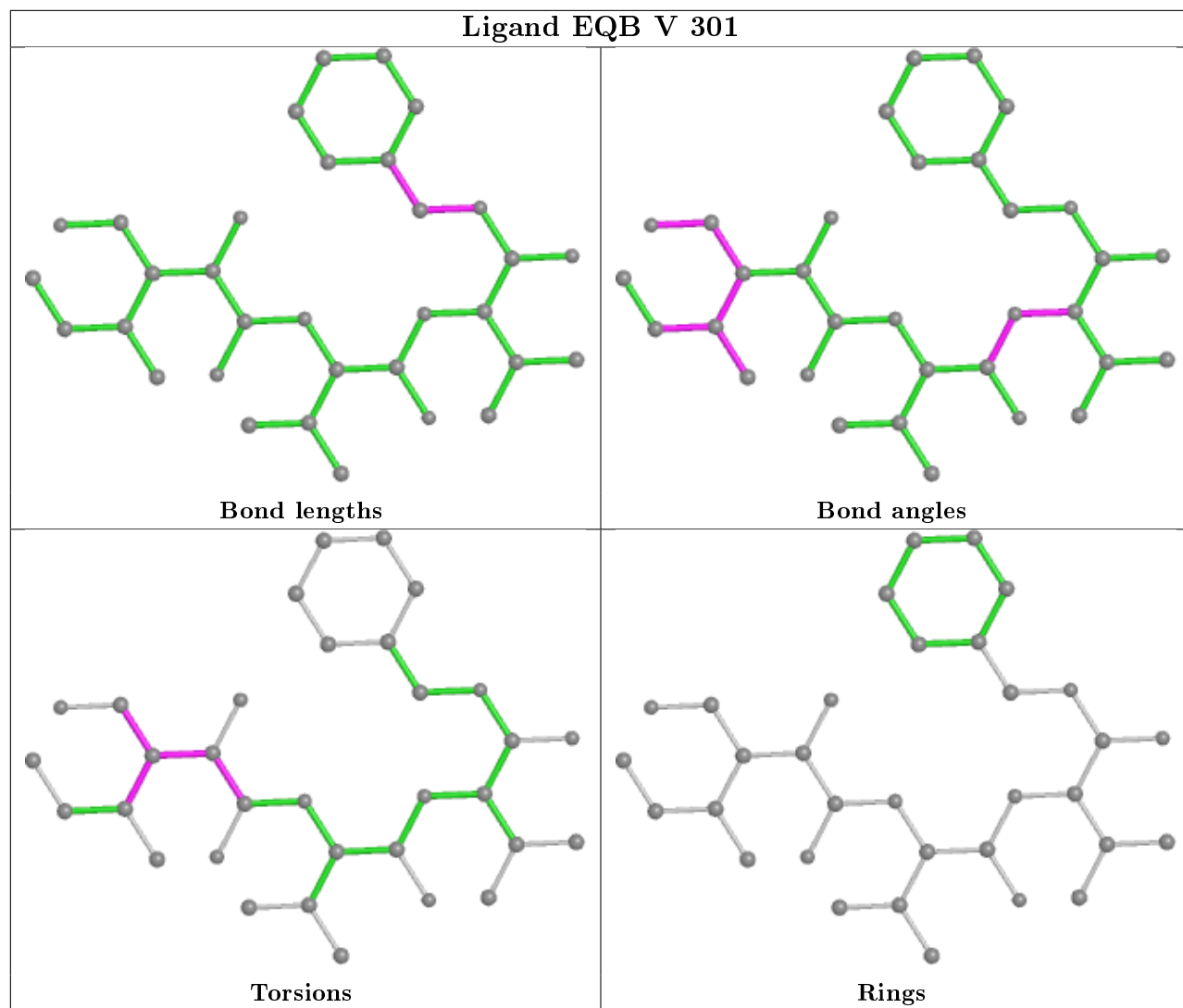


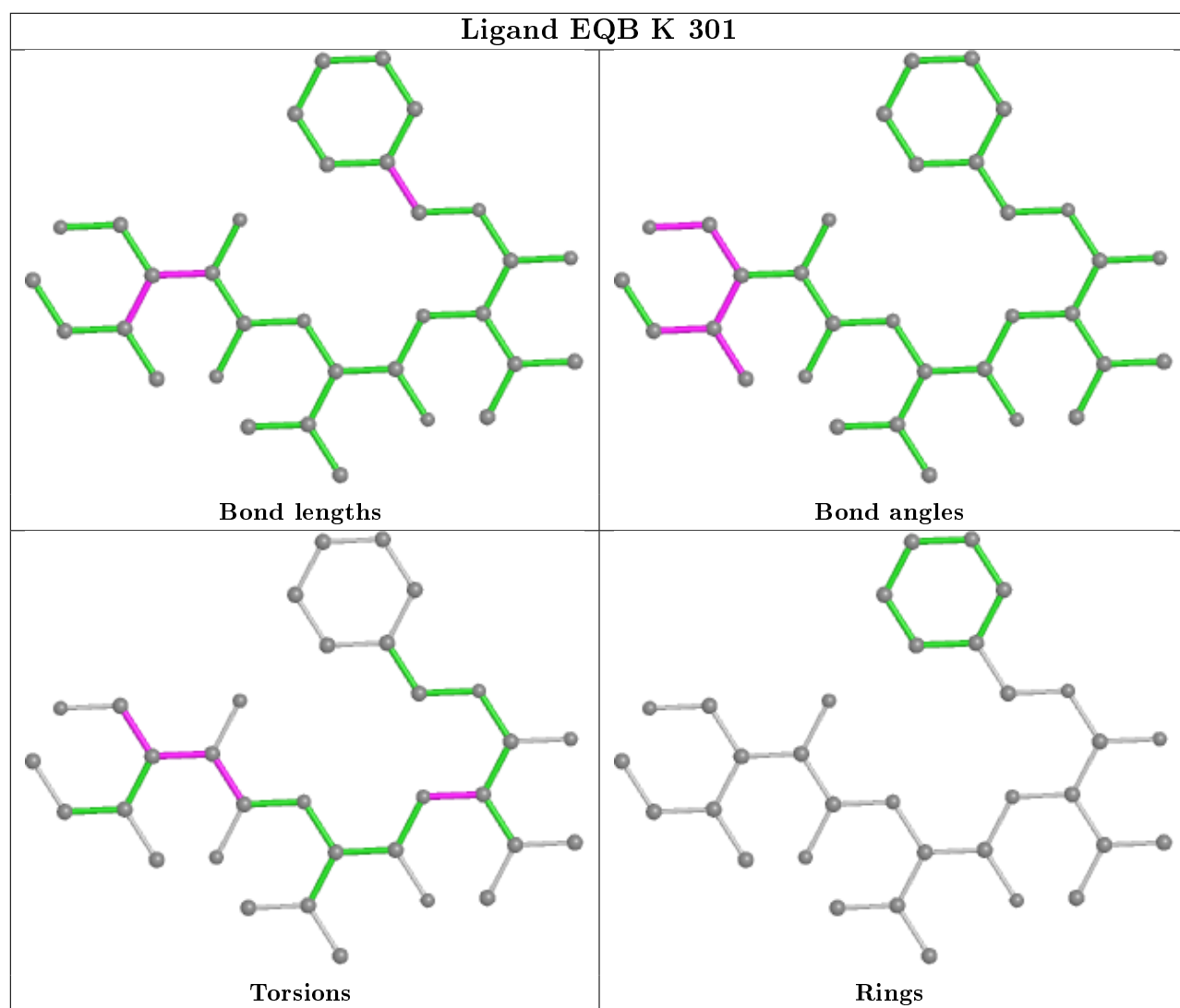
Rings



Ligand EQB b 201







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	250/250 (100%)	-0.58	3 (1%) 79 54	59, 74, 110, 150	0
1	O	250/250 (100%)	-0.59	1 (0%) 92 79	62, 80, 124, 155	0
2	B	244/258 (94%)	-0.48	6 (2%) 57 29	59, 82, 133, 196	0
2	P	244/258 (94%)	-0.50	5 (2%) 65 36	63, 83, 134, 185	0
3	C	240/254 (94%)	-0.51	3 (1%) 77 51	56, 84, 141, 167	0
3	Q	240/254 (94%)	-0.39	5 (2%) 63 34	65, 94, 171, 191	0
4	D	235/260 (90%)	-0.59	0 100 100	62, 85, 115, 146	0
4	R	235/260 (90%)	-0.51	2 (0%) 84 63	67, 91, 132, 164	0
5	E	231/234 (98%)	-0.50	1 (0%) 92 79	67, 88, 126, 156	0
5	S	231/234 (98%)	-0.46	1 (0%) 92 79	68, 93, 136, 166	0
6	F	243/288 (84%)	-0.61	1 (0%) 92 79	62, 82, 128, 161	0
6	T	243/288 (84%)	-0.58	0 100 100	60, 89, 137, 172	0
7	G	241/252 (95%)	-0.67	0 100 100	59, 78, 114, 153	0
7	U	241/252 (95%)	-0.64	0 100 100	63, 80, 114, 154	0
8	H	226/232 (97%)	-0.63	6 (2%) 54 26	57, 73, 106, 173	0
8	V	226/232 (97%)	-0.60	6 (2%) 54 26	57, 75, 109, 181	0
9	I	204/205 (99%)	-0.83	0 100 100	52, 69, 94, 122	0
9	W	204/205 (99%)	-0.78	1 (0%) 91 75	55, 70, 96, 133	0
10	J	195/198 (98%)	-0.71	2 (1%) 82 59	56, 74, 101, 149	0
10	X	195/198 (98%)	-0.67	3 (1%) 73 46	58, 76, 100, 167	0
11	K	212/212 (100%)	-0.76	0 100 100	52, 70, 95, 112	0
11	Y	212/212 (100%)	-0.76	0 100 100	58, 74, 98, 121	0
12	L	222/222 (100%)	-0.72	0 100 100	55, 72, 103, 137	0
12	Z	222/222 (100%)	-0.70	0 100 100	55, 72, 107, 140	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	229/246 (93%)	-0.70	1 (0%) 92 79	54, 75, 101, 118	0
13	a	232/246 (94%)	-0.69	0 100 100	53, 73, 99, 114	0
14	N	196/196 (100%)	-0.76	0 100 100	57, 70, 97, 129	0
14	b	196/196 (100%)	-0.69	1 (0%) 91 75	57, 71, 101, 133	0
All	All	6339/6614 (95%)	-0.62	48 (0%) 86 65	52, 78, 124, 196	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	P	220	ASN	5.8
8	V	226	GLU	4.6
8	V	222	ASP	4.0
2	B	220	ASN	3.9
8	V	224	GLN	3.6
2	B	221	ASP	3.6
8	H	226	GLU	3.4
3	Q	50	LEU	3.4
8	V	225	GLU	3.2
5	S	202	ASP	3.1
8	H	224	GLN	3.0
2	B	51	VAL	2.9
8	H	222	ASP	2.9
8	H	225	GLU	2.9
1	A	2	THR	2.8
5	E	202	ASP	2.8
3	Q	236	GLN	2.8
3	Q	49	THR	2.8
9	W	1	SER	2.7
2	B	218	GLY	2.7
10	X	194	ASP	2.7
3	C	239	GLN	2.6
8	H	223	ILE	2.6
6	F	205	GLU	2.6
10	X	1	MET	2.6
2	P	51	VAL	2.5
8	V	221	CYS	2.5
3	Q	206	LYS	2.5
10	J	194	ASP	2.5
2	B	244	THR	2.5
8	V	223	ILE	2.5
3	C	236	GLN	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
4	R	1	ASP	2.5
2	P	59	ASP	2.4
2	B	203	SER	2.4
2	P	221	ASP	2.4
8	H	221	CYS	2.3
10	J	1	MET	2.3
14	b	195	GLN	2.3
10	X	193	ASP	2.2
4	R	241	ALA	2.2
1	A	202	GLY	2.2
1	O	2	THR	2.1
3	Q	238	LYS	2.1
3	C	206	LYS	2.1
13	M	1	THR	2.0
2	P	219	ALA	2.0
1	A	201	GLU	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 carbohydrates 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.

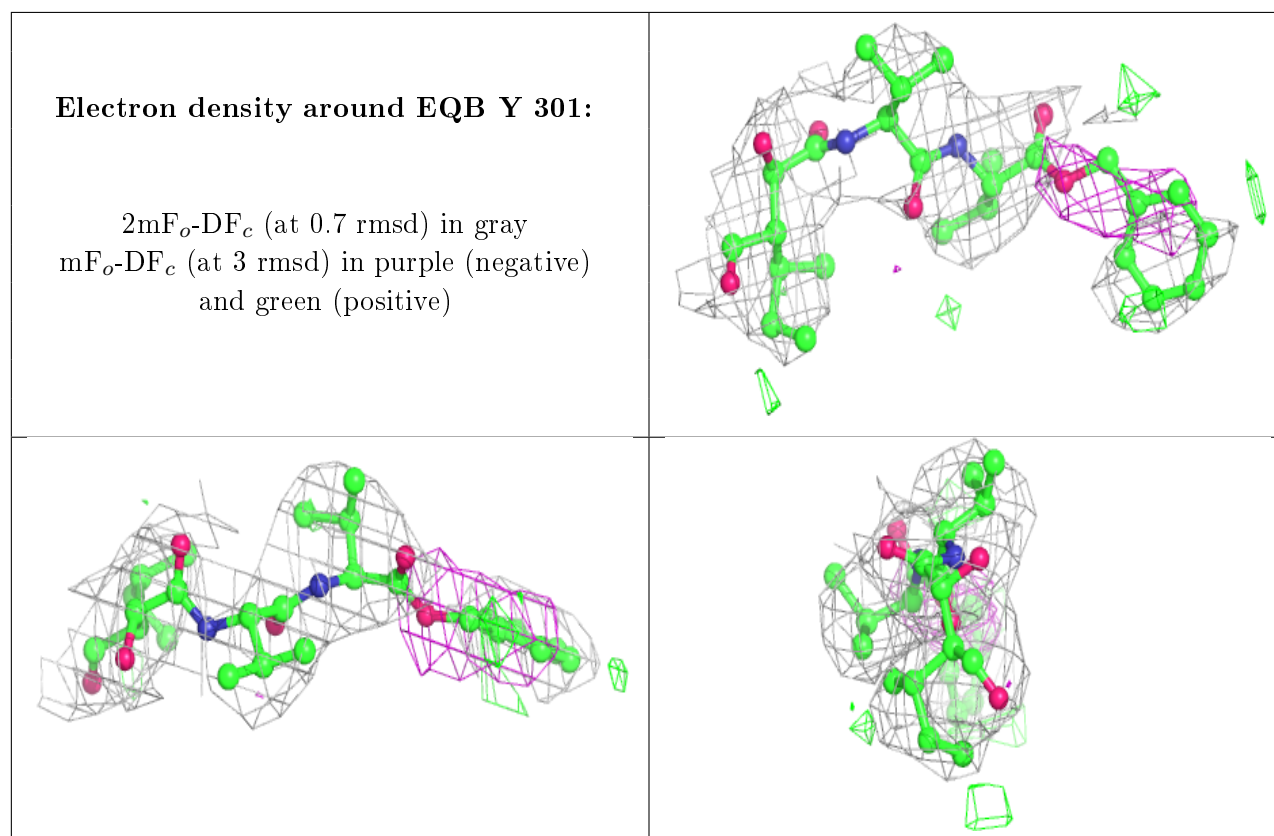
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
17	EQB	Y	301	33/34	0.82	0.31	73,85,120,133	0
17	EQB	K	301	33/34	0.88	0.30	65,85,104,117	0
15	MG	I	301	1/1	0.89	0.47	96,96,96,96	0
17	EQB	N	201	33/34	0.90	0.27	70,82,110,136	0
17	EQB	b	201	33/34	0.91	0.28	66,83,101,130	0
15	MG	Y	302	1/1	0.91	0.26	92,92,92,92	0
15	MG	V	302	1/1	0.91	0.16	105,105,105,105	0

Continued on next page...

Continued from previous page...

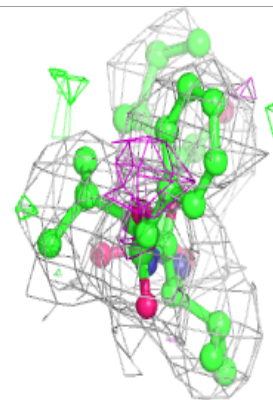
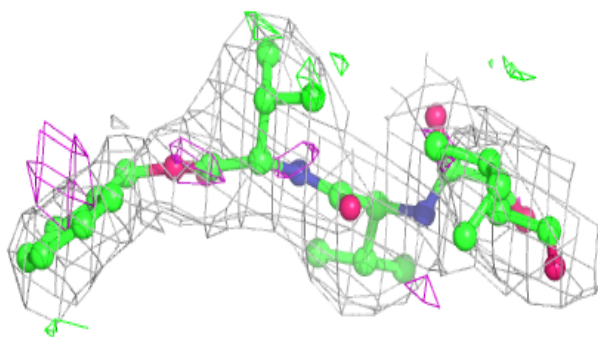
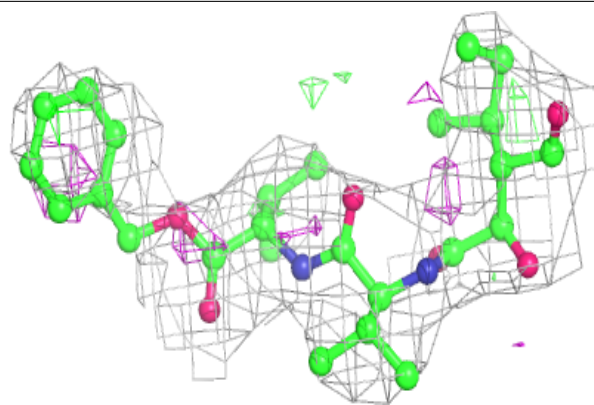
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
17	EQB	V	301	33/34	0.92	0.24	57,72,91,99	0
17	EQB	H	301	33/34	0.94	0.23	59,75,96,101	0
15	MG	K	302	1/1	0.95	0.18	92,92,92,92	0
16	CL	G	302	1/1	0.96	0.23	82,82,82,82	0
15	MG	W	301	1/1	0.96	0.35	84,84,84,84	0
16	CL	U	301	1/1	0.97	0.18	75,75,75,75	0
15	MG	N	202	1/1	0.97	0.11	55,55,55,55	0
15	MG	G	301	1/1	0.98	0.10	83,83,83,83	0
15	MG	Z	301	1/1	0.99	0.10	61,61,61,61	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.

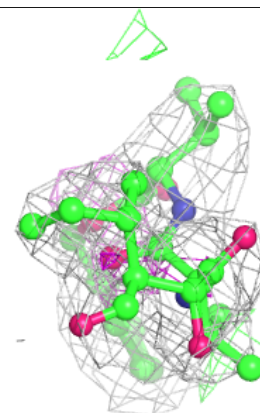
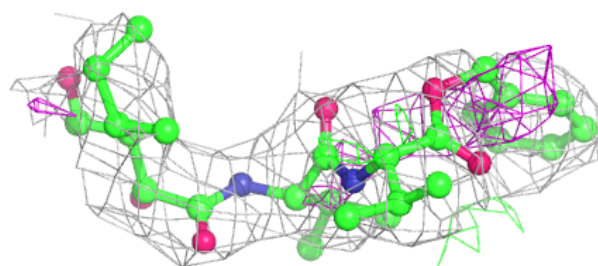
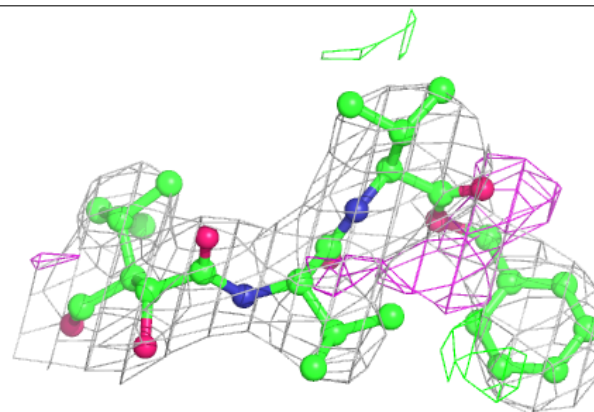


Electron density around EQB K 301:

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

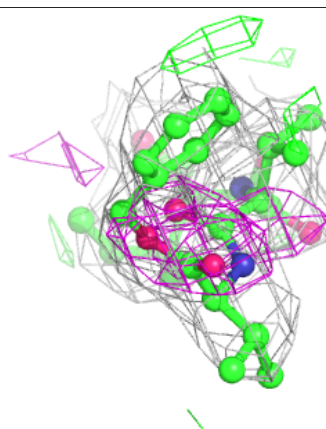
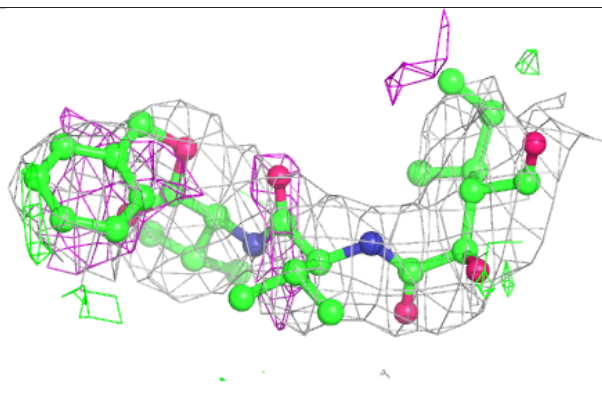
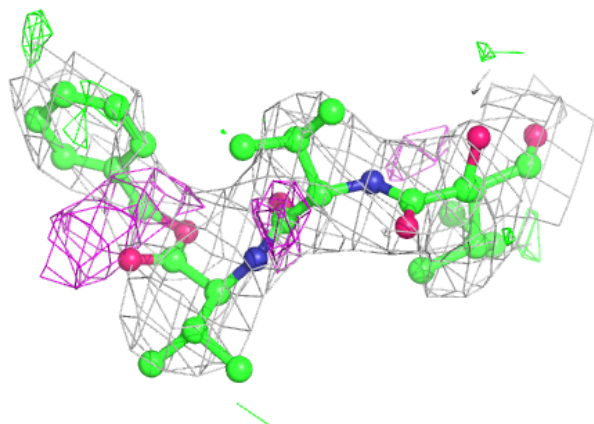
**Electron density around EQB N 201:**

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

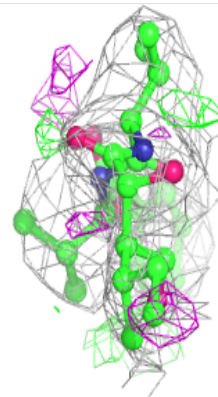
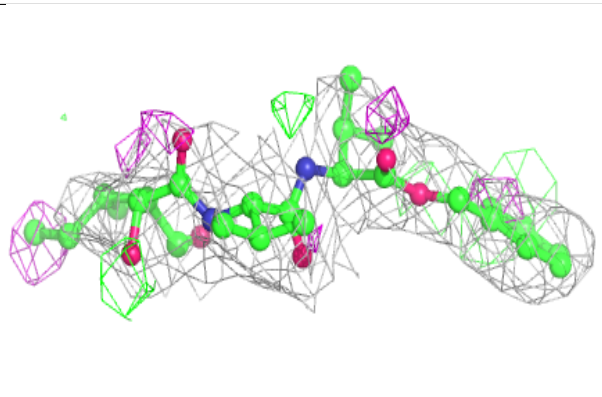
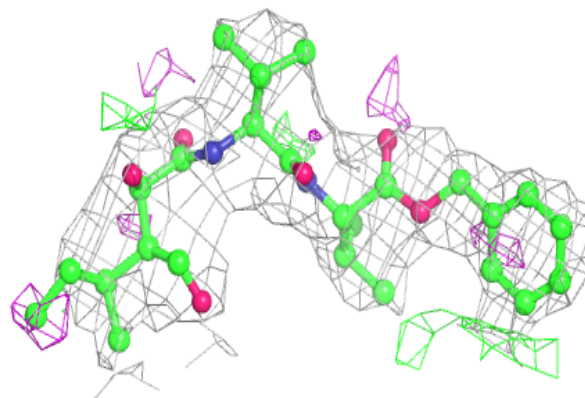


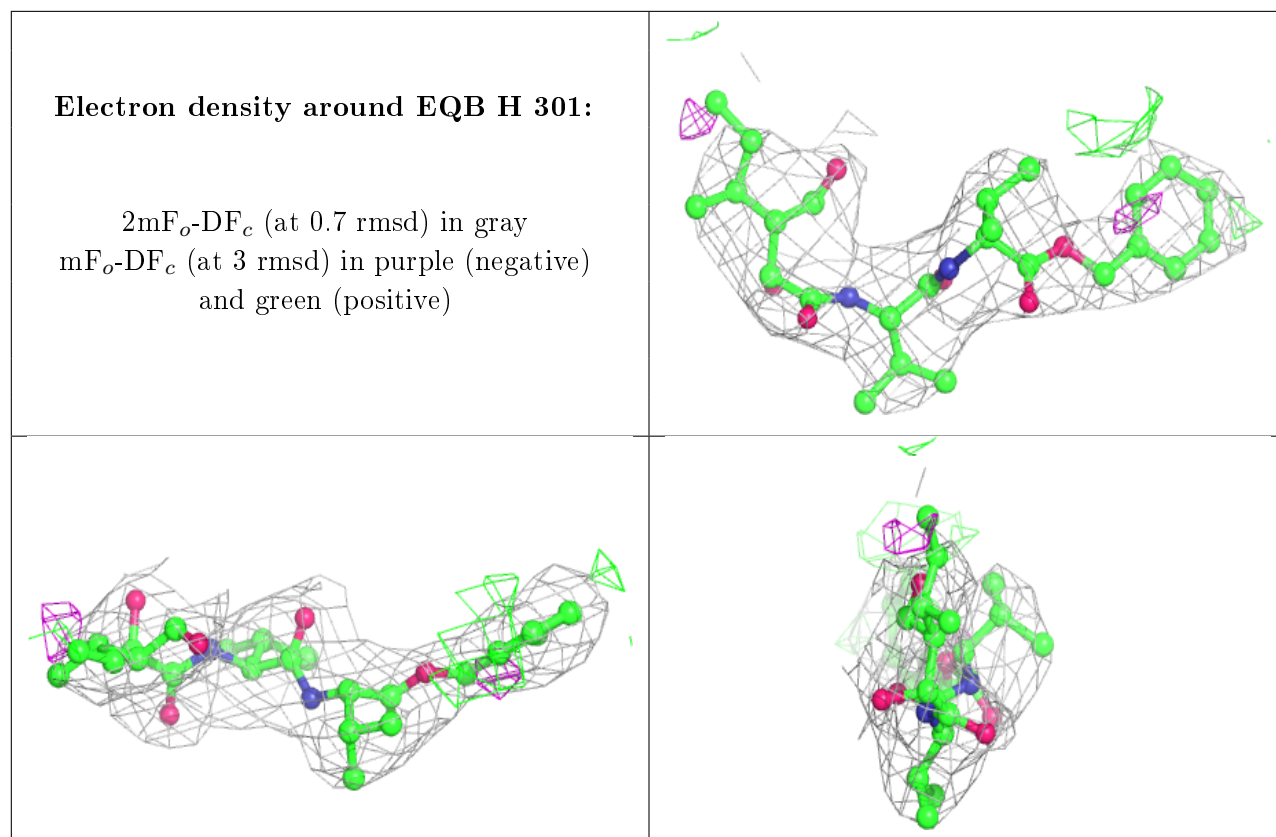
Electron density around EQB b 201:

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

**Electron density around EQB V 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.