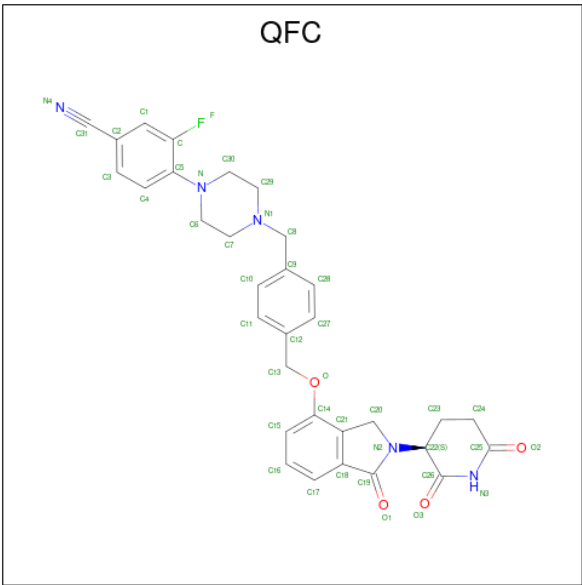




wwPDB X-ray Structure Validation Summary Report ⓘ</



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
4	A	1	Total	C	F	N	O	0	0
			42	32	1	5	4		
4	D	1	Total	C	F	N	O	0	0
			42	32	1	5	4		

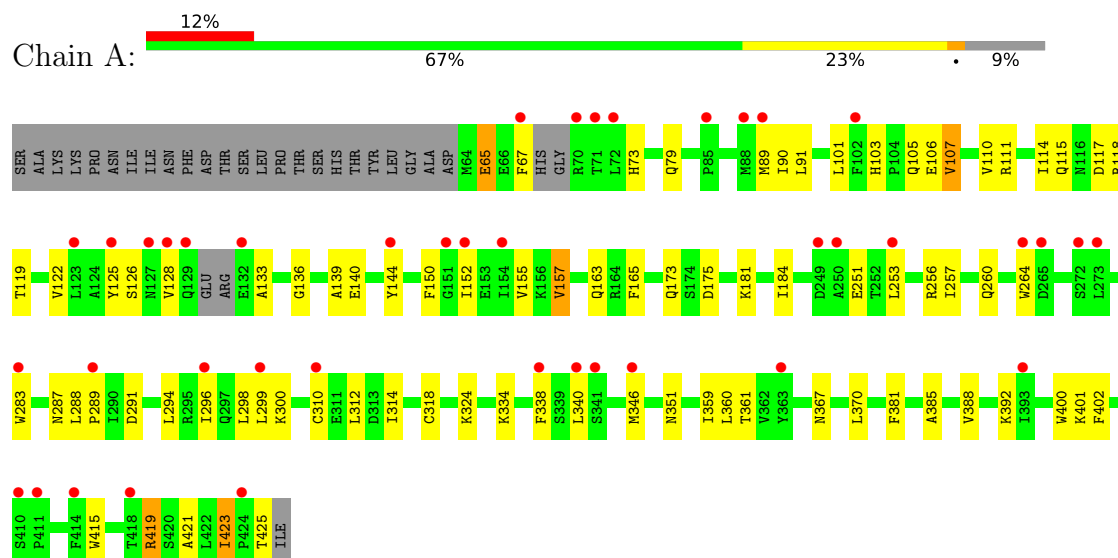
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	75	Total	O	0	0
			75	75		
5	B	11	Total	O	0	0
			11	11		
5	D	83	Total	O	0	0
			83	83		
5	E	10	Total	O	0	0
			10	10		

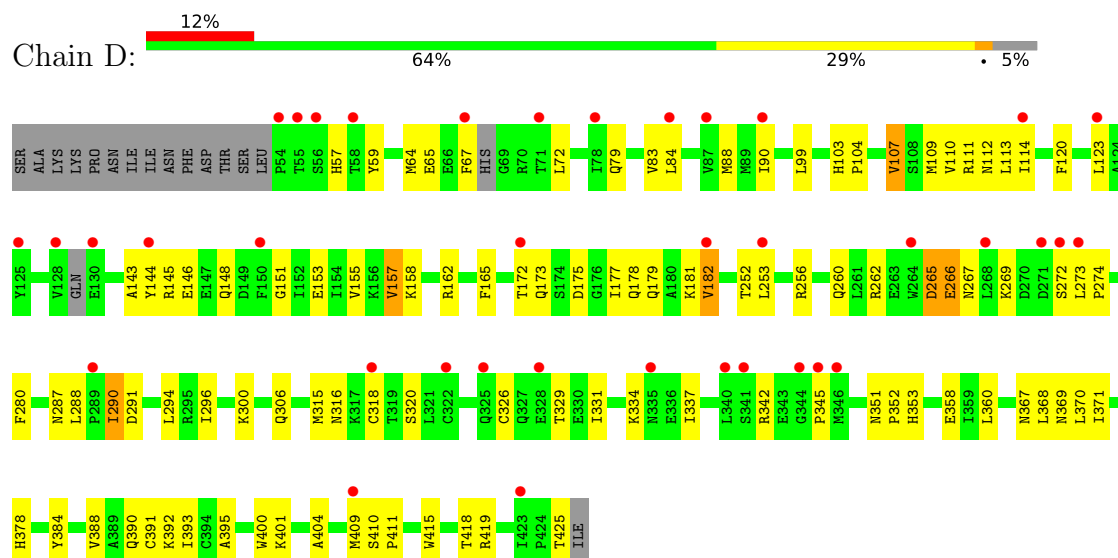
3 Residue-property plots [i](#)

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: Protein cereblon

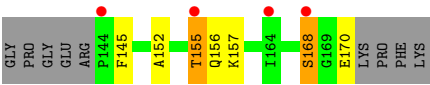


• Molecule 1: Protein cereblon

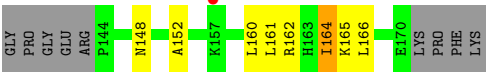


• Molecule 2: DNA-binding protein Ikaros





● Molecule 2: DNA-binding protein Ikaros



Continued from previous page...

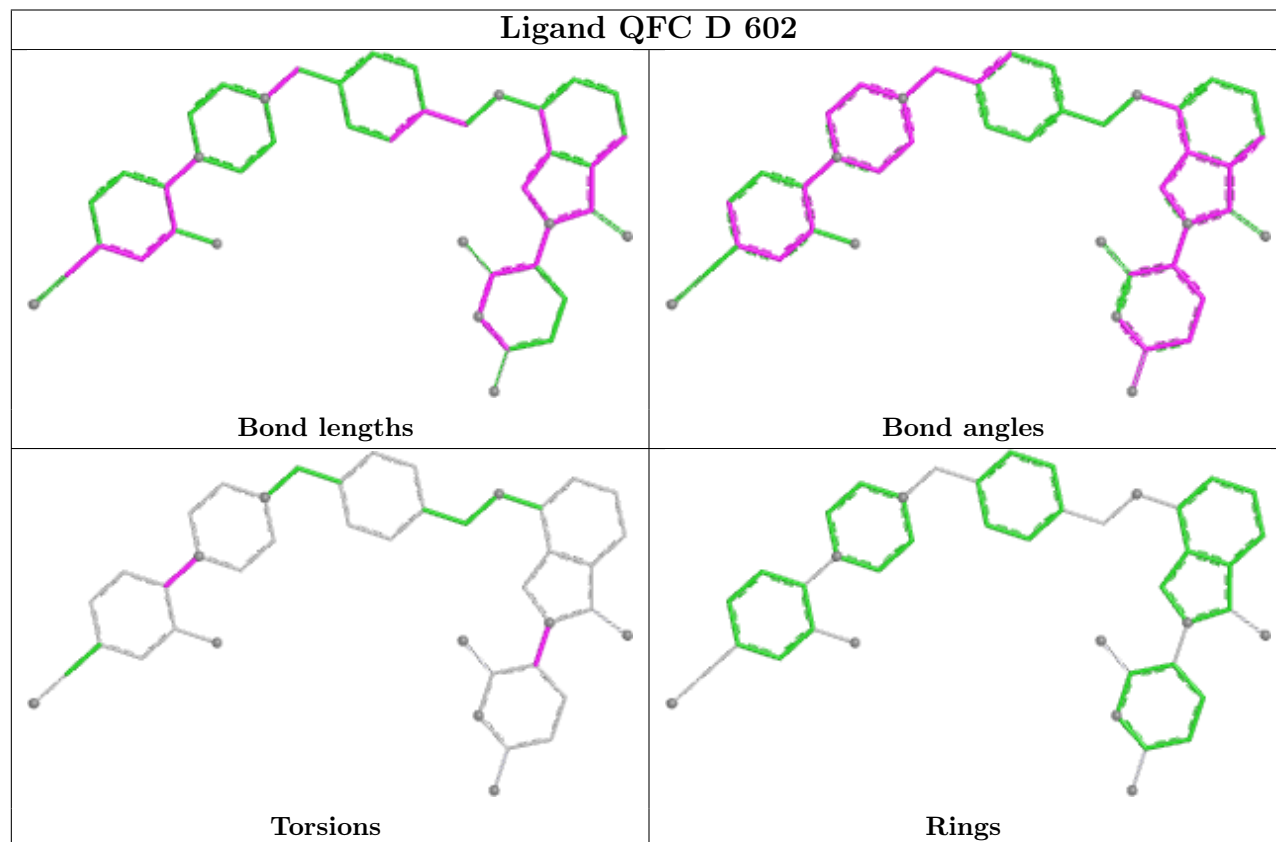
Continued from previous page...

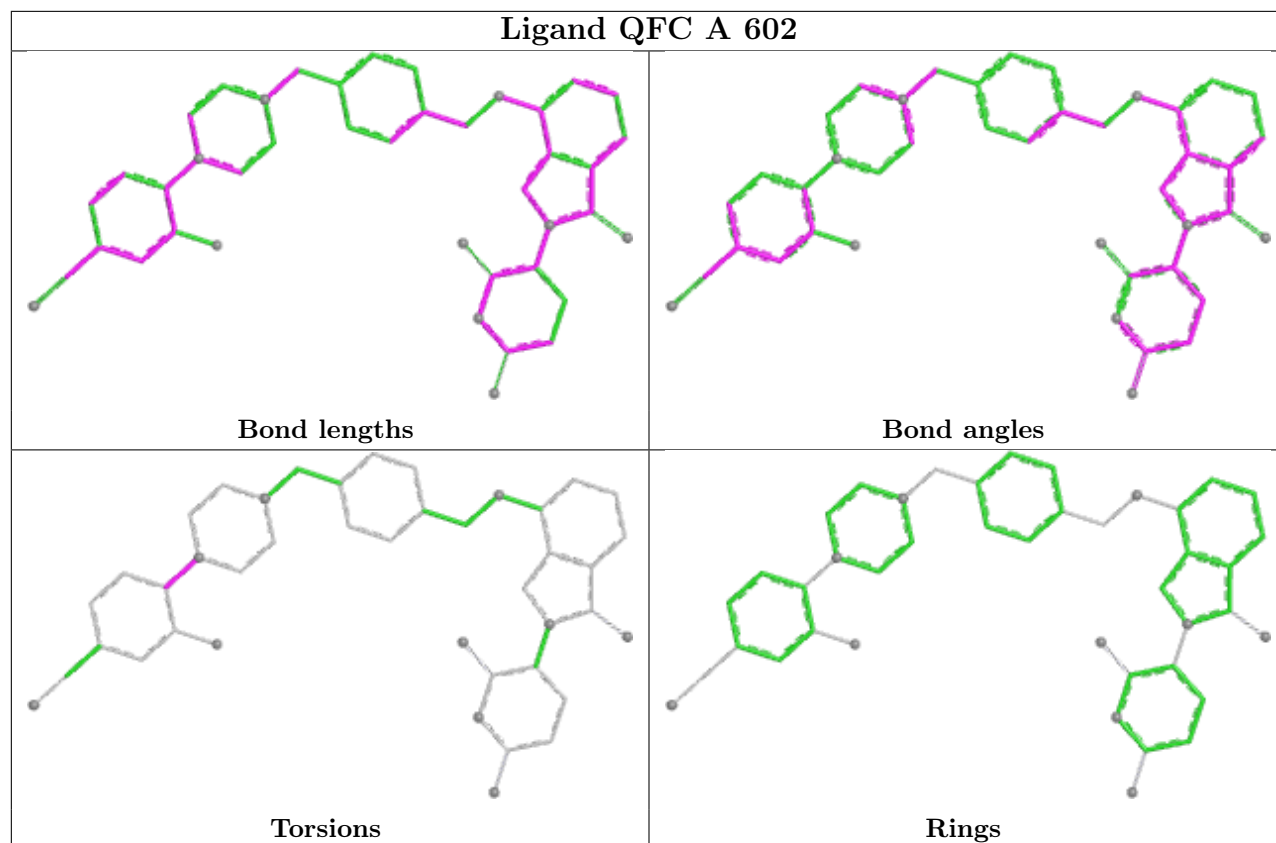
Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	QFC	A	602	-	-	2/19/54/54	0/6/6/6

The worst 5 of 42 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	602	QFC	C8-N1	10.15	1.67	1.47
4	D	602	QFC	C8-N1	9.71	1.66	1.47
4	A	602	QFC	C19-N2	9.62	1.45	1.36
4	D	602	QFC	C19-N2	9.29	1.45	1.36
4	A	6					

within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

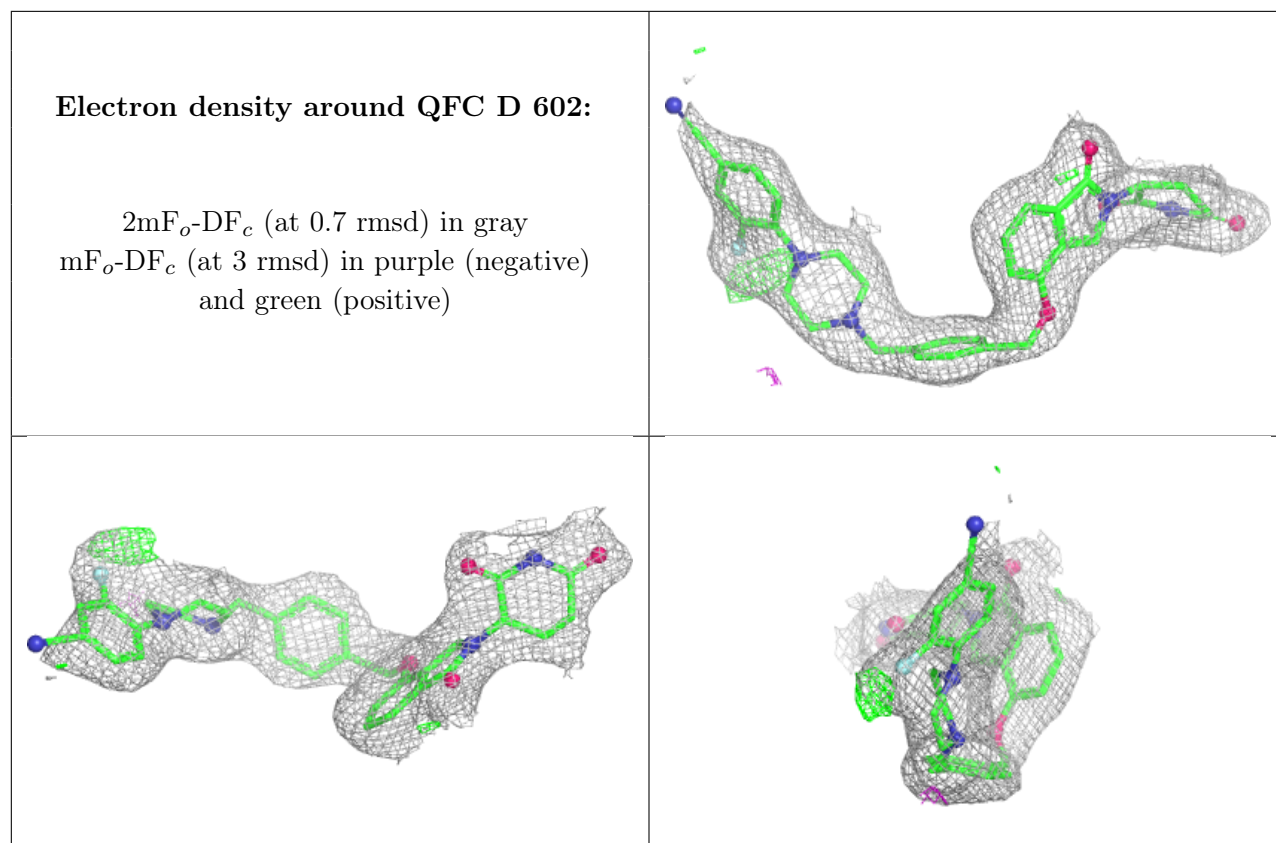
In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	300/329 (91%)	0.98	41 (13%) 6 7	42, 59, 101, 129	0
1	D	312/329 (94%)	0.86	38 (12%) 8 9	39, 60, 97, 152	1 (0%)
2	B	27/36 (75%)	0.69	4 (14%) 5 6	46, 58, 79, 85	0
2	E	27/36 (75%)	0.57	1 (3%) 45 49	44, 55, 71, 75	0
All	All	666/730 (91%)	0.89	84 (12%) 8 8	39, 59, 98, 152	1 (0%)

The worst 5 of 84 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	253	LEU	4.7
1	A	264	TRP	4.4
1	D	182	VAL	4.3
1	A	363	TYR	4.2
1	A	129	GLN	4.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)</



6.5 Other polymers [i](#)

There are no such residues in this entry.