



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:31 PM UTC

PDB ID : 8U17 / pdb_00008u17
Title : The ternary complex structure of DDB1-CRBN-SALL4(ZF1,2)-long bound to Pomalidomide
Authors : Clifton, M.C.; Ma, X.; Ornelas, E.
Deposited on : 2023-08-30
Resolution : 3.10 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

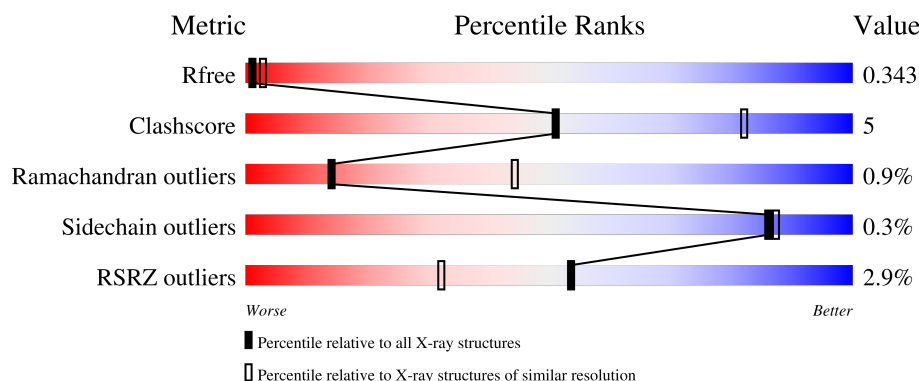
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	373	2% 80% 10% 10%
1	D	373	2% 82% 11% 6%
2	B	836	4% 83% 11% 6%
2	E	836	2% 83% 12% 5%
3	C	86	0% 51% 10% 37%

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Mol	Chain	Length	Quality of chain
3	F	86	6% 55% 7% 35%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 17033 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 Protein cereblon.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	0	0	0
			2459	1571	424	447	17			
1	D	349	Total	C	N	O	S	0	0	0
			2530	1626	429	455	20			

- Molecule 2 is a protein called DNA damage-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	787	Total	C	N	O	S	0	0	0
			5557	3494	949	1084	30			
2	E	797	Total	C	N	O	S	0	0	0
			5676	3585	957	1105	29			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	700	GLY	-	linker	UNP Q16531
B	701	ASN	-	linker	UNP Q16531
B	702	GLY	-	linker	UNP Q16531
B	703	ASN	-	linker	UNP Q16531
B	704	SER	-	linker	UNP Q16531
B	705	GLY	-	linker	UNP Q16531
E	700	GLY	-	linker	UNP Q16531
E	701	ASN	-	linker	UNP Q16531
E	702	GLY	-	linker	UNP Q16531
E	703	ASN	-	linker	UNP Q16531
E	704	SER	-	linker	UNP Q16531
E	705	GLY	-	linker	UNP Q16531

- Molecule 3 is a protein called Sal-like protein 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	54	Total	C	N	O	S	0	0	0
			394	246	77	67	4			
3	F	56	Total	C	N	O	S	0	0	0
			371	229	71	67	4			

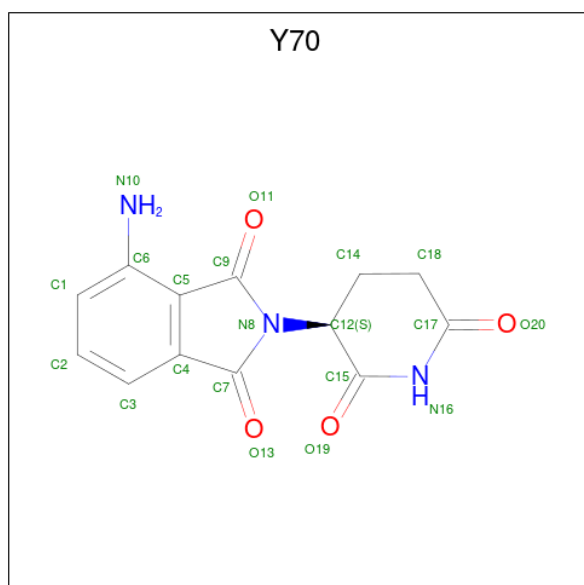
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	369	SER	-	expression tag	UNP Q9UJQ4
F	369	SER	-	expression tag	UNP Q9UJQ4

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 5 is S-Pomalidomide (CCD ID: Y70) (formula: C₁₃H₁₁N₃O₄) (labeled as "Ligand of Interest" by depositor).

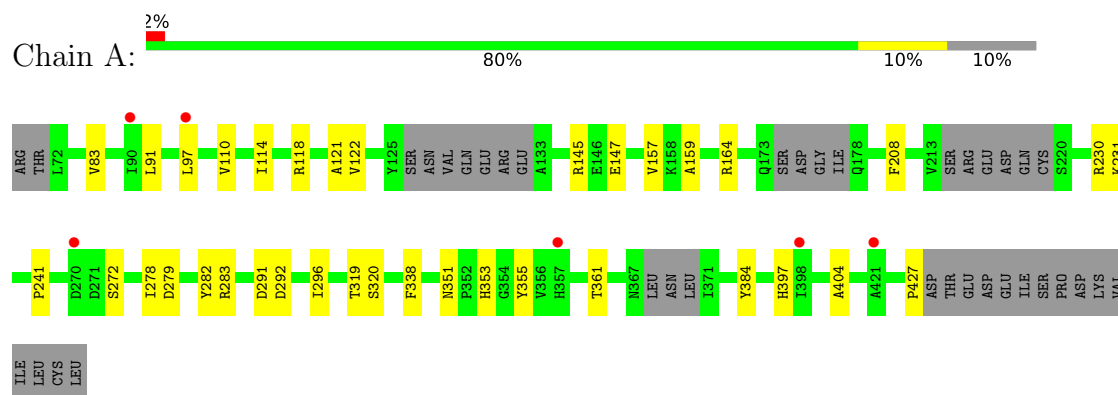


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			20	13	3	4		
5	D	1	Total	C	N	O	0	0
			20	13	3	4		

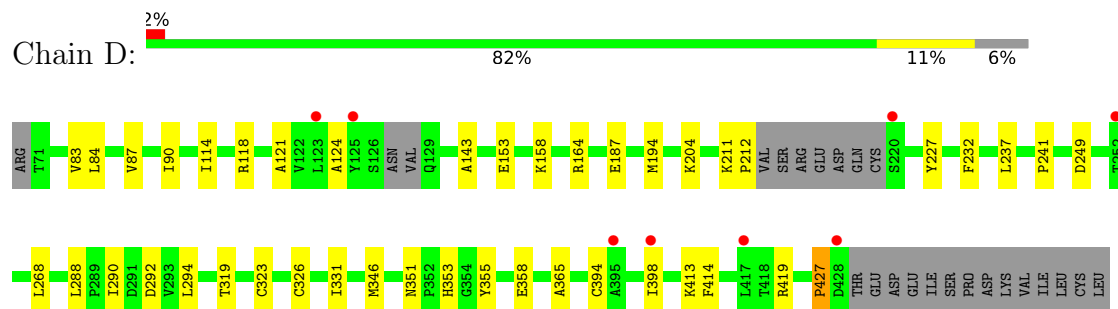
3 Residue-property plots [i](#)

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.

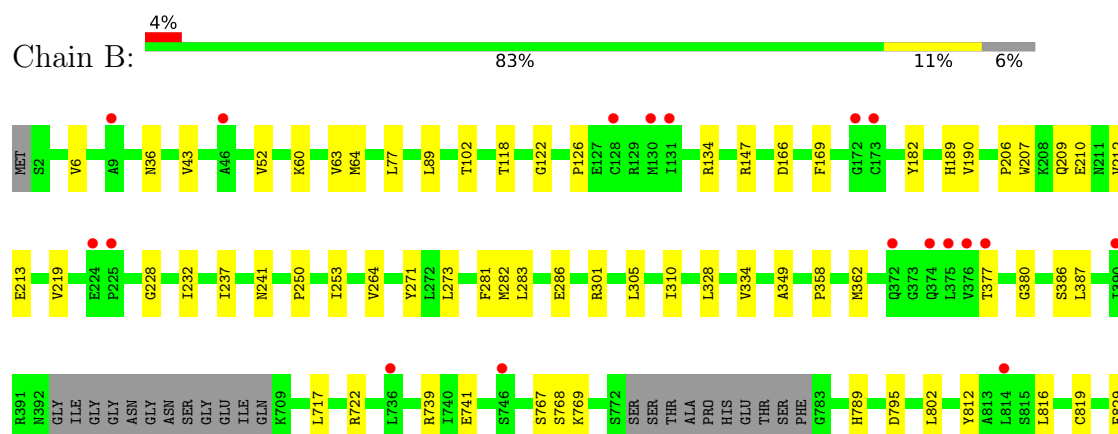
- Molecule 1: Protein cereblon

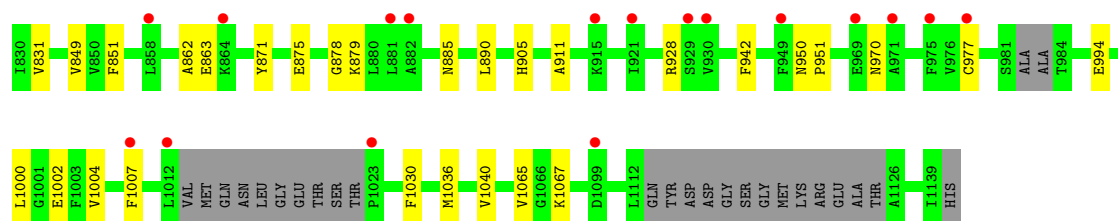


- Molecule 1: Protein cereblon

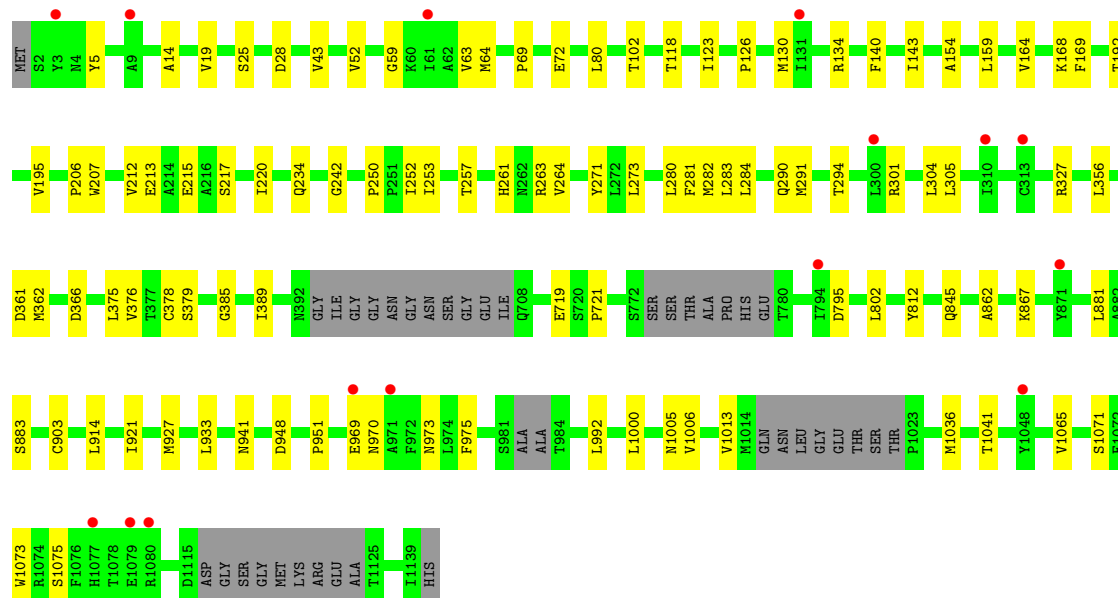
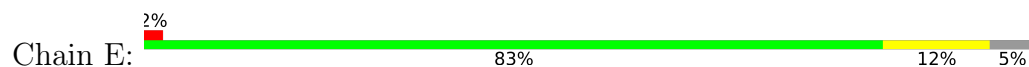


- Molecule 2: DNA damage-binding protein 1





• Molecule 2: DNA damage-binding protein 1



• Molecule 3: Sal-like protein 4



• Molecule 3: Sal-like protein 4



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	116.08Å 151.66Å 195.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.90 – 3.10 49.90 – 3.10	Depositor EDS
% Data completeness (in resolution range)	96.0 (49.90-3.10) 99.5 (49.90-3.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.21	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.23 (at 3.12Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.305 , 0.346 0.303 , 0.343	Depositor DCC
R_{free} test set	3185 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	82.6	Xtriage
Anisotropy	0.684	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 81.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	17033	wwPDB-VP
Average B, all atoms (Å ²)	122.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.01% 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: Y70, ZN

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	0.10	0/2517	0.28	0/3445
1	D	0.14	0/2592	0.33	0/3556
2	B	0.09	0/5659	0.29	0/7731
2	E	0.09	0/5778	0.29	0/7890
3	C	0.13	0/407	0.40	0/553
3	F	0.30	0/381	0.49	0/521
All	All	0.11	0/17334	0.30	0/23696

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	2459	0	2232	24	0
1	D	2530	0	2259	28	0
2	B	5557	0	4834	55	0
2	E	5676	0	5042	58	0
3	C	394	0	329	7	0
3	F	371	0	285	4	0
4	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	2	0	0	0	0
4	D	1	0	0	0	0
4	F	2	0	0	0	0
5	A	20	0	11	0	0
5	D	20	0	11	0	0
All	All	17033	0	15003	166	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 5.

All (166) 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)
2:B:118:THR:OG1	2:B:134:ARG:NH2	2.18	0.75
2:E:969:GLU:HB2	2:E:973:ASN:HB2	1.68	0.75
2:E:252:ILE:HD11	2:E:304:LEU:HB2	1.70	0.71
1:D:143:ALA:HB3	1:D:158:LYS:HB2	1.74	0.70
1:A:114:ILE:HA	1:A:118:ARG:HG3	1.74	0.69
2:B:767:SER:O	2:B:769:LYS:N	2.25	0.69
2:E:69:PRO:HG2	2:E:72:GLU:HG3	1.74	0.68
2:E:948:ASP:HB2	2:E:992:LEU:HB2	1.76	0.67
1:D:204:LYS:HG3	2:E:217:SER:HB2	1.78	0.66
1:A:320:SER:HB3	1:A:427:PRO:HG3	1.76	0.66
2:E:130:MET:HE1	2:E:195:VAL:HG11	1.78	0.66
1:D:292:ASP:OD1	1:D:419:ARG:NH2	2.29	0.66
3:F:432:HIS:HB2	3:F:433:PRO:HD2	1.77	0.65
1:A:83:VAL:HG22	1:A:121:ALA:HB3	1.77	0.65
2:E:273:LEU:HB2	2:E:281:PHE:HB2	1.79	0.64
2:B:36:ASN:OD1	2:B:60:LYS:NZ	2.29	0.64
2:E:282:MET:HB2	2:E:305:LEU:HD21	1.79	0.63
1:D:353:HIS:NE2	3:F:387:CYS:O	2.32	0.62
2:B:36:ASN:ND2	2:B:1002:GLU:OE2	2.33	0.62
2:E:102:THR:OG1	2:E:1065:VAL:O	2.17	0.61
1:A:145:ARG:NH1	1:A:147:GLU:OE2	2.33	0.61
2:B:212:VAL:HG22	2:B:213:GLU:H	1.68	0.59
3:C:432:HIS:O	3:C:434:GLN:N	2.35	0.59
2:E:123:ILE:HG21	2:E:168:LYS:HA	1.85	0.59
2:E:118:THR:OG1	2:E:134:ARG:NH2	2.26	0.59
1:D:351:ASN:OD1	1:D:355:TYR:N	2.36	0.58
2:E:271:TYR:HB2	2:E:283:LEU:HB3	1.85	0.58
1:A:351:ASN:OD1	1:A:355:TYR:N	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:114:ILE:HA	1:D:118:ARG:HG2	1.85	0.58
2:B:6:VAL:HG22	2:B:1040:VAL:HG22	1.86	0.57
2:B:362:MET:HB3	2:B:377:THR:HG22	1.87	0.56
2:B:819:CYS:HB2	2:B:875:GLU:HG3	1.87	0.56
1:D:319:THR:HB	1:D:427:PRO:HG2	1.87	0.56
1:A:272:SER:O	1:A:283:ARG:NH1	2.39	0.56
2:B:273:LEU:HB2	2:B:281:PHE:HB2	1.88	0.56
2:E:234:GLN:OE1	2:E:257:THR:OG1	2.22	0.56
2:B:182:TYR:CE1	2:B:189:HIS:HB2	2.41	0.55
1:D:164:ARG:HH21	1:D:187:GLU:HG2	1.71	0.55
2:B:250:PRO:HG2	2:B:253:ILE:HG12	1.87	0.55
2:E:1071:SER:O	2:E:1075:SER:OG	2.24	0.55
1:D:153:GLU:H	1:D:153:GLU:CD	2.16	0.53
1:A:353:HIS:NE2	3:C:387:CYS:O	2.41	0.53
1:A:208:PHE:HE2	1:A:230:ARG:HB3	1.74	0.53
2:E:212:VAL:HG22	2:E:213:GLU:H	1.72	0.53
2:B:206:PRO:HB2	2:B:207:TRP:CD1	2.45	0.52
2:B:334:VAL:HG12	2:B:349:ALA:HA	1.92	0.52
2:B:928:ARG:HD3	2:B:950:ASN:HB3	1.91	0.52
2:B:885:ASN:O	2:B:911:ALA:N	2.42	0.52
1:D:331:ILE:HG22	1:D:365:ALA:HB1	1.92	0.51
2:E:280:LEU:HG	2:E:305:LEU:HD12	1.92	0.51
2:E:19:VAL:HG22	2:E:64:MET:HE3	1.93	0.51
1:D:227:TYR:OH	1:D:249:ASP:OD2	2.29	0.51
1:A:338:PHE:O	1:A:361:THR:OG1	2.29	0.51
1:D:237:LEU:O	2:E:1005:ASN:ND2	2.44	0.50
2:B:1000:LEU:HD11	2:B:1036:MET:HE1	1.93	0.50
2:E:881:LEU:HG	2:E:914:LEU:HD21	1.94	0.50
2:B:816:LEU:HD13	2:B:831:VAL:HG22	1.93	0.50
2:B:829:PHE:O	2:B:851:PHE:N	2.41	0.50
2:B:43:VAL:HG23	2:B:52:VAL:HG21	1.94	0.50
1:D:90:ILE:HG12	1:D:124:ALA:HB1	1.93	0.49
2:E:250:PRO:HG2	2:E:253:ILE:HG12	1.94	0.49
2:B:189:HIS:ND1	2:B:210:GLU:O	2.41	0.49
2:B:890:LEU:HB2	2:B:942:PHE:HZ	1.76	0.49
2:E:126:PRO:HD3	2:E:169:PHE:HB3	1.95	0.49
2:E:143:ILE:HG12	2:E:154:ALA:HB2	1.94	0.49
1:D:153:GLU:OE1	1:D:153:GLU:N	2.46	0.48
1:D:83:VAL:HG22	1:D:121:ALA:HB3	1.93	0.48
2:B:795:ASP:HB2	2:B:802:LEU:HD11	1.94	0.48
1:D:241:PRO:HB3	2:E:812:TYR:CZ	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:397:HIS:HB2	3:C:432:HIS:CE1	2.49	0.47
1:A:319:THR:HB	1:A:427:PRO:HG2	1.96	0.47
2:B:282:MET:HE2	2:B:305:LEU:HD11	1.96	0.47
3:C:415:CYS:SG	3:C:417:HIS:HB2	2.55	0.47
1:D:323:CYS:SG	1:D:331:ILE:HD11	2.54	0.47
1:A:278:ILE:HG13	1:A:279:ASP:N	2.29	0.47
2:B:63:VAL:HG11	2:B:122:GLY:HA3	1.97	0.46
2:E:927:MET:HE2	2:E:927:MET:HB3	1.80	0.46
2:B:871:TYR:HE2	2:B:885:ASN:HA	1.79	0.46
2:E:356:LEU:O	2:E:379:SER:OG	2.29	0.46
2:B:1067:LYS:HB3	2:B:1067:LYS:HE3	1.74	0.46
1:D:194:MET:HE2	1:D:232:PHE:HA	1.96	0.46
2:E:903:CYS:SG	2:E:941:ASN:HA	2.56	0.46
2:B:228:GLY:HA3	2:B:241:ASN:HB2	1.98	0.46
2:E:130:MET:HE2	2:E:169:PHE:HZ	1.80	0.46
1:D:84:LEU:O	1:D:87:VAL:HG12	2.16	0.46
2:B:1004:VAL:HG13	2:B:1030:PHE:HB2	1.98	0.46
3:C:414:VAL:HB	3:C:432:HIS:HD2	1.81	0.46
1:A:292:ASP:O	1:A:296:ILE:HG13	2.16	0.46
2:B:1007:PHE:CD1	2:B:1030:PHE:HB3	2.51	0.46
1:A:291:ASP:OD1	1:A:291:ASP:N	2.49	0.45
2:B:905:HIS:HB2	2:B:942:PHE:HD2	1.81	0.45
1:A:97:LEU:N	1:A:159:ALA:O	2.44	0.45
1:A:384:TYR:HA	1:A:404:ALA:HB2	1.98	0.45
2:B:739:ARG:NE	2:B:741:GLU:OE2	2.46	0.45
2:E:63:VAL:HB	2:E:80:LEU:HB3	1.98	0.45
2:B:166:ASP:HB3	2:B:219:VAL:HG23	1.99	0.45
3:F:396:SER:HA	3:F:399:ILE:HD12	1.98	0.45
2:E:206:PRO:HB2	2:E:207:TRP:CD1	2.52	0.45
2:B:206:PRO:HB2	2:B:207:TRP:HD1	1.83	0.44
2:E:25:SER:HB3	2:E:28:ASP:HB2	1.99	0.44
2:B:232:ILE:HG12	2:B:237:ILE:HG23	1.99	0.44
2:B:387:LEU:HG	2:B:717:LEU:HD11	1.99	0.44
2:E:59:GLY:HA2	2:E:1073:TRP:CZ3	2.53	0.44
2:E:883:SER:OG	2:E:914:LEU:HD22	2.17	0.44
2:E:14:ALA:HB1	2:E:327:ARG:HD2	1.99	0.44
2:E:362:MET:HB2	2:E:375:LEU:HD11	2.00	0.44
2:E:5:TYR:N	2:E:1041:THR:O	2.50	0.44
2:E:220:ILE:HG23	2:E:261:HIS:CE1	2.52	0.44
1:A:208:PHE:HZ	1:A:231:LYS:HB2	1.83	0.44
3:C:428:HIS:CE1	3:C:432:HIS:CE1	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:102:THR:OG1	2:B:1065:VAL:O	2.36	0.43
1:D:288:LEU:HD23	1:D:288:LEU:HA	1.88	0.43
1:A:241:PRO:HB3	2:B:812:TYR:OH	2.19	0.43
2:B:386:SER:HA	2:B:717:LEU:HD12	1.99	0.43
2:B:286:GLU:OE2	2:B:301:ARG:NH1	2.51	0.43
2:E:140:PHE:HB2	2:E:159:LEU:HD11	1.99	0.43
1:A:164:ARG:NE	1:A:282:TYR:OH	2.41	0.43
1:D:326:CYS:HB3	1:D:394:CYS:HB3	1.99	0.43
2:E:291:MET:HA	2:E:291:MET:HE2	2.00	0.43
2:B:1002:GLU:HG3	2:B:1036:MET:HE3	2.00	0.43
2:E:284:LEU:HB2	2:E:301:ARG:HG2	2.01	0.43
2:B:722:ARG:HG3	2:B:789:HIS:CE1	2.53	0.43
2:B:126:PRO:HD3	2:B:169:PHE:HB3	2.00	0.43
1:D:398:ILE:HD13	1:D:398:ILE:HA	1.86	0.43
2:B:147:ARG:NE	2:B:147:ARG:HA	2.34	0.43
2:E:263:ARG:HG3	2:E:271:TYR:CE1	2.53	0.43
2:E:921:ILE:HB	2:E:933:LEU:HB2	2.01	0.43
2:B:271:TYR:HB2	2:B:283:LEU:HB3	2.01	0.42
2:E:845:GLN:HA	2:E:867:LYS:HA	2.01	0.42
2:B:722:ARG:HG3	2:B:789:HIS:HE1	1.84	0.42
2:E:376:VAL:HG13	2:E:389:ILE:HG13	2.01	0.42
3:F:436:LYS:HE2	3:F:436:LYS:HB2	1.59	0.42
1:A:397:HIS:HB2	3:C:432:HIS:HE1	1.85	0.42
2:B:977:CYS:HA	2:B:994:GLU:HA	2.02	0.42
1:D:241:PRO:HB3	2:E:812:TYR:OH	2.20	0.42
2:E:215:GLU:OE1	2:E:234:GLN:NE2	2.53	0.42
1:A:110:VAL:O	1:A:114:ILE:HG13	2.20	0.42
2:B:849:VAL:HG22	2:B:863:GLU:HB2	2.01	0.42
2:E:378:CYS:HB3	2:E:721:PRO:HG2	2.02	0.41
1:A:110:VAL:HG11	1:A:157:VAL:HG21	2.02	0.41
1:D:211:LYS:HA	1:D:212:PRO:HD3	1.95	0.41
2:E:290:GLN:HB2	2:E:294:THR:O	2.20	0.41
2:B:875:GLU:OE2	2:B:878:GLY:N	2.44	0.41
2:E:969:GLU:HG2	2:E:975:PHE:HD2	1.84	0.41
2:B:879:LYS:HD3	2:B:879:LYS:HA	1.87	0.41
1:D:346:MET:HE3	1:D:358:GLU:HB3	2.02	0.41
2:E:134:ARG:NH1	2:E:164:VAL:HG13	2.36	0.41
2:E:1000:LEU:HD11	2:E:1036:MET:HE1	2.00	0.41
2:E:366:ASP:N	2:E:366:ASP:OD1	2.52	0.41
2:B:64:MET:HG3	2:B:77:LEU:HD11	2.02	0.41
2:B:328:LEU:HA	2:B:358:PRO:HD3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:290:ILE:HD12	1:D:294:LEU:HB3	2.02	0.41
2:E:43:VAL:HG23	2:E:52:VAL:HG21	2.02	0.41
2:E:192:THR:HG22	2:E:207:TRP:O	2.21	0.41
2:E:282:MET:HE2	2:E:305:LEU:HD11	2.03	0.41
1:A:91:LEU:HD22	1:A:122:VAL:HG21	2.03	0.41
2:B:190:VAL:HG13	2:B:209:GLN:HB3	2.02	0.41
2:E:207:TRP:HB3	2:E:242:GLY:HA2	2.04	0.41
2:E:361:ASP:HA	2:E:1006:VAL:HG11	2.03	0.41
2:E:795:ASP:HB2	2:E:802:LEU:HD11	2.02	0.41
1:D:323:CYS:HB2	1:D:326:CYS:SG	2.60	0.40
2:E:385:GLY:HA3	2:E:719:GLU:O	2.21	0.40
2:B:77:LEU:HB3	2:B:89:LEU:HB2	2.04	0.40
1:A:241:PRO:HB3	2:B:812:TYR:CZ	2.56	0.40
2:B:358:PRO:HD2	2:B:380:GLY:HA2	2.04	0.40
1:D:204:LYS:HE2	1:D:204:LYS:HB3	1.98	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	326/373 (87%)	297 (91%)	29 (9%)	0	100	100
1	D	343/373 (92%)	312 (91%)	27 (8%)	4 (1%)	10	37
2	B	775/836 (93%)	697 (90%)	72 (9%)	6 (1%)	16	47
2	E	785/836 (94%)	703 (90%)	77 (10%)	5 (1%)	21	52
3	C	52/86 (60%)	40 (77%)	9 (17%)	3 (6%)	1	8
3	F	54/86 (63%)	44 (82%)	7 (13%)	3 (6%)	1	8
All	All	2335/2590 (90%)	2093 (90%)	221 (10%)	21 (1%)	14	44

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	768	SER
3	C	405	THR
3	F	433	PRO
3	C	433	PRO
1	D	268	LEU
1	D	414	PHE
2	B	862	ALA
1	D	413	LYS
3	F	409	PRO
3	C	409	PRO
2	E	862	ALA
2	E	970	ASN
2	B	264	VAL
2	B	970	ASN
2	E	951	PRO
3	F	434	GLN
2	B	951	PRO
2	E	264	VAL
1	D	427	PRO
2	E	1013	VAL
2	B	310	ILE

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	234/340 (69%)	234 (100%)	0	100	100
1	D	231/340 (68%)	231 (100%)	0	100	100
2	B	509/727 (70%)	509 (100%)	0	100	100
2	E	533/727 (73%)	533 (100%)	0	100	100
3	C	39/74 (53%)	38 (97%)	1 (3%)	40	68
3	F	32/74 (43%)	29 (91%)	3 (9%)	8	31
All	All	1578/2282 (69%)	1574 (100%)	4 (0%)	86	87

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	432	HIS
3	F	432	HIS
3	F	435	VAL
3	F	436	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	100	GLN
1	A	378	HIS
2	B	149	ASN
2	B	234	GLN
2	B	267	ASN
2	B	797	HIS
2	B	905	HIS
2	B	1034	ASN
1	D	198	GLN
1	D	206	GLN
2	E	203	ASN
2	E	267	ASN
2	E	796	GLN
2	E	905	HIS
2	E	1059	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 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	$\# Z > 2$
5	Y70	A	502	-	22,22,22	0.27	0	31,33,33	0.84	1 (3%)
5	Y70	D	502	-	22,22,22	0.26	0	31,33,33	0.93	1 (3%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	Y70	A	502	-	-	1/4/33/33	0/3/3/3
5	Y70	D	502	-	-	0/4/33/33	0/3/3/3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
5	D	502	Y70	C15-C12-N8	4.65	113.23	109.08
5	A	502	Y70	C15-C12-N8	4.03	112.68	109.08

There are no chirality outliers.

All (1) torsion outliers are listed below:

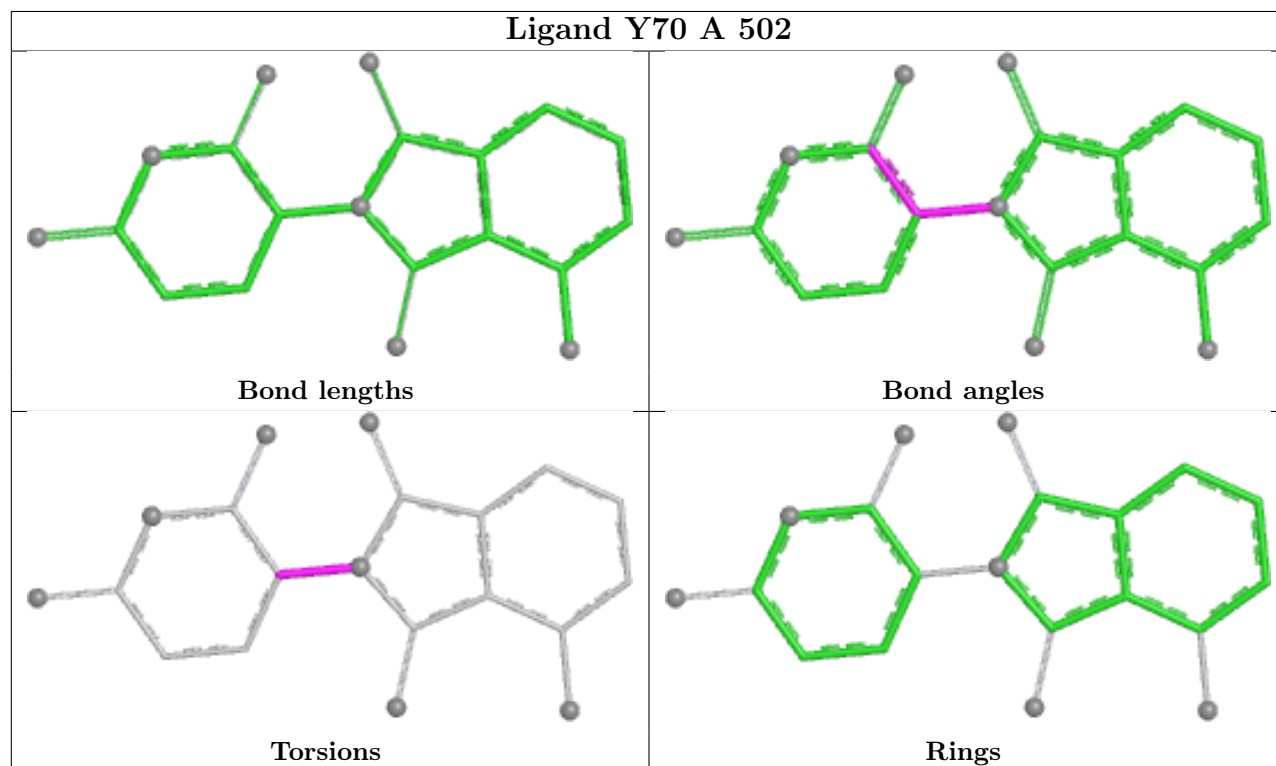
Mol	Chain	Res	Type	Atoms
5	A	502	Y70	C14-C12-N8-C9

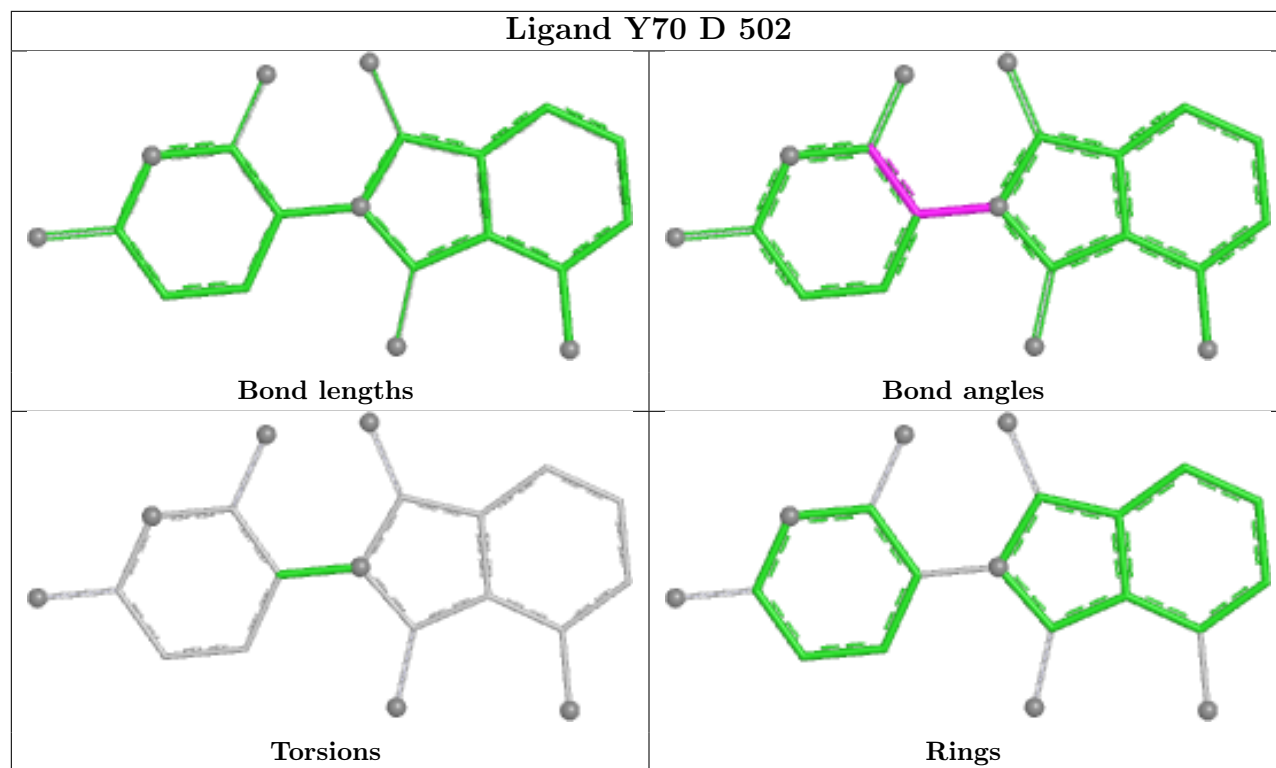
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	336/373 (90%)	0.24	6 (1%) 67 47	72, 115, 177, 228	0
1	D	349/373 (93%)	0.28	8 (2%) 61 39	62, 115, 178, 249	0
2	B	787/836 (94%)	0.33	35 (4%) 39 21	62, 126, 190, 246	0
2	E	797/836 (95%)	0.21	15 (1%) 66 45	63, 114, 177, 226	0
3	C	54/86 (62%)	0.14	1 (1%) 66 45	123, 136, 176, 248	0
3	F	56/86 (65%)	0.53	5 (8%) 15 8	109, 158, 212, 279	0
All	All	2379/2590 (91%)	0.27	70 (2%) 53 32	62, 121, 184, 279	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	882	ALA	8.6
1	A	357	HIS	5.1
2	B	858	LEU	4.7
2	B	975	PHE	4.5
2	B	390	ILE	4.4
2	B	9	ALA	4.3
1	D	220	SER	4.0
2	B	977	CYS	4.0
2	E	313	CYS	3.7
3	F	433	PRO	3.6
1	A	270	ASP	3.6
2	B	1023	PRO	3.6
2	B	1099	ASP	3.5
1	D	398	ILE	3.5
1	A	398	ILE	3.3
2	B	930	VAL	3.3
2	B	372	GLN	3.1
1	D	395	ALA	3.1
2	B	377	THR	3.1

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Mol	Chain	Res	Type	RSRZ
2	B	969	GLU	3.1
2	E	1077	HIS	3.0
2	B	971	ALA	3.0
2	E	300	LEU	2.9
3	F	386	TYR	2.9
2	B	1007	PHE	2.9
2	B	374	GLN	2.9
2	E	971	ALA	2.9
3	F	409	PRO	2.8
2	B	225	PRO	2.8
2	E	1079	GLU	2.8
2	E	61	ILE	2.8
3	F	427	VAL	2.7
2	B	131	ILE	2.7
2	E	9	ALA	2.5
2	B	224	GLU	2.5
1	A	90	ILE	2.4
2	B	746	SER	2.4
2	B	929	SER	2.4
3	F	435	VAL	2.4
2	B	949	PHE	2.4
2	E	310	ILE	2.3
3	C	434	GLN	2.3
2	E	3	TYR	2.3
2	E	871	TYR	2.3
2	B	915	LYS	2.3
2	B	814	LEU	2.3
2	B	130	MET	2.3
1	A	97	LEU	2.3
2	B	1012	LEU	2.3
2	E	131	ILE	2.2
2	E	794	ILE	2.2
2	B	375	LEU	2.2
1	D	428	ASP	2.2
2	B	864	LYS	2.2
2	B	921	ILE	2.2
2	B	736	LEU	2.1
1	D	123	LEU	2.1
1	A	421	ALA	2.1
2	B	173	CYS	2.1
1	D	252	THR	2.1
2	B	172	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
2	E	969	GLU	2.1
2	B	376	VAL	2.1
2	B	46	ALA	2.1
1	D	417	LEU	2.1
1	D	125	TYR	2.1
2	B	128	CYS	2.1
2	E	1080	ARG	2.0
2	E	1048	TYR	2.0
2	B	881	LEU	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](#)

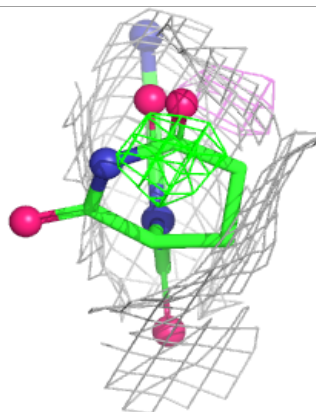
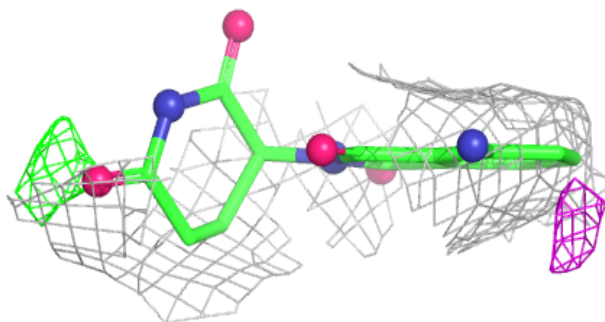
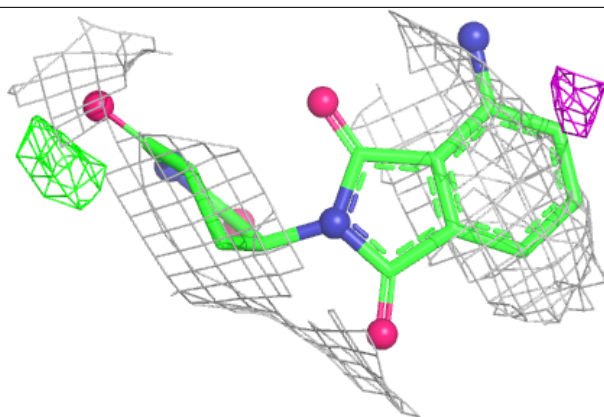
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	Y70	D	502	20/20	0.81	0.12	93,118,122,126	0
4	ZN	F	501	1/1	0.86	0.12	143,143,143,143	0
5	Y70	A	502	20/20	0.88	0.12	100,111,139,157	0
4	ZN	F	502	1/1	0.90	0.09	140,140,140,140	0
4	ZN	D	501	1/1	0.93	0.06	139,139,139,139	0
4	ZN	C	502	1/1	0.95	0.05	105,105,105,105	0
4	ZN	A	501	1/1	0.96	0.05	121,121,121,121	0
4	ZN	C	501	1/1	0.98	0.04	129,129,129,129	0

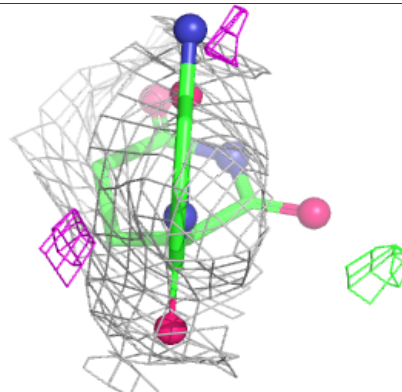
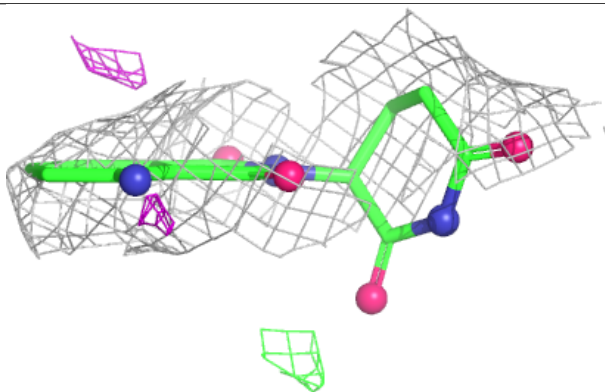
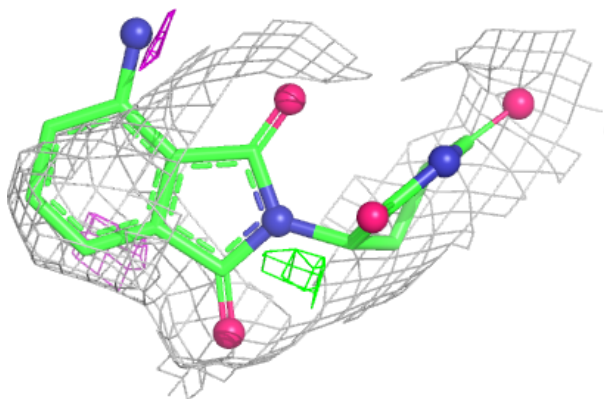
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Y70 D 502:

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

**Electron density around Y70 A 502:**

$2mF_o-DF_c$ (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.