



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 03:30 PM UTC

PDB ID : 8OIZ / pdb_00008oiz
Title : Crystal structure of human CRBN-DDB1 in complex with Pomalidomide
Authors : Le Bihan, Y.-V.; Cabry, M.P.; van Montfort, R.L.M.
Deposited on : 2023-03-23
Resolution : 2.50 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

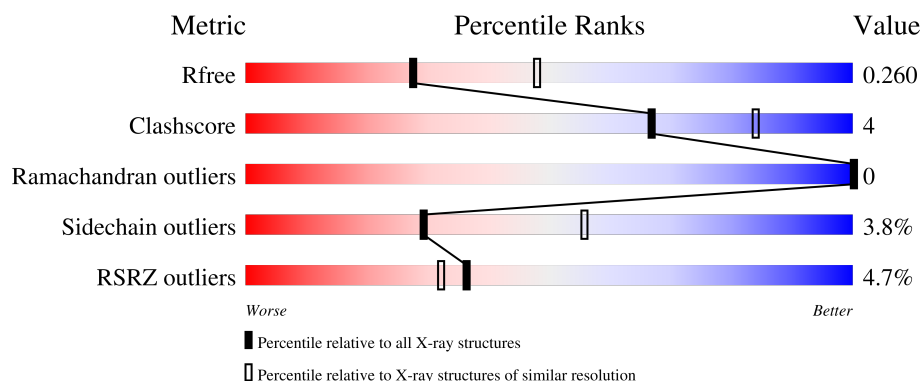
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	1148	4% 85% 12% .
2	B	407	5% 83% 10% 7%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 11765 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 DNA damage-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1116	Total	C	N	O	S	6	7	1
			8329	5313	1382	1586	48			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1141	TRP	-	expression tag	UNP Q16531
A	1142	SER	-	expression tag	UNP Q16531
A	1143	HIS	-	expression tag	UNP Q16531
A	1144	PRO	-	expression tag	UNP Q16531
A	1145	GLN	-	expression tag	UNP Q16531
A	1146	PHE	-	expression tag	UNP Q16531
A	1147	GLU	-	expression tag	UNP Q16531
A	1148	LYS	-	expression tag	UNP Q16531

- Molecule 2 is a protein called Protein cereblon.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	379	Total	C	N	O	S	0	3	0
			2900	1865	480	530	25			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	36	GLY	-	expression tag	UNP Q96SW2
B	37	PRO	-	expression tag	UNP Q96SW2
B	38	HIS	-	expression tag	UNP Q96SW2
B	39	MET	-	expression tag	UNP Q96SW2

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).

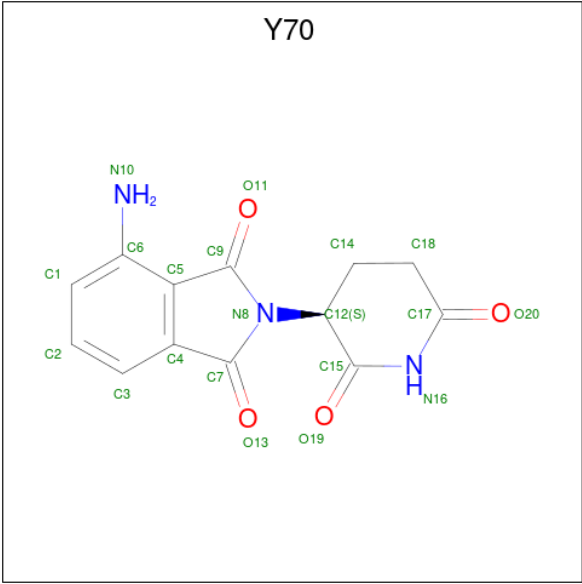


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Zn	0	0
			1	1		

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



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

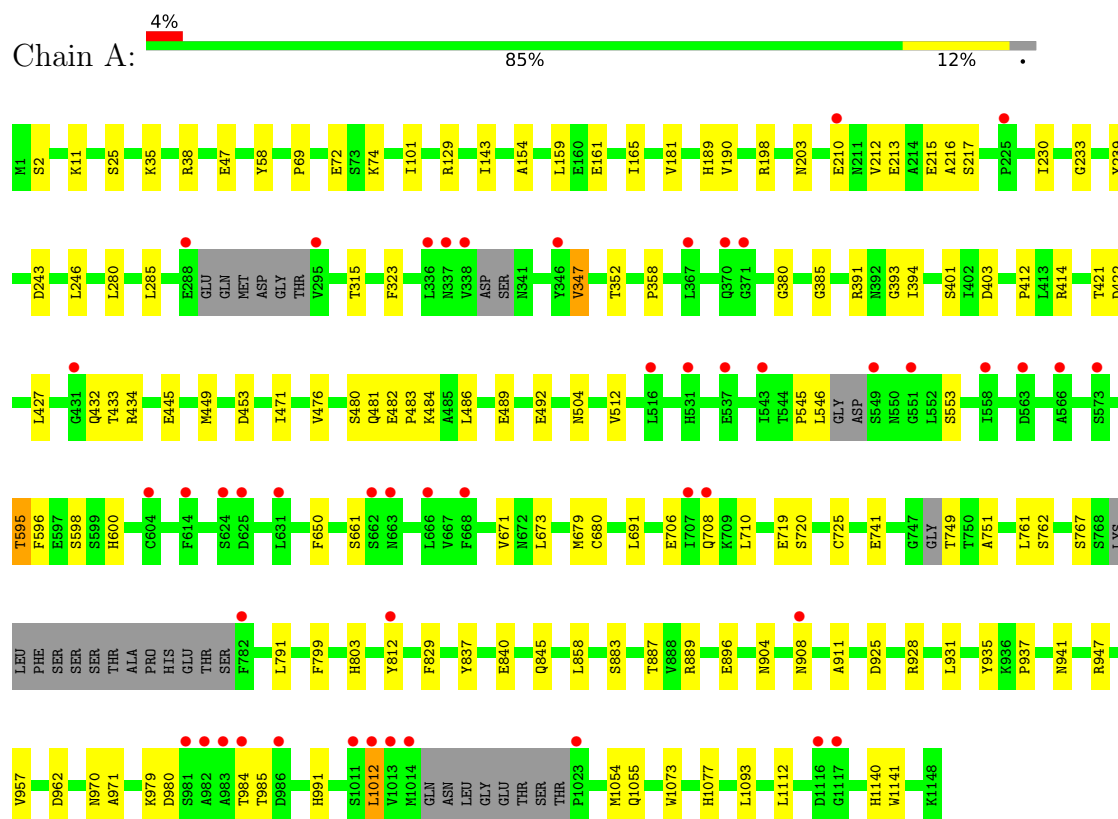
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	377	Total	O	0	3
			379	379		
6	B	112	Total	O	0	0
			112	112		

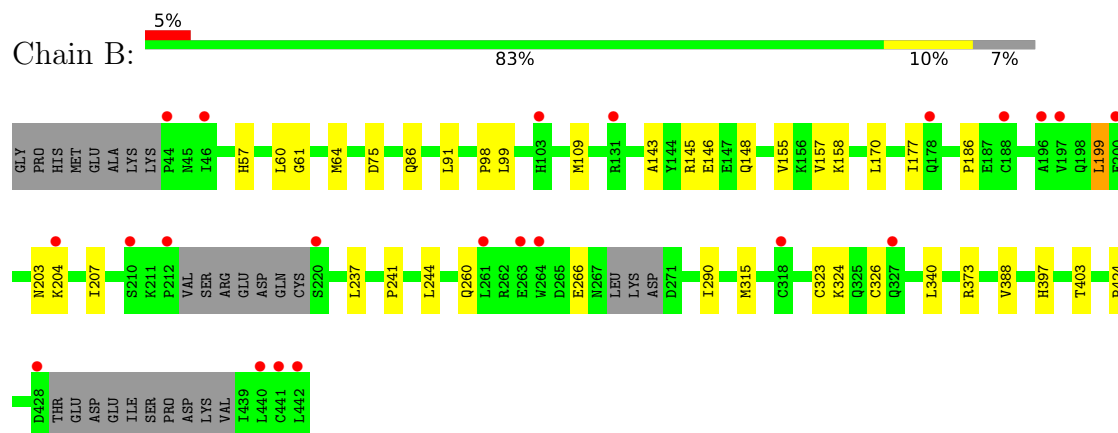
3 Residue-property plots [i](#)

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: DNA damage-binding protein 1



- Molecule 2: Protein cereblon



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	71.84Å 128.51Å 198.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.59 – 2.50 49.59 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.59-2.50) 100.0 (49.59-2.50)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 2.51Å)	Xtriage
Refinement program	BUSTER 2.10.4 (17-FEB-2023)	Depositor
R, R_{free}	0.213 , 0.262 0.208 , 0.260	Depositor DCC
R_{free} test set	3287 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	55.7	Xtriage
Anisotropy	0.425	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 69.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11765	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.76% 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: Y70, ZN, EDO

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	0.69	0/8487	1.01	10/11516 (0.1%)
2	B	0.64	0/2972	0.96	0/4045
All	All	0.68	0/11459	1.00	10/15561 (0.1%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	453	ASP	CA-C-N	8.08	131.45	120.54
1	A	453	ASP	C-N-CA	8.08	131.45	120.54
1	A	980	ASP	N-CA-C	7.38	121.10	110.10
1	A	1077	HIS	N-CA-C	6.41	119.96	109.06
1	A	720	SER	N-CA-C	6.07	117.68	109.24
1	A	481	GLN	N-CA-C	5.70	117.29	111.14
1	A	403	ASP	CA-CB-CG	5.54	118.14	112.60
1	A	925	ASP	CA-CB-CG	5.23	117.83	112.60
1	A	504	ASN	CA-CB-CG	5.19	117.79	112.60
1	A	799	PHE	CA-CB-CG	-5.08	108.72	113.80

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	8329	0	7749	64	0
2	B	2900	0	2661	19	0
3	A	24	0	36	1	0
4	B	1	0	0	0	0
5	B	20	0	11	0	0
6	A	379	0	0	3	0
6	B	112	0	0	0	0
All	All	11765	0	10457	80	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 4.

All (80) 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:A:69:PRO:HG2	1:A:72:GLU:HG3	1.52	0.90
1:A:908:ASN:HD21	1:A:947:ARG:HH12	1.19	0.86
1:A:596:PHE:HB3	1:A:661:SER:HB2	1.57	0.84
1:A:545:PRO:HA	1:A:553:SER:HB2	1.65	0.75
1:A:47:GLU:H	1:A:47:GLU:CD	2.00	0.70
1:A:984:THR:HG23	1:A:985:THR:HG22	1.79	0.65
1:A:449:MET:HG2	1:A:484:LYS:O	1.97	0.64
1:A:812:TYR:CZ	2:B:241:PRO:HB3	2.32	0.64
1:A:35:LYS:NZ	6:A:1301:HOH:O	2.31	0.63
1:A:217:SER:HB2	2:B:204:LYS:HB2	1.80	0.63
1:A:482:GLU:CB	1:A:483:PRO:HD3	2.29	0.62
1:A:1012:LEU:HD23	1:A:1140:HIS:HA	1.80	0.62
2:B:146:GLU:OE2	2:B:148:GLN:NE2	2.33	0.62
2:B:143:ALA:HB3	2:B:158:LYS:HB2	1.82	0.61
1:A:545:PRO:CA	1:A:553:SER:HB2	2.31	0.61
1:A:181:VAL:HG22	1:A:190:VAL:HG22	1.84	0.60
1:A:908:ASN:HD21	1:A:947:ARG:NH1	1.96	0.59
1:A:595:THR:HG22	1:A:600:HIS:CD2	2.38	0.58
1:A:239:TYR:HB3	1:A:246:LEU:HB2	1.85	0.58
1:A:1055:GLN:HG2	1:A:1093:LEU:HD23	1.86	0.58
2:B:60:LEU:HD13	2:B:64:MET:HE1	1.87	0.57
1:A:840:GLU:HG3	6:A:1385:HOH:O	2.06	0.56
1:A:837:TYR:HB2	1:A:840:GLU:HG2	1.87	0.56
1:A:280:LEU:HD23	1:A:347:VAL:HG21	1.88	0.55
1:A:11:LYS:HD3	1:A:38:ARG:HD2	1.88	0.55
2:B:75:ASP:HB3	2:B:186:PRO:HB3	1.87	0.55
1:A:165:ILE:HG13	2:B:207:ILE:HD12	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:290:ILE:HA	2:B:424:PRO:HG3	1.90	0.53
1:A:434:ARG:HD3	1:A:445:GLU:OE1	2.08	0.53
1:A:546:LEU:HD22	1:A:595:THR:HG23	1.91	0.53
1:A:471:ILE:HG12	1:A:476:VAL:HG13	1.89	0.52
2:B:260:GLN:HB2	2:B:315:MET:HE3	1.91	0.51
1:A:358:PRO:HD2	1:A:380:GLY:HA2	1.93	0.51
1:A:161:GLU:HA	3:A:1205:EDO:H11	1.92	0.51
1:A:791:LEU:HD23	1:A:858:LEU:HD21	1.94	0.49
1:A:315:THR:HG22	1:A:323:PHE:HB3	1.95	0.49
1:A:393:GLY:HA2	1:A:708:GLN:HE21	1.77	0.49
1:A:595:THR:CG2	1:A:600:HIS:CD2	2.96	0.49
2:B:61:GLY:HA3	2:B:145:ARG:NH2	2.26	0.49
1:A:480:SER:HB2	1:A:483:PRO:HD2	1.94	0.49
1:A:143:ILE:HG12	1:A:154:ALA:HB2	1.95	0.49
1:A:25:SER:HA	1:A:74:LYS:HD3	1.95	0.48
1:A:725[A]:CYS:SG	1:A:829:PHE:CE1	3.06	0.48
1:A:414:ARG:HG2	1:A:422:ASP:HA	1.96	0.48
1:A:492:GLU:HG3	1:A:512:VAL:HG21	1.95	0.48
2:B:199:LEU:HD13	2:B:237:LEU:HD11	1.96	0.48
1:A:889:ARG:HE	1:A:904:ASN:HD21	1.62	0.48
1:A:962:ASP:O	1:A:979:LYS:NZ	2.46	0.47
1:A:213:GLU:OE2	1:A:215:GLU:HB2	2.15	0.47
2:B:146:GLU:HG2	2:B:155:VAL:HG22	1.97	0.47
1:A:883:SER:HB2	1:A:911:ALA:CB	2.45	0.46
1:A:883:SER:HB2	1:A:911:ALA:HB3	1.95	0.46
1:A:984:THR:HG23	1:A:985:THR:N	2.30	0.46
1:A:216:ALA:HA	1:A:233:GLY:HA2	1.97	0.46
1:A:725[A]:CYS:SG	1:A:829:PHE:HE1	2.38	0.46
1:A:47:GLU:CD	1:A:47:GLU:N	2.73	0.45
1:A:189:HIS:HB3	1:A:210:GLU:HA	1.98	0.45
1:A:710:LEU:HD21	1:A:1141:TRP:CD2	2.51	0.45
1:A:412:PRO:HD3	1:A:680:CYS:HB2	1.98	0.45
1:A:190:VAL:HG23	1:A:212:VAL:HG11	1.99	0.44
1:A:979:LYS:HA	6:A:1302:HOH:O	2.16	0.44
1:A:432:GLN:HG2	1:A:433:THR:N	2.32	0.44
1:A:762:SER:O	1:A:803:HIS:HA	2.18	0.43
1:A:385:GLY:HA3	1:A:719:GLU:O	2.18	0.43
1:A:671:VAL:HG12	1:A:673:LEU:HB2	2.00	0.43
2:B:323:CYS:HB3	2:B:326:CYS:HB2	2.01	0.43
1:A:970:ASN:HA	1:A:971:ALA:HA	1.85	0.42
1:A:58:TYR:HB3	1:A:1073:TRP:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:486:LEU:HD21	1:A:489:GLU:HB2	2.01	0.42
2:B:109:MET:HE2	2:B:177:ILE:CG2	2.49	0.42
2:B:99:LEU:HB2	2:B:157:VAL:HG22	2.02	0.41
1:A:1054:MET:HG3	1:A:1112:LEU:HD11	2.01	0.41
2:B:57:HIS:CE1	2:B:98:PRO:HG3	2.55	0.41
2:B:60:LEU:HD23	2:B:60:LEU:HA	1.80	0.41
2:B:109:MET:HE2	2:B:177:ILE:HG23	2.02	0.41
1:A:650:PHE:CD1	1:A:679:MET:HG2	2.55	0.41
1:A:230:ILE:HD11	1:A:285:LEU:HD21	2.03	0.41
2:B:388:VAL:HG13	2:B:397:HIS:HD2	1.86	0.40
1:A:741:GLU:HG2	1:A:751:ALA:HA	2.04	0.40
1:A:935:TYR:O	1:A:937:PRO:HD3	2.21	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	1109/1148 (97%)	1066 (96%)	43 (4%)	0	100	100
2	B	374/407 (92%)	366 (98%)	8 (2%)	0	100	100
All	All	1483/1555 (95%)	1432 (97%)	51 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	812/1007 (81%)	782 (96%)	30 (4%)	30	57
2	B	279/369 (76%)	268 (96%)	11 (4%)	28	55
All	All	1091/1376 (79%)	1050 (96%)	41 (4%)	29	56

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	101	ILE
1	A	129	ARG
1	A	159	LEU
1	A	198	ARG
1	A	203	ASN
1	A	243	ASP
1	A	347	VAL
1	A	352	THR
1	A	391	ARG
1	A	394	ILE
1	A	401	SER
1	A	421	THR
1	A	427	LEU
1	A	595	THR
1	A	598	SER
1	A	691	LEU
1	A	706	GLU
1	A	749	THR
1	A	761	LEU
1	A	767	SER
1	A	845	GLN
1	A	887	THR
1	A	896	GLU
1	A	928	ARG
1	A	931	LEU
1	A	941	ASN
1	A	957	VAL
1	A	991	HIS
1	A	1012	LEU
2	B	86	GLN
2	B	91	LEU
2	B	170	LEU
2	B	199	LEU

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Mol	Chain	Res	Type
2	B	203	ASN
2	B	244	LEU
2	B	266	GLU
2	B	324	LYS
2	B	340	LEU
2	B	373	ARG
2	B	403	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	105	HIS
1	A	203	ASN
1	A	255	GLN
1	A	455	GLN
1	A	456	GLN
1	A	600	HIS
1	A	648	ASN
1	A	677	ASN
1	A	696	ASN
1	A	790	ASN
1	A	904	ASN
1	A	907	ASN
1	A	908	ASN
1	A	978	GLN
1	A	1056	ASN
1	A	1059	ASN
2	B	68	HIS
2	B	86	GLN
2	B	203	ASN
2	B	260	GLN
2	B	316	ASN
2	B	397	HIS

5.3.3 RNA ⓘ

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, 1 is monoatomic - leaving 7 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	$\# Z > 2$
3	EDO	A	1201	-	3,3,3	0.25	0	2,2,2	0.10	0
3	EDO	A	1205	-	3,3,3	0.33	0	2,2,2	0.15	0
3	EDO	A	1204	-	3,3,3	0.38	0	2,2,2	0.24	0
5	Y70	B	502	-	22,22,22	0.41	0	31,33,33	0.62	2 (6%)
3	EDO	A	1202	-	3,3,3	0.27	0	2,2,2	0.28	0
3	EDO	A	1206	-	3,3,3	0.43	0	2,2,2	0.09	0
3	EDO	A	1203	-	3,3,3	0.18	0	2,2,2	0.35	0

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
3	EDO	A	1201	-	-	1/1/1/1	-
3	EDO	A	1205	-	-	1/1/1/1	-
3	EDO	A	1204	-	-	0/1/1/1	-
5	Y70	B	502	-	-	0/4/33/33	0/3/3/3
3	EDO	A	1202	-	-	0/1/1/1	-
3	EDO	A	1206	-	-	1/1/1/1	-
3	EDO	A	1203	-	-	1/1/1/1	-

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	B	502	Y70	C14-C12-N8	-2.21	108.68	113.60
5	B	502	Y70	C15-C12-N8	2.10	110.95	109.08

There are no chirality outliers.

All (4) torsion outliers are listed below:

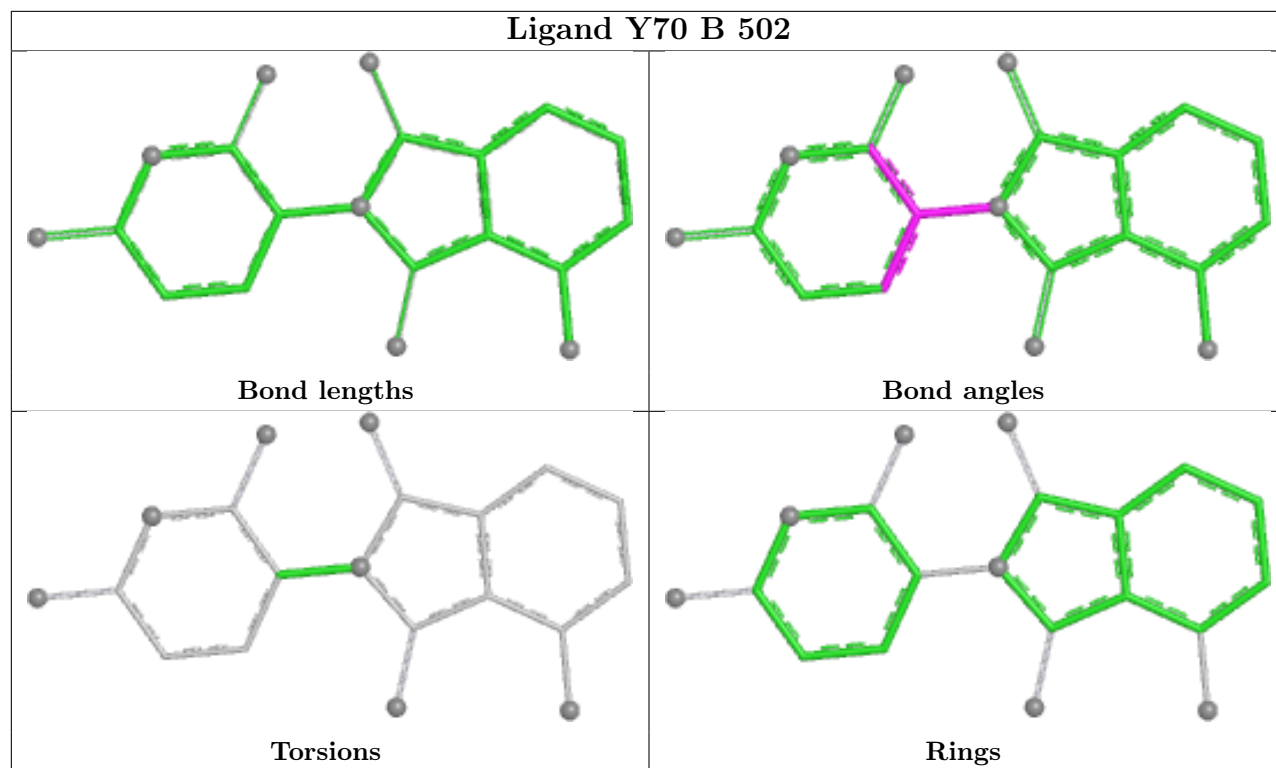
Mol	Chain	Res	Type	Atoms
3	A	1206	EDO	O1-C1-C2-O2
3	A	1203	EDO	O1-C1-C2-O2
3	A	1205	EDO	O1-C1-C2-O2
3	A	1201	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1205	EDO	1	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.



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	1115/1148 (97%)	0.34	48 (4%) 40 35	24, 61, 116, 129	9 (0%)
2	B	379/407 (93%)	0.39	22 (5%) 29 25	27, 67, 97, 131	3 (0%)
All	All	1494/1555 (96%)	0.35	70 (4%) 36 32	24, 62, 112, 131	12 (0%)

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	782	PHE	7.7
1	A	531[A]	HIS	4.4
1	A	1023	PRO	4.4
1	A	338	VAL	4.2
1	A	1011	SER	3.9
1	A	908	ASN	3.9
1	A	1012	LEU	3.9
2	B	442	LEU	3.8
1	A	983	ALA	3.8
1	A	295	VAL	3.2
2	B	440	LEU	3.2
1	A	371	GLY	3.2
2	B	428	ASP	3.1
1	A	288	GLU	3.0
2	B	318	CYS	2.9
1	A	225	PRO	2.9
2	B	263	GLU	2.8
2	B	131	ARG	2.8
2	B	220	SER	2.8
1	A	516	LEU	2.8
1	A	370	GLN	2.8
2	B	327	GLN	2.7
1	A	367	LEU	2.7
2	B	44	PRO	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	662	SER	2.6
1	A	566	ALA	2.5
2	B	210	SER	2.5
2	B	441	CYS	2.5
1	A	625	ASP	2.5
1	A	1013	VAL	2.5
1	A	984	THR	2.5
2	B	197	VAL	2.5
1	A	431	GLY	2.4
1	A	543	ILE	2.4
1	A	707	ILE	2.4
2	B	46	ILE	2.4
1	A	210	GLU	2.4
1	A	624	SER	2.4
1	A	346	TYR	2.4
1	A	663	ASN	2.3
2	B	212	PRO	2.3
2	B	204	LYS	2.3
1	A	1014	MET	2.3
1	A	563	ASP	2.3
1	A	812	TYR	2.3
1	A	708	GLN	2.2
2	B	103[A]	HIS	2.2
2	B	200	GLU	2.2
2	B	261	LEU	2.2
1	A	981	SER	2.2
1	A	986	ASP	2.2
1	A	337	ASN	2.2
1	A	604	CYS	2.2
1	A	1117	GLY	2.2
1	A	537	GLU	2.2
1	A	573	SER	2.2
1	A	631	LEU	2.1
1	A	614	PHE	2.1
2	B	264	TRP	2.1
1	A	558	ILE	2.1
1	A	549	SER	2.1
2	B	196	ALA	2.1
2	B	188	CYS	2.1
2	B	178	GLN	2.1
1	A	982	ALA	2.1
1	A	668	PHE	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	336	LEU	2.0
1	A	666	LEU	2.0
1	A	551	GLY	2.0
1	A	1116	ASP	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](#)

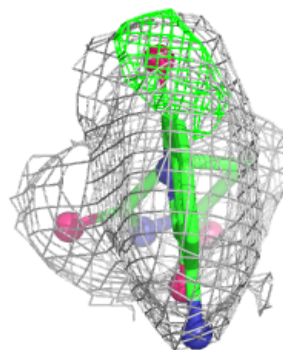
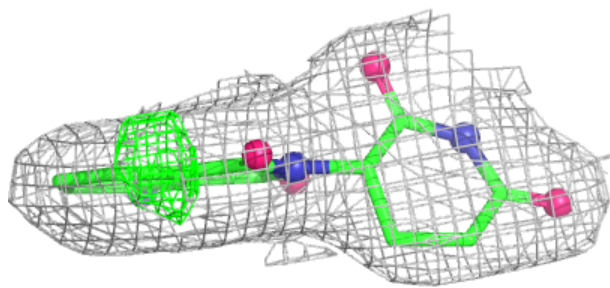
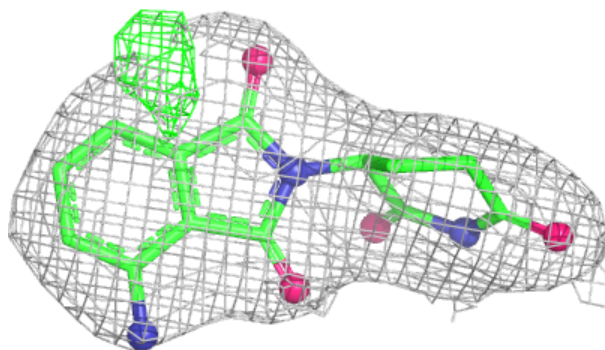
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	EDO	A	1206	4/4	0.81	0.14	65,65,65,65	0
3	EDO	A	1204	4/4	0.83	0.20	76,76,77,77	0
3	EDO	A	1205	4/4	0.85	0.16	71,71,71,71	0
3	EDO	A	1201	4/4	0.89	0.17	56,57,58,58	0
5	Y70	B	502	20/20	0.92	0.09	48,51,51,51	0
3	EDO	A	1203	4/4	0.95	0.09	59,59,59,59	0
3	EDO	A	1202	4/4	0.97	0.06	47,47,48,48	0
4	ZN	B	501	1/1	1.00	0.04	62,62,62,62	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 B 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.