



wwPDB X-ray Structure Validation Summary Report ⓘ

May 13, 2020 – 09:36 pm BST

PDB ID : 6NJH
Title : Crystal Structure of the PDE4D Catalytic Domain and UCR2 Regulatory Helix with T-48
Authors : Fox III, D.; Fairman, J.W.; Gurney, M.E.
Deposited on : 2019-01-03
Resolution : 2.15 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

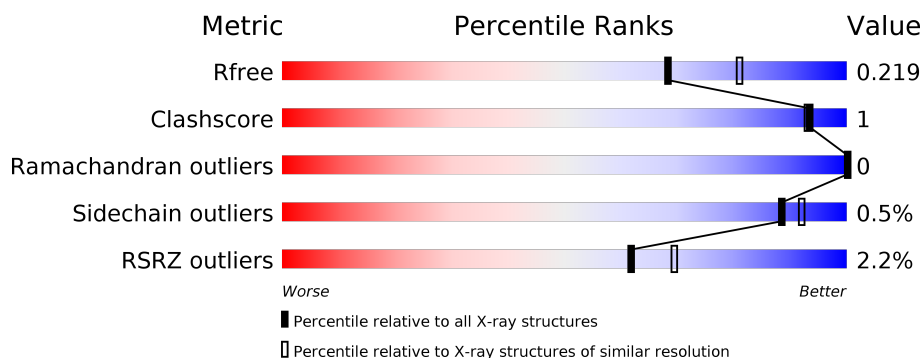
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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	370	<div> <div>2%</div> <div> <div></div> <div>85%</div> <div>5%</div> <div>10%</div> </div> </div>
1	B	370	<div> <div>2%</div> <div> <div></div> <div>87%</div> <div>•</div> <div>9%</div> </div> </div>
1	C	370	<div> <div>•</div> <div> <div></div> <div>88%</div> <div>•</div> <div>9%</div> </div> </div>
1	D	370	<div> <div>3%</div> <div> <div></div> <div>85%</div> <div>5%</div> <div>10%</div> </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11211 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called cAMP-specific 3',5'-cyclic phosphodiesterase 4D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	334	Total	C	N	O	S	0	2	0
			2652	1681	451	505	15			
1	B	335	Total	C	N	O	S	0	1	0
			2620	1663	442	500	15			
1	C	337	Total	C	N	O	S	0	3	0
			2639	1676	441	507	15			
1	D	333	Total	C	N	O	S	0	2	0
			2623	1663	446	499	15			

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	243	MET	-	expression tag	UNP Q08499
A	579	ALA	SER	engineered mutation	UNP Q08499
A	581	ALA	SER	engineered mutation	UNP Q08499
A	583	PRO	-	linker	UNP Q08499
A	584	LEU	-	linker	UNP Q08499
A	585	ASP	-	linker	UNP Q08499
A	586	GLU	-	linker	UNP Q08499
A	587	GLN	-	linker	UNP Q08499
A	588	ASN	-	linker	UNP Q08499
A	589	ARG	-	linker	UNP Q08499
A	590	ASP	-	linker	UNP Q08499
A	591	SER	-	linker	UNP Q08499
A	592	GLN	-	linker	UNP Q08499
A	607	GLU	-	expression tag	UNP Q08499
A	608	ASN	-	expression tag	UNP Q08499
A	609	LEU	-	expression tag	UNP Q08499
A	610	TYR	-	expression tag	UNP Q08499
A	611	PHE	-	expression tag	UNP Q08499
A	612	GLN	-	expression tag	UNP Q08499
B	243	MET	-	expression tag	UNP Q08499
B	579	ALA	SER	engineered mutation	UNP Q08499

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	581	ALA	SER	engineered mutation	UNP Q08499
B	583	PRO	-	linker	UNP Q08499
B	584	LEU	-	linker	UNP Q08499
B	585	ASP	-	linker	UNP Q08499
B	586	GLU	-	linker	UNP Q08499
B	587	GLN	-	linker	UNP Q08499
B	588	ASN	-	linker	UNP Q08499
B	589	ARG	-	linker	UNP Q08499
B	590	ASP	-	linker	UNP Q08499
B	591	SER	-	linker	UNP Q08499
B	592	GLN	-	linker	UNP Q08499
B	607	GLU	-	expression tag	UNP Q08499
B	608	ASN	-	expression tag	UNP Q08499
B	609	LEU	-	expression tag	UNP Q08499
B	610	TYR	-	expression tag	UNP Q08499
B	611	PHE	-	expression tag	UNP Q08499
B	612	GLN	-	expression tag	UNP Q08499
C	243	MET	-	expression tag	UNP Q08499
C	579	ALA	SER	engineered mutation	UNP Q08499
C	581	ALA	SER	engineered mutation	UNP Q08499
C	583	PRO	-	linker	UNP Q08499
C	584	LEU	-	linker	UNP Q08499
C	585	ASP	-	linker	UNP Q08499
C	586	GLU	-	linker	UNP Q08499
C	587	GLN	-	linker	UNP Q08499
C	588	ASN	-	linker	UNP Q08499
C	589	ARG	-	linker	UNP Q08499
C	590	ASP	-	linker	UNP Q08499
C	591	SER	-	linker	UNP Q08499
C	592	GLN	-	linker	UNP Q08499
C	607	GLU	-	expression tag	UNP Q08499
C	608	ASN	-	expression tag	UNP Q08499
C	609	LEU	-	expression tag	UNP Q08499
C	610	TYR	-	expression tag	UNP Q08499
C	611	PHE	-	expression tag	UNP Q08499
C	612	GLN	-	expression tag	UNP Q08499
D	243	MET	-	expression tag	UNP Q08499
D	579	ALA	SER	engineered mutation	UNP Q08499
D	581	ALA	SER	engineered mutation	UNP Q08499
D	583	PRO	-	linker	UNP Q08499
D	584	LEU	-	linker	UNP Q08499
D	585	ASP	-	linker	UNP Q08499

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	586	GLU	-	linker	UNP Q08499
D	587	GLN	-	linker	UNP Q08499
D	588	ASN	-	linker	UNP Q08499
D	589	ARG	-	linker	UNP Q08499
D	590	ASP	-	linker	UNP Q08499
D	591	SER	-	linker	UNP Q08499
D	592	GLN	-	linker	UNP Q08499
D	607	GLU	-	expression tag	UNP Q08499
D	608	ASN	-	expression tag	UNP Q08499
D	609	LEU	-	expression tag	UNP Q08499
D	610	TYR	-	expression tag	UNP Q08499
D	611	PHE	-	expression tag	UNP Q08499
D	612	GLN	-	expression tag	UNP Q08499

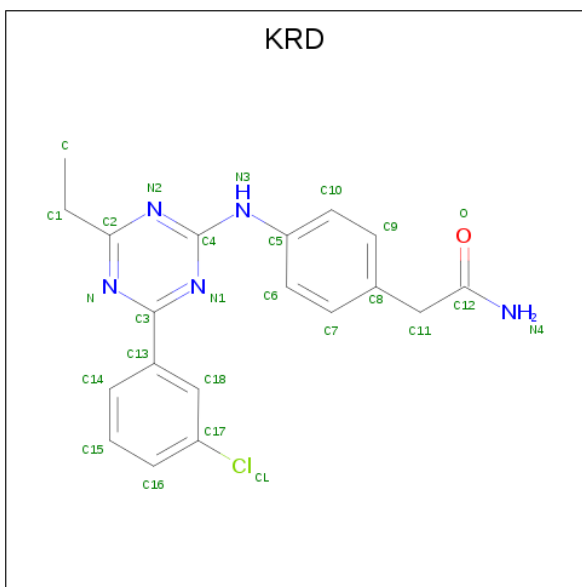
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 4 is 2-(4-([4-(3-chlorophenyl)-6-ethyl-1,3,5-triazin-2-yl]amino}phenyl)acetamide (three-letter code: KRD) (formula: C₁₉H₁₈ClN₅O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Cl	N	O	0	0
			26	19	1	5	1		
4	B	1	Total	C	Cl	N	O	0	0
			26	19	1	5	1		
4	C	1	Total	C	Cl	N	O	0	0
			26	19	1	5	1		
4	D	1	Total	C	Cl	N	O	0	0
			26	19	1	5	1		

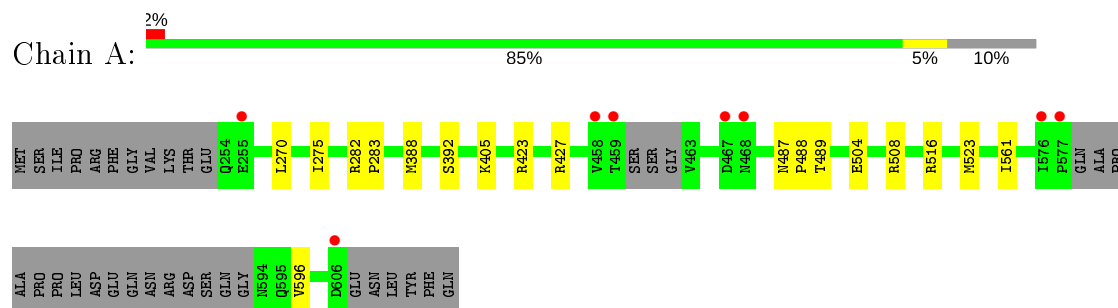
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	156	Total	O	0	0
			156	156		
5	B	129	Total	O	0	0
			129	129		
5	C	161	Total	O	0	0
			161	161		
5	D	117	Total	O	0	0
			117	117		

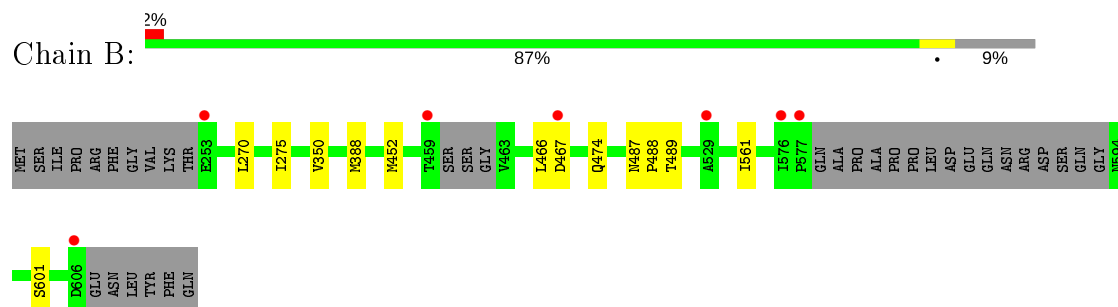
3 Residue-property plots [i](#)

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.

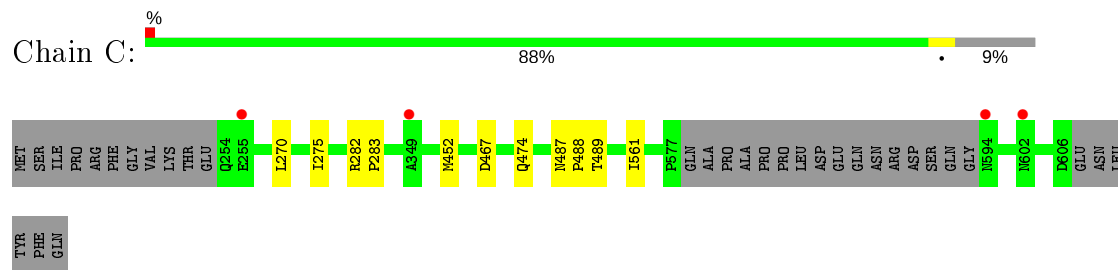
- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



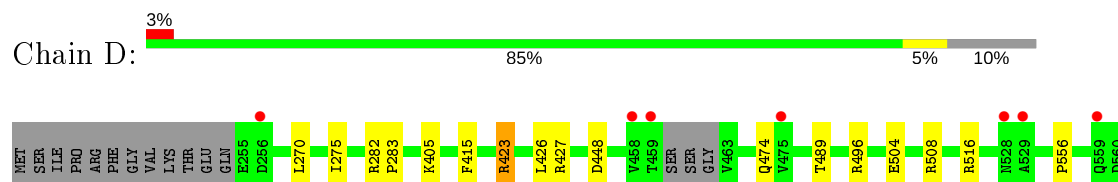
- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



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



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





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	81.64Å 82.07Å 116.53Å 90.00° 110.23° 90.00°	Depositor
Resolution (Å)	19.91 – 2.15 19.86 – 2.15	Depositor EDS
% Data completeness (in resolution range)	98.4 (19.91-2.15) 97.9 (19.86-2.15)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.74 (at 2.15Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.172 , 0.210 0.182 , 0.219	Depositor DCC
R_{free} test set	3879 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	24.3	Xtriage
Anisotropy	0.064	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 45.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11211	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 32.53 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 9.2553e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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, ZN, KRD

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	0.83	1/2709 (0.0%)	0.82	4/3692 (0.1%)
1	B	0.77	0/2674	0.78	1/3651 (0.0%)
1	C	0.83	0/2703	0.82	1/3692 (0.0%)
1	D	0.75	0/2683	0.82	5/3659 (0.1%)
All	All	0.80	1/10769 (0.0%)	0.81	11/14694 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	392	SER	CB-OG	-5.58	1.34	1.42

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	516	ARG	NE-CZ-NH1	-7.65	116.48	120.30
1	D	423	ARG	NE-CZ-NH2	-7.43	116.58	120.30
1	D	423	ARG	NE-CZ-NH1	6.82	123.71	120.30
1	A	427	ARG	NE-CZ-NH1	5.87	123.23	120.30
1	A	516	ARG	NE-CZ-NH2	5.66	123.13	120.30

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	2652	0	2533	8	0
1	B	2620	0	2471	7	0
1	C	2639	0	2491	5	0
1	D	2623	0	2483	7	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	2	0	0	0	0
4	A	26	0	0	1	0
4	B	26	0	0	0	0
4	C	26	0	0	1	0
4	D	26	0	0	1	0
5	A	156	0	0	0	0
5	B	129	0	0	0	0
5	C	161	0	0	0	0
5	D	117	0	0	1	0
All	All	11211	0	9978	28	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.

The worst 5 of 28 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:496:ARG:HD2	5:D:889:HOH:O	1.90	0.70
1:A:504:GLU:OE2	1:A:508:ARG:NH2	2.25	0.69
1:D:504:GLU:OE2	1:D:508:ARG:NH2	2.26	0.68
1:A:388[B]:MET:SD	1:B:388[B]:MET:SD	2.91	0.68
1:A:388[A]:MET:SD	1:B:388[A]:MET:SD	3.00	0.60

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	330/370 (89%)	320 (97%)	10 (3%)	0	100	100
1	B	330/370 (89%)	322 (98%)	8 (2%)	0	100	100
1	C	336/370 (91%)	326 (97%)	10 (3%)	0	100	100
1	D	329/370 (89%)	323 (98%)	6 (2%)	0	100	100
All	All	1325/1480 (90%)	1291 (97%)	34 (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	290/338 (86%)	288 (99%)	2 (1%)	84	89
1	B	282/338 (83%)	281 (100%)	1 (0%)	91	93
1	C	285/338 (84%)	285 (100%)	0	100	100
1	D	283/338 (84%)	280 (99%)	3 (1%)	73	78
All	All	1140/1352 (84%)	1134 (100%)	6 (0%)	88	92

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	601	SER
1	D	556	PRO
1	D	405	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	423	ARG
1	D	423	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	535	GLN
1	C	474	GLN
1	C	535	GLN
1	D	474	GLN
1	D	535	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 10 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	KRD	C	702	-	28,28,28	0.95	3 (10%)	37,38,38	2.08	9 (24%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	KRD	B	703	-	28,28,28	1.11	4 (14%)	37,38,38	2.01	8 (21%)
4	KRD	D	704	-	28,28,28	1.19	4 (14%)	37,38,38	2.10	7 (18%)
4	KRD	A	703	-	28,28,28	1.15	2 (7%)	37,38,38	2.08	6 (16%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	KRD	C	702	-	-	5/14/14/14	0/3/3/3
4	KRD	B	703	-	-	5/14/14/14	0/3/3/3
4	KRD	D	704	-	-	5/14/14/14	0/3/3/3
4	KRD	A	703	-	-	7/14/14/14	0/3/3/3

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	703	KRD	C3-N	3.08	1.41	1.34
4	A	703	KRD	C5-N3	-2.92	1.34	1.40
4	B	703	KRD	C11-C8	2.67	1.56	1.51
4	B	703	KRD	C17-CL	2.61	1.80	1.74
4	B	703	KRD	C2-N	2.29	1.37	1.33

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	703	KRD	C4-N2-C2	7.16	124.54	114.47
4	D	704	KRD	C4-N1-C3	6.63	118.83	114.60
4	B	703	KRD	C4-N1-C3	6.10	118.49	114.60
4	C	702	KRD	C4-N2-C2	6.06	123.00	114.47
4	A	703	KRD	N2-C2-N	-5.99	118.15	126.06

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	703	KRD	C-C1-C2-N
4	C	702	KRD	C18-C13-C3-N
4	D	704	KRD	C18-C13-C3-N

Continued on next page...

Continued from previous page...

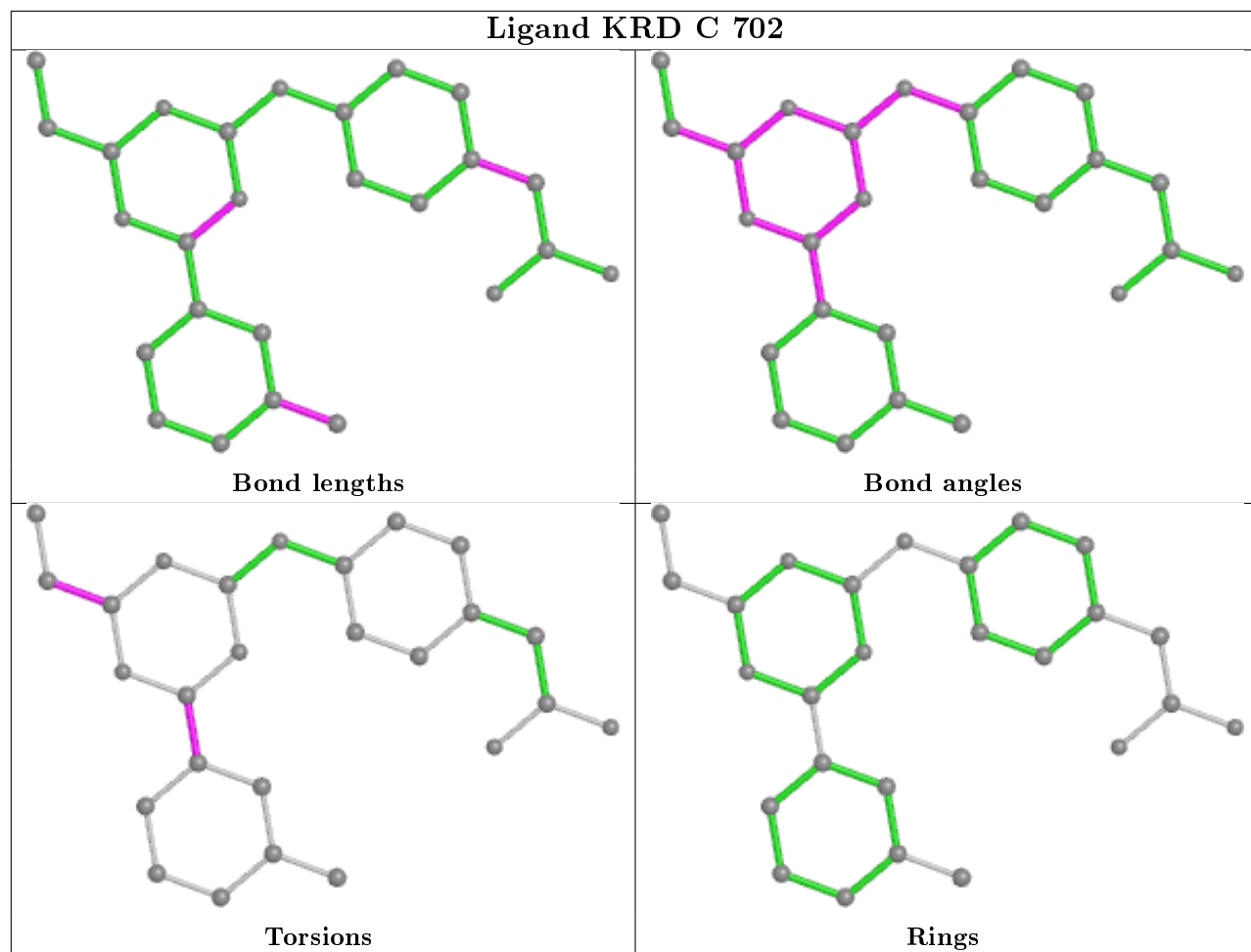
Mol	Chain	Res	Type	Atoms
4	C	702	KRD	C18-C13-C3-N1
4	D	704	KRD	C18-C13-C3-N1

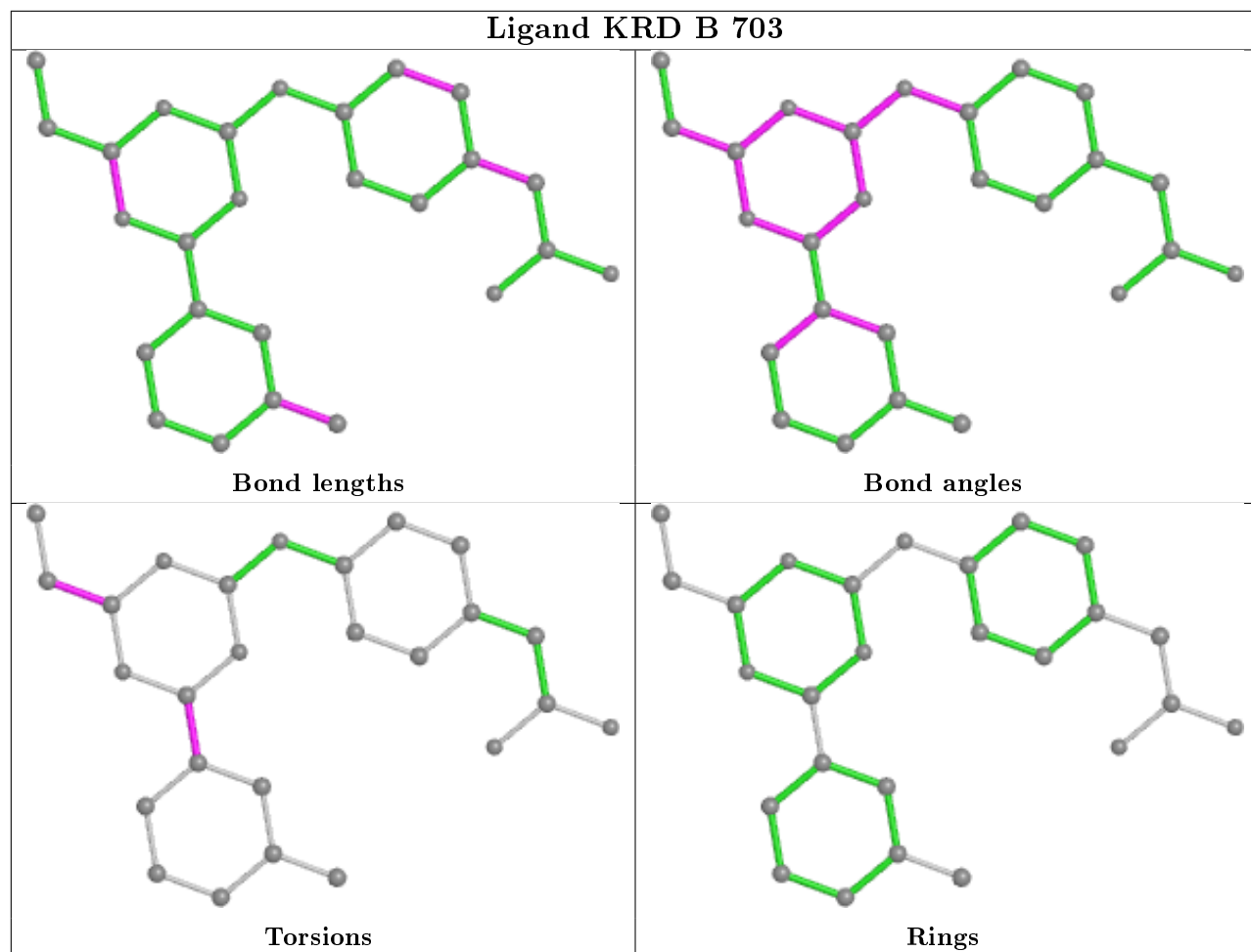
There are no ring outliers.

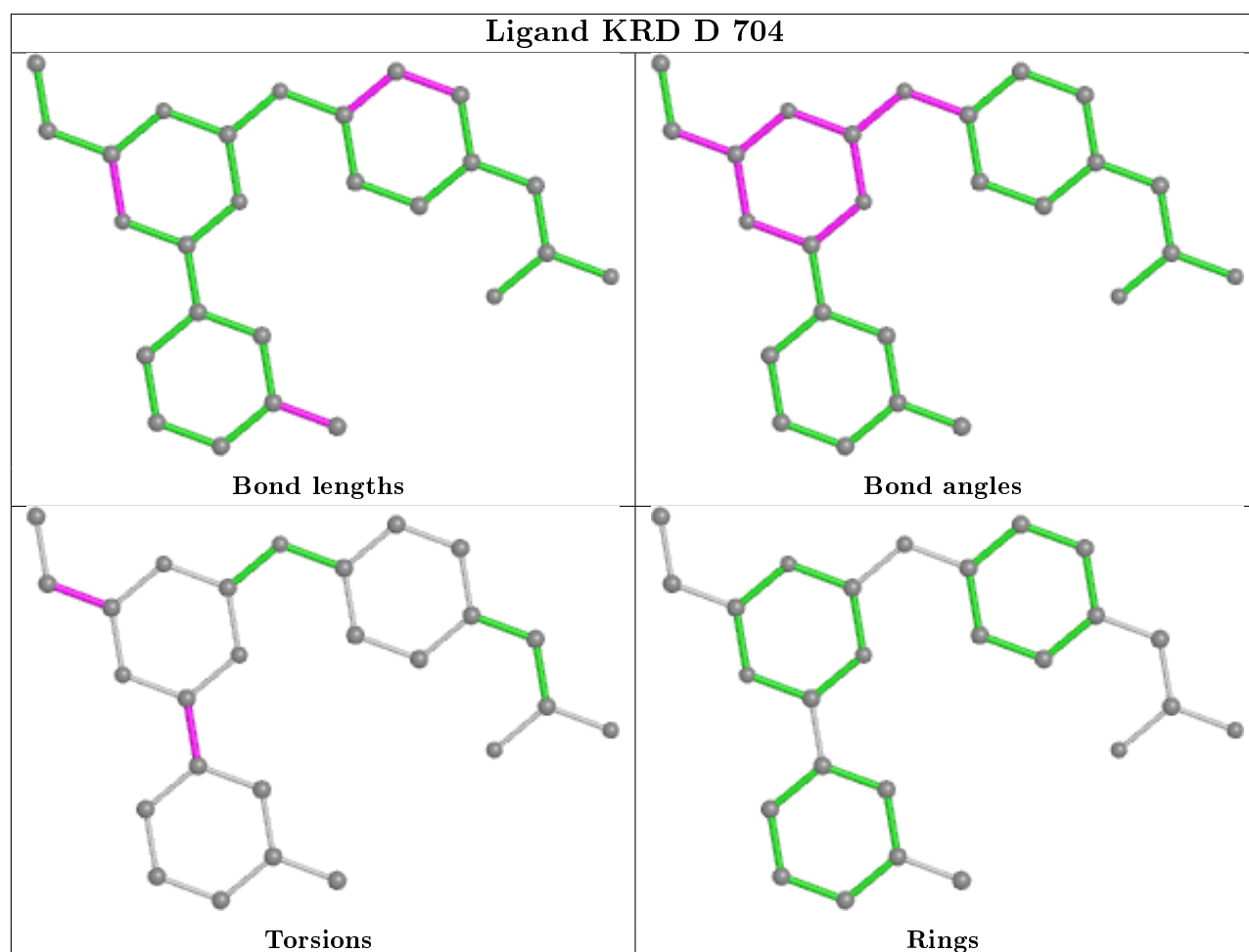
3 monomers are involved in 3 short contacts:

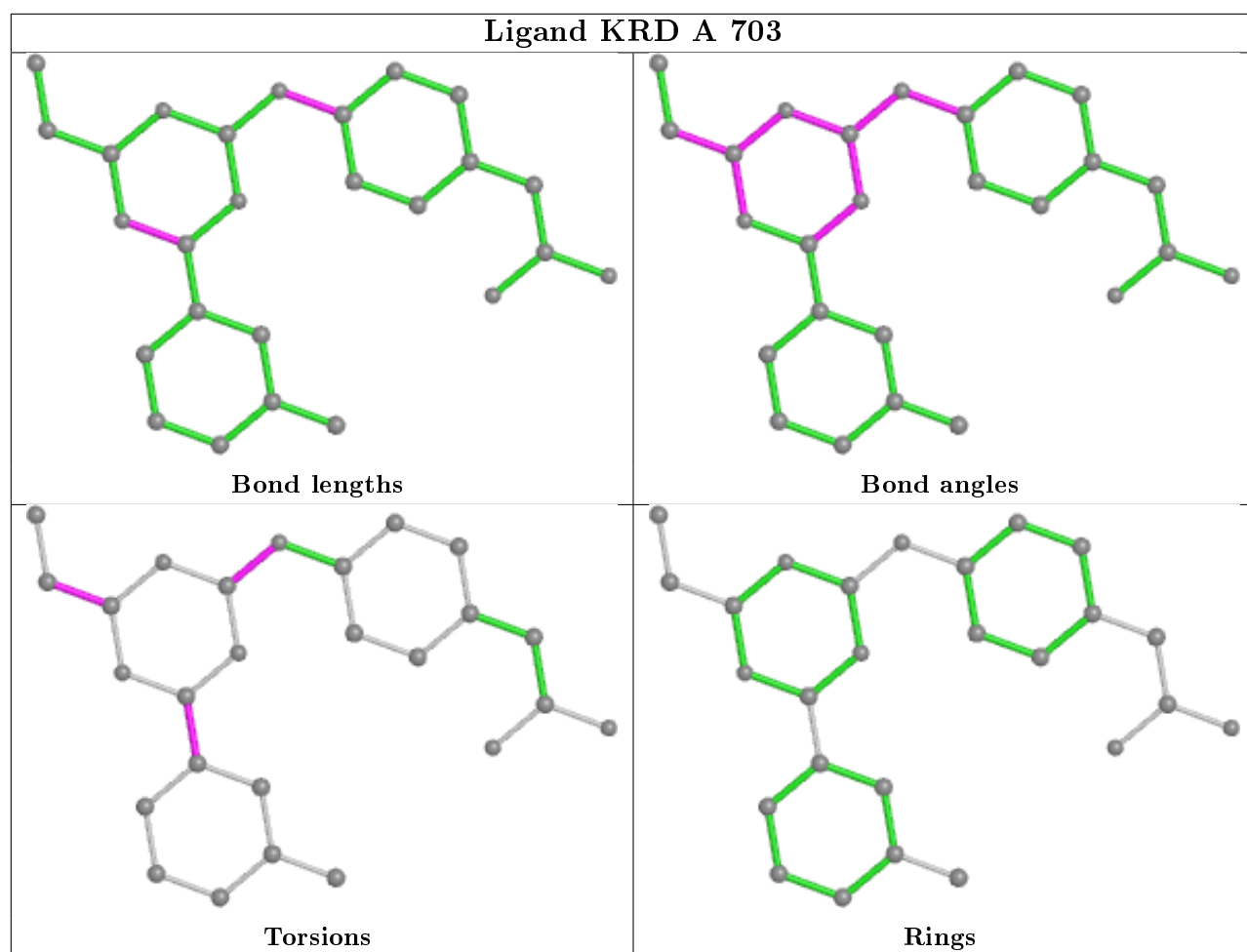
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	702	KRD	1	0
4	D	704	KRD	1	0
4	A	703	KRD	1	0

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 [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	334/370 (90%)	-0.25	8 (2%) 59 67	13, 25, 44, 71	0
1	B	335/370 (90%)	-0.17	7 (2%) 63 71	14, 28, 50, 83	0
1	C	337/370 (91%)	-0.29	4 (1%) 79 83	14, 24, 43, 60	0
1	D	333/370 (90%)	-0.07	11 (3%) 46 55	16, 30, 55, 82	0
All	All	1339/1480 (90%)	-0.19	30 (2%) 62 69	13, 27, 49, 83	0

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	577	PRO	4.5
1	D	594	ASN	3.4
1	D	458	VAL	3.4
1	A	577	PRO	3.3
1	B	606	ASP	3.2

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](#)

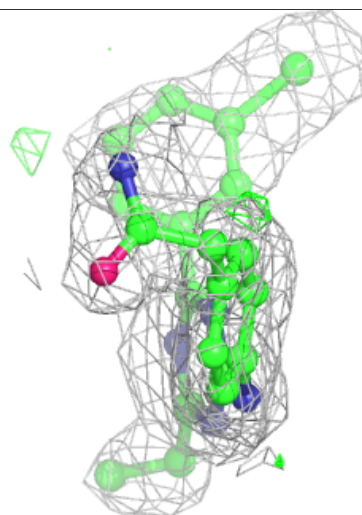
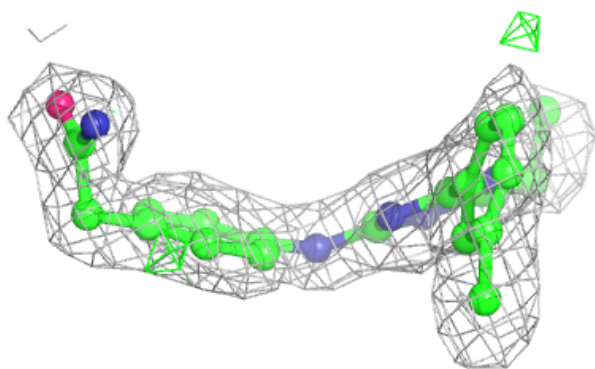
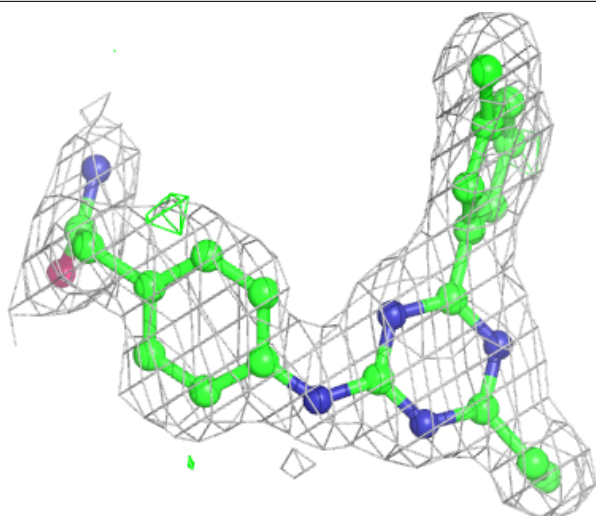
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	KRD	D	704	26/26	0.92	0.24	24,29,33,40	26
4	KRD	B	703	26/26	0.93	0.13	26,30,34,43	0
3	MG	B	702	1/1	0.95	0.05	28,28,28,28	0
3	MG	A	702	1/1	0.95	0.05	24,24,24,24	0
3	MG	D	703	1/1	0.97	0.03	30,30,30,30	0
4	KRD	C	702	26/26	0.97	0.10	21,28,32,32	0
3	MG	D	701	1/1	0.97	0.05	12,12,12,12	0
4	KRD	A	703	26/26	0.97	0.12	21,25,29,30	0
3	MG	A	704	1/1	0.99	0.04	10,10,10,10	0
3	MG	C	701	1/1	0.99	0.08	21,21,21,21	0
2	ZN	C	700	1/1	1.00	0.04	16,16,16,16	0
2	ZN	A	701	1/1	1.00	0.05	16,16,16,16	0
2	ZN	D	702	1/1	1.00	0.04	22,22,22,22	0
2	ZN	B	701	1/1	1.00	0.04	20,20,20,20	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.

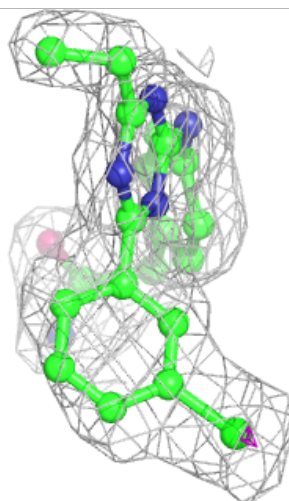
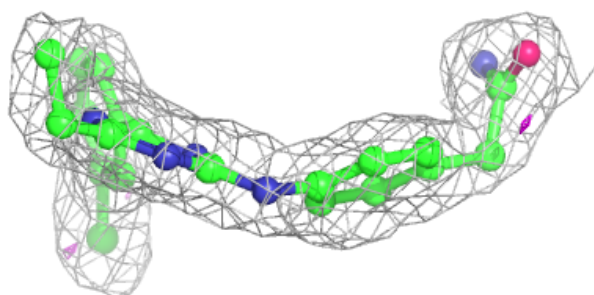
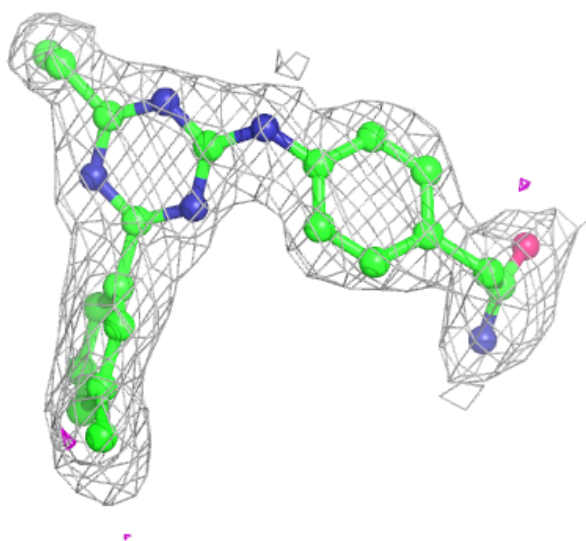
Electron density around KRD D 704:

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



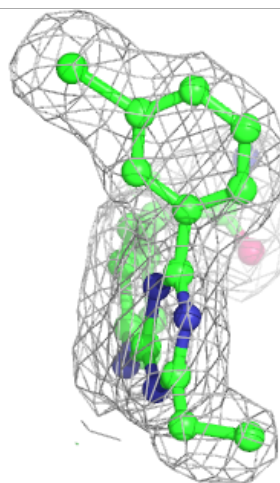
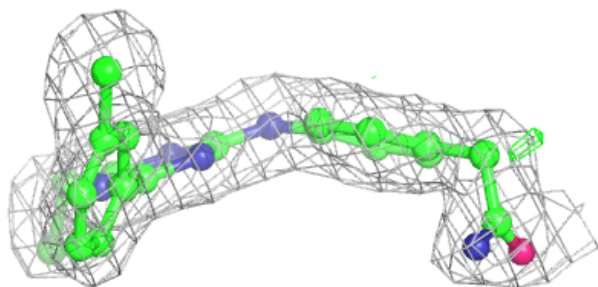
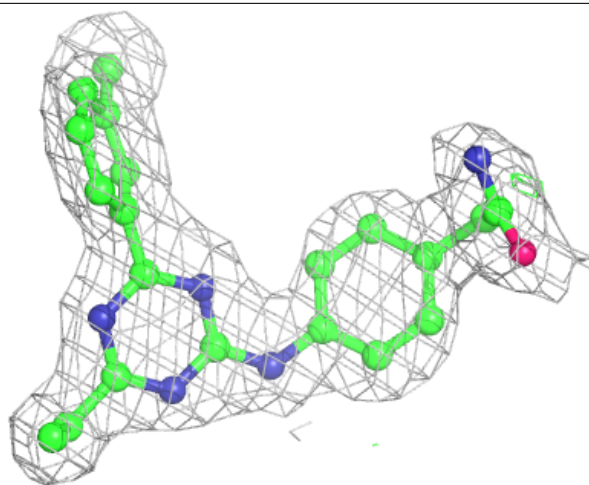
Electron density around KRD B 703:

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



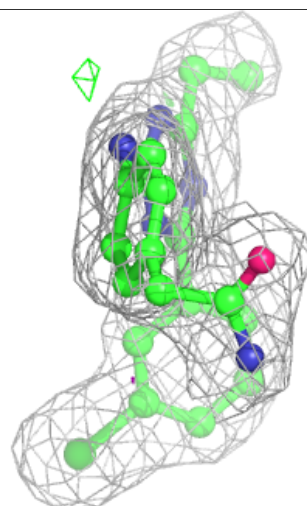
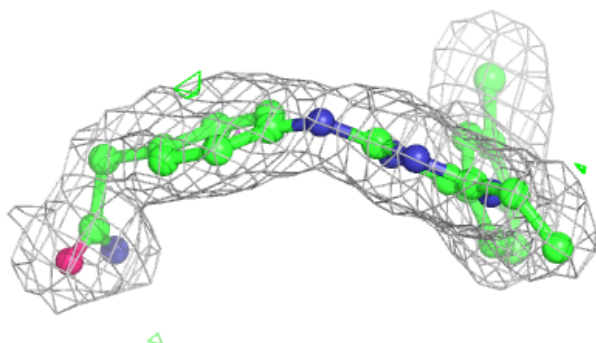
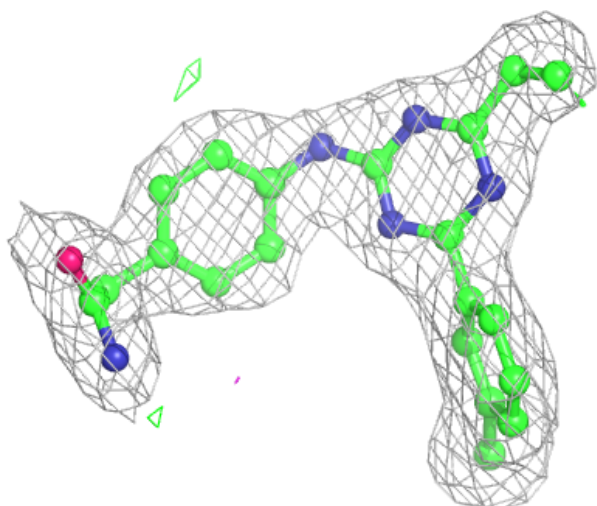
Electron density around KRD C 702:

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



Electron density around KRD A 703:

$2mF_o-DF_c$ (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.