



Full wwPDB X-ray Structure Validation Report ⓘ

May 23, 2022 – 04:27 pm BST

PDB ID : 7OJO
Title : Tankyrase 2 in complex with two small molecule fragments
Authors : Sowa, S.T.; Lehtio, L.
Deposited on : 2021-05-17
Resolution : 2.30 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 : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.28.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.28.1

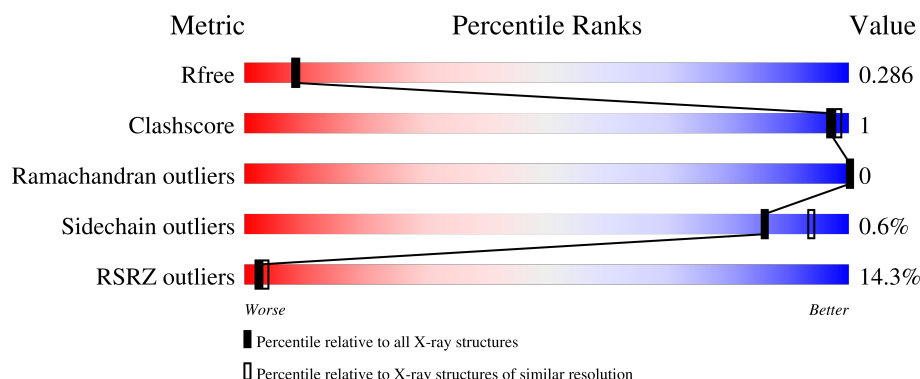
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	AAA	171	<div> <div>13%</div> <div>91%</div> <div>7%</div> </div>
1	BBB	171	<div> <div>10%</div> <div>91%</div> <div>6%</div> </div>
2	A	48	<div> <div>8%</div> <div>77%</div> <div>19%</div> </div>
2	B	48	<div> <div>31%</div> <div>94%</div> <div>• •</div> </div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 3486 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 Poly [ADP-ribose] polymerase tankyrase-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	159	Total	C	N	O	S	0	2	0
			1286	803	239	236	8			
1	BBB	160	Total	C	N	O	S	0	0	0
			1270	796	235	231	8			

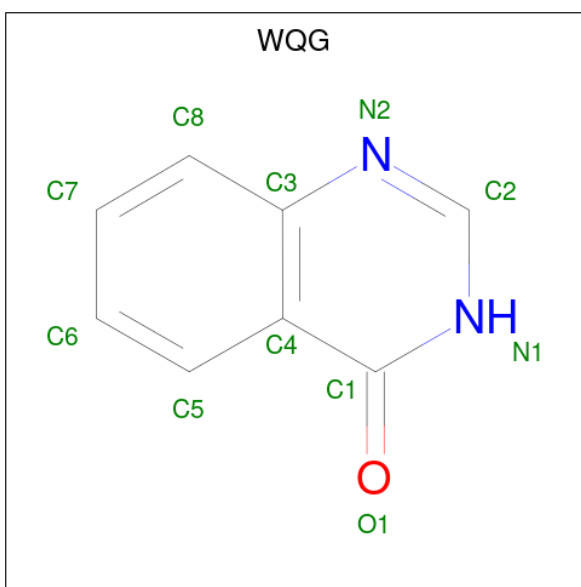
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	944	SER	-	expression tag	UNP Q9H2K2
AAA	945	MET	-	expression tag	UNP Q9H2K2
BBB	944	SER	-	expression tag	UNP Q9H2K2
BBB	945	MET	-	expression tag	UNP Q9H2K2

- Molecule 2 is a protein called Poly [ADP-ribose] polymerase tankyrase-2.

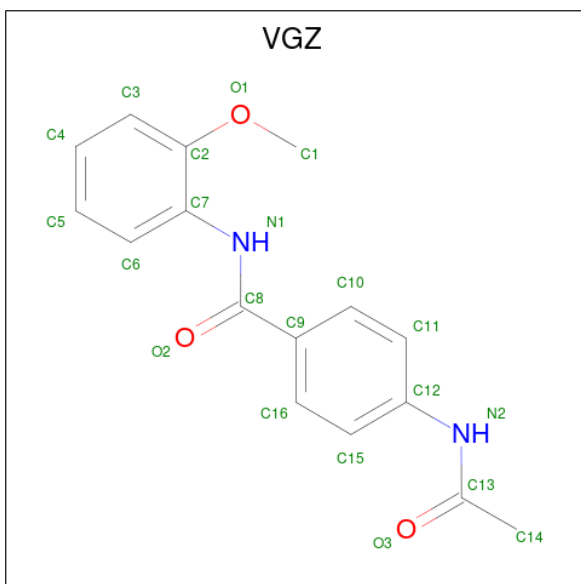
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	39	Total	C	N	O	S	0	0	0
			316	202	56	56	2			
2	B	47	Total	C	N	O	S	0	0	0
			369	236	65	66	2			

- Molecule 3 is quinazolin-4(3H)-one (three-letter code: WQG) (formula: C₈H₆N₂O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	AAA	1	Total	C	N	O	0	0
			11	8	2	1		
3	BBB	1	Total	C	N	O	0	0
			11	8	2	1		

- Molecule 4 is 4-acetamido- {N}-(2-methoxyphenyl)benzamide (three-letter code: VGZ) (formula: C₁₆H₁₆N₂O₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	AAA	1	Total	C	N	O	0	0
			21	16	2	3		

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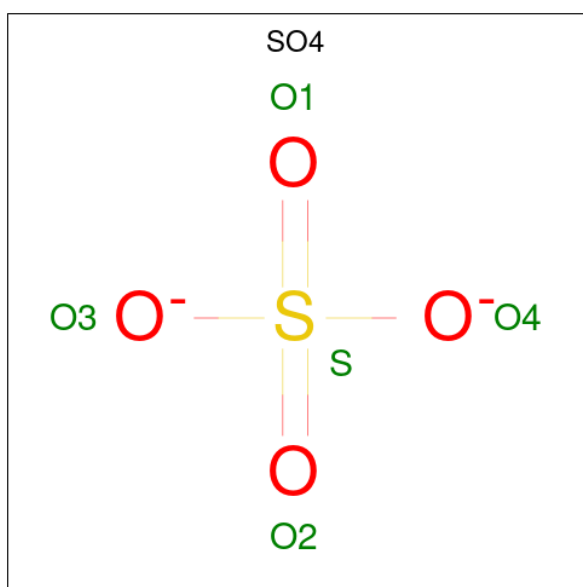
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	BBB	1	Total	C	N	O	0	0
			21	16	2	3		

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	AAA	1	Total	Zn	0	0
			1	1		
5	BBB	1	Total	Zn	0	0
			1	1		

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	BBB	1	Total	O	S	0	0
			5	4	1		
6	BBB	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is water.

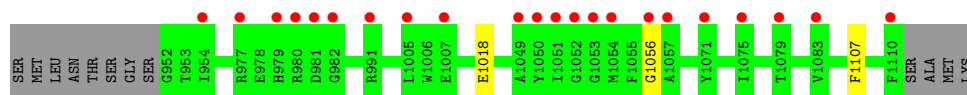
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	AAA	60	Total 60	O 60	0	0
7	A	9	Total 9	O 9	0	0
7	BBB	73	Total 73	O 73	0	0
7	B	7	Total 7	O 7	0	0

3 Residue-property plots

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.

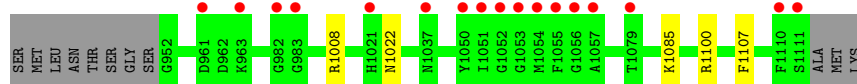
- Molecule 1: Poly [ADP-ribose] polymerase tankyrase-2

Chain AAA: 




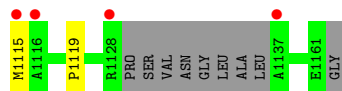
- Molecule 1: Poly [ADP-ribose] polymerase tankyrase-2

Chain BBB: 



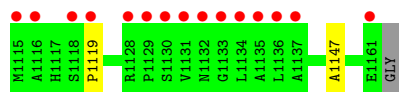
- Molecule 2: Poly [ADP-ribose] polymerase tankyrase-2

Chain A: 



- Molecule 2: Poly [ADP-ribose] polymerase tankyrase-2

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	41.65Å 76.39Å 148.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	74.55 – 2.30 74.44 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (74.55-2.30) 99.9 (74.44-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.57 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.232 , 0.277 0.242 , 0.286	Depositor DCC
R_{free} test set	1107 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	10.3	Xtriage
Anisotropy	2.222	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	3486	wwPDB-VP
Average B, all atoms (Å ²)	17.0	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 23.84 % 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 4.3067e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: ZN, VGZ, SO4, WQG

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	AAA	0.64	0/1319	0.72	0/1770
1	BBB	0.64	0/1300	0.72	0/1745
2	A	0.61	0/326	0.73	0/442
2	B	0.62	0/381	0.74	0/520
All	All	0.64	0/3326	0.72	0/4477

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	AAA	1286	0	1215	2	0
1	BBB	1270	0	1203	4	0
2	A	316	0	295	2	0
2	B	369	0	353	2	0
3	AAA	11	0	0	0	0
3	BBB	11	0	0	0	0
4	AAA	21	0	0	0	0
4	BBB	21	0	0	0	0
5	AAA	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	BBB	1	0	0	0	0
6	A	10	0	0	0	0
6	B	10	0	0	0	0
6	BBB	10	0	0	0	0
7	A	9	0	0	0	0
7	AAA	60	0	0	0	0
7	B	7	0	0	0	0
7	BBB	73	0	0	1	0
All	All	3486	0	3066	6	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 (6) 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:BBB:1008:ARG:NH2	7:BBB:1305:HOH:O	2.50	0.44
1:BBB:1022:ASN:CG	1:BBB:1022:ASN:O	2.58	0.42
1:BBB:1107:PHE:CG	2:B:1119:PRO:HG2	2.54	0.42
1:AAA:1107:PHE:CG	2:A:1119:PRO:HG2	2.55	0.41
1:AAA:1056:GLY:HA3	2:A:1115:MET:O	2.21	0.41
1:BBB:1100:ARG:O	2:B:1147:ALA:HA	2.21	0.41

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	AAA	159/171 (93%)	157 (99%)	2 (1%)	0	100	100
1	BBB	158/171 (92%)	157 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	35/48 (73%)	35 (100%)	0	0	100	100
2	B	45/48 (94%)	43 (96%)	2 (4%)	0	100	100
All	All	397/438 (91%)	392 (99%)	5 (1%)	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	AAA	135/146 (92%)	133 (98%)	2 (2%)	65	79
1	BBB	133/146 (91%)	132 (99%)	1 (1%)	81	91
2	A	32/39 (82%)	32 (100%)	0	100	100
2	B	38/39 (97%)	38 (100%)	0	100	100
All	All	338/370 (91%)	335 (99%)	3 (1%)	86	89

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	1018[A]	GLU
1	AAA	1018[B]	GLU
1	BBB	1085	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 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	VGZ	AAA	1202	-	22,22,22	0.20	0	29,29,29	0.49	0
6	SO4	A	1202	-	4,4,4	0.38	0	6,6,6	0.08	0
6	SO4	BBB	1205	-	4,4,4	0.38	0	6,6,6	0.05	0
6	SO4	B	1202	-	4,4,4	0.39	0	6,6,6	0.05	0
6	SO4	A	1201	-	4,4,4	0.35	0	6,6,6	0.08	0
4	VGZ	BBB	1202	-	22,22,22	0.18	0	29,29,29	0.43	0
6	SO4	BBB	1204	-	4,4,4	0.36	0	6,6,6	0.10	0
3	WQG	AAA	1201	-	11,12,12	1.31	1 (9%)	13,16,16	1.70	2 (15%)
6	SO4	B	1201	-	4,4,4	0.34	0	6,6,6	0.10	0
3	WQG	BBB	1201	-	11,12,12	1.30	1 (9%)	13,16,16	1.72	3 (23%)

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	VGZ	AAA	1202	-	-	0/14/14/14	0/2/2/2
4	VGZ	BBB	1202	-	-	8/14/14/14	0/2/2/2
3	WQG	BBB	1201	-	-	-	0/2/2/2
3	WQG	AAA	1201	-	-	-	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	AAA	1201	WQG	C1-N1	2.99	1.38	1.33
3	BBB	1201	WQG	C1-N1	2.95	1.38	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	BBB	1201	WQG	C2-N1-C1	4.28	123.05	115.88
3	AAA	1201	WQG	C2-N1-C1	4.25	123.00	115.88
3	BBB	1201	WQG	N2-C2-N1	-3.00	123.99	128.68
3	AAA	1201	WQG	N2-C2-N1	-2.93	124.09	128.68
3	BBB	1201	WQG	C2-N2-C3	2.07	118.25	115.40

There are no chirality outliers.

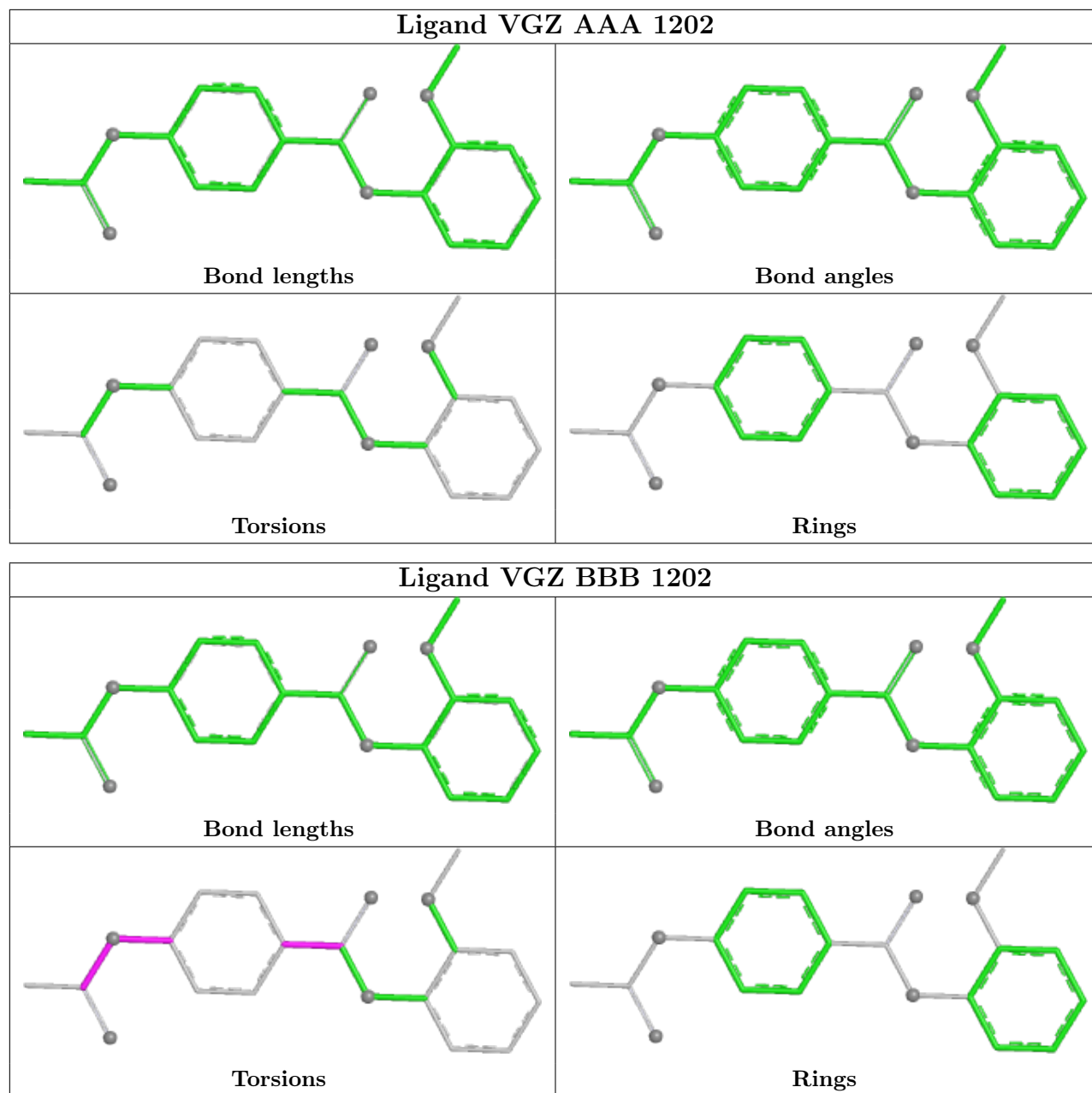
All (8) torsion outliers are listed below:

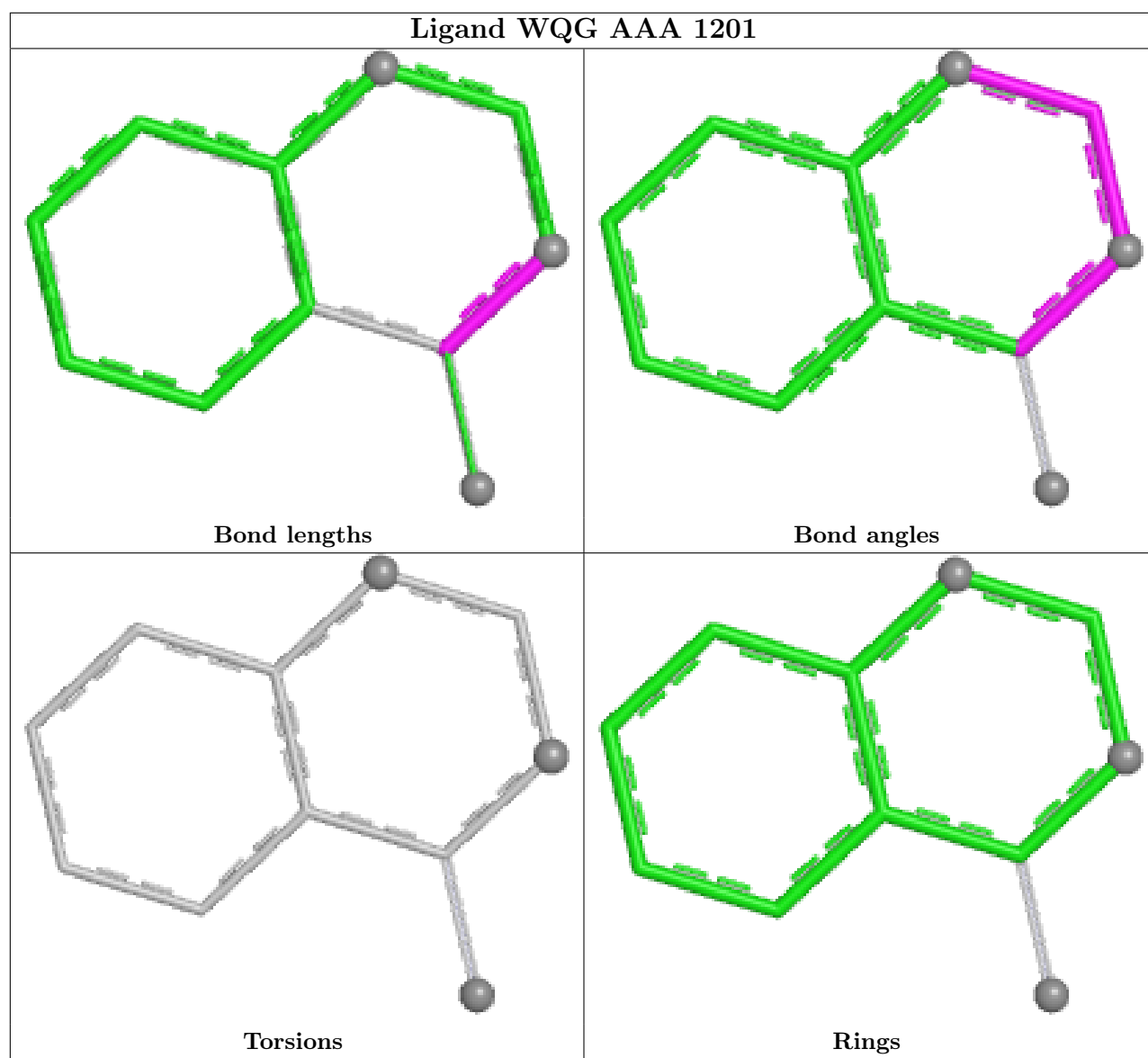
Mol	Chain	Res	Type	Atoms
4	BBB	1202	VGZ	O2-C8-C9-C10
4	BBB	1202	VGZ	N1-C8-C9-C10
4	BBB	1202	VGZ	O2-C8-C9-C16
4	BBB	1202	VGZ	N1-C8-C9-C16
4	BBB	1202	VGZ	O3-C13-N2-C12
4	BBB	1202	VGZ	C14-C13-N2-C12
4	BBB	1202	VGZ	C11-C12-N2-C13
4	BBB	1202	VGZ	C15-C12-N2-C13

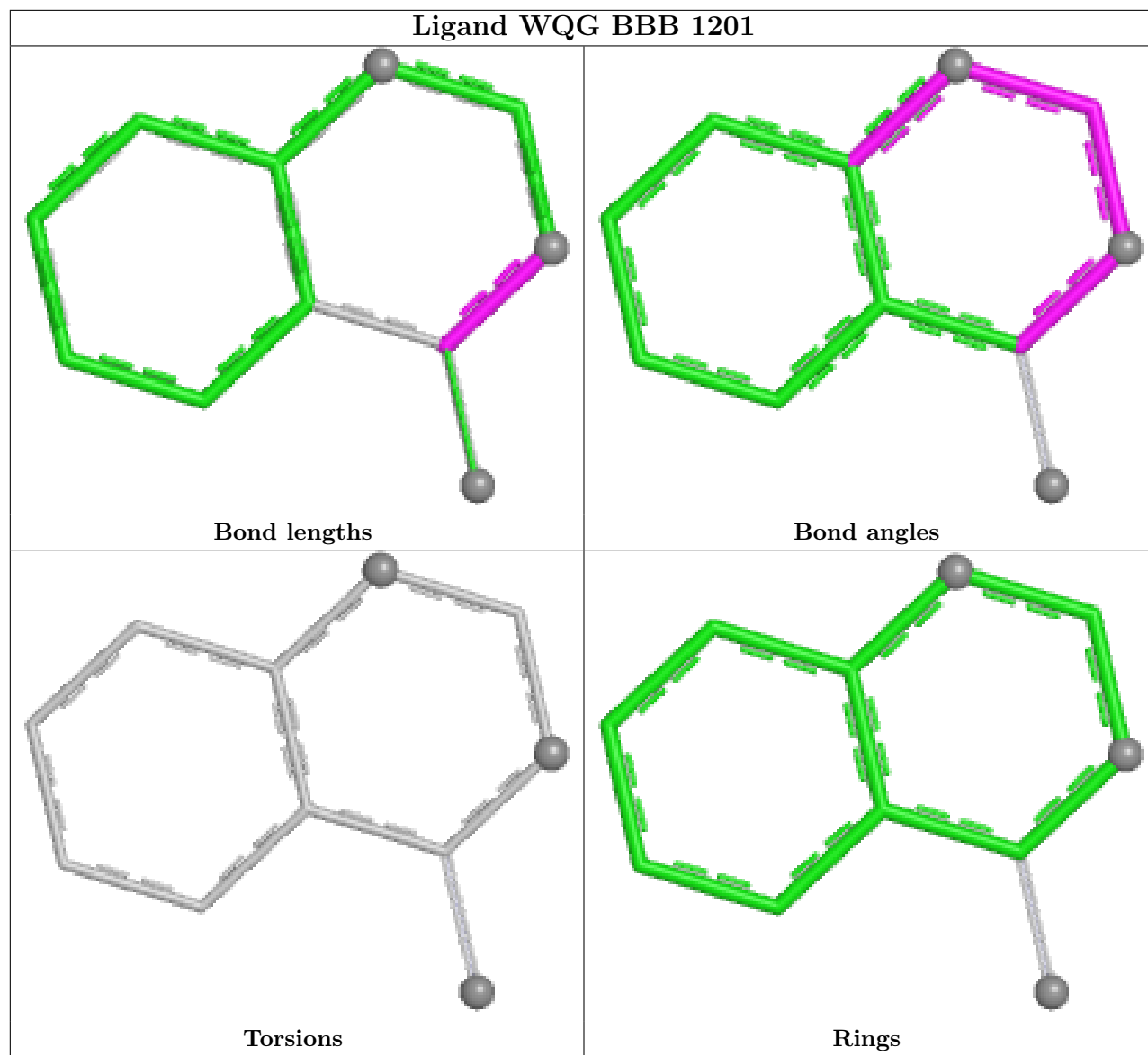
There are no ring outliers.

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	AAA	159/171 (92%)	1.30	22 (13%) 2 4	9, 17, 40, 79	0
1	BBB	160/171 (93%)	1.02	17 (10%) 6 8	5, 12, 34, 62	0
2	A	39/48 (81%)	1.22	4 (10%) 6 9	8, 13, 39, 53	0
2	B	47/48 (97%)	1.76	15 (31%) 0 0	4, 11, 54, 64	0
All	All	405/438 (92%)	1.23	58 (14%) 2 3	4, 14, 41, 79	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	1051	ILE	11.6
1	AAA	1050	TYR	11.3
2	A	1137	ALA	7.4
1	BBB	1051	ILE	7.1
2	B	1132	ASN	7.0
1	BBB	1052	GLY	6.8
1	AAA	1052	GLY	6.5
2	B	1131	VAL	6.2
1	BBB	1050	TYR	5.9
2	B	1115	MET	5.9
1	AAA	1056	GLY	5.8
1	BBB	1111	SER	5.6
2	B	1130	SER	4.7
1	BBB	1110	PHE	4.6
1	AAA	980	ARG	4.3
1	AAA	1079	THR	4.3
1	BBB	1057	ALA	4.2
2	B	1133	GLY	4.1
1	AAA	982	GLY	4.1
1	BBB	1054	MET	4.0
2	A	1128	ARG	3.7

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Mol	Chain	Res	Type	RSRZ
2	A	1115	MET	3.7
2	B	1137	ALA	3.6
1	AAA	1054	MET	3.6
1	AAA	1057	ALA	3.5
1	AAA	1110	PHE	3.4
2	B	1134	LEU	3.4
2	B	1116	ALA	3.2
2	B	1135	ALA	3.2
2	B	1136	LEU	3.2
1	BBB	982	GLY	3.1
1	AAA	1053	GLY	3.1
1	BBB	1056	GLY	3.0
1	AAA	954	ILE	3.0
2	B	1161	GLU	3.0
2	B	1129	PRO	2.9
1	AAA	1075	ILE	2.9
1	AAA	1083	VAL	2.9
1	AAA	981	ASP	2.7
1	BBB	961	ASP	2.7
2	A	1116	ALA	2.7
1	AAA	991	ARG	2.7
1	BBB	963	LYS	2.7
1	BBB	1053	GLY	2.7
1	AAA	1007	GLU	2.6
1	BBB	1055	PHE	2.5
1	AAA	1005	LEU	2.5
1	BBB	1079	THR	2.5
1	AAA	977	ARG	2.4
1	BBB	1037	ASN	2.3
2	B	1118	SER	2.3
1	AAA	979	HIS	2.1
1	AAA	1049	ALA	2.1
1	BBB	1021	HIS	2.1
1	AAA	1071	TYR	2.1
1	BBB	983	GLY	2.1
2	B	1128	ARG	2.0
2	B	1119	PRO	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

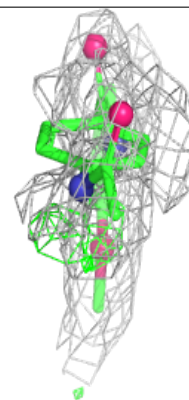
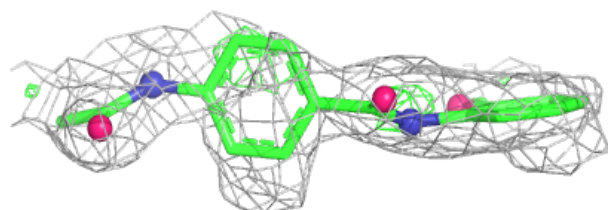
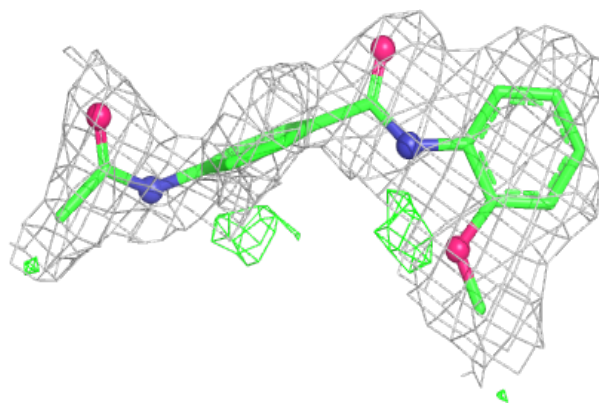
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	SO4	BBB	1204	5/5	0.63	0.38	43,44,47,47	0
4	VGZ	BBB	1202	21/21	0.67	0.29	37,40,44,45	0
4	VGZ	AAA	1202	21/21	0.81	0.25	27,28,31,31	0
3	WQG	AAA	1201	11/11	0.85	0.19	16,16,17,17	0
3	WQG	BBB	1201	11/11	0.86	0.18	10,11,11,11	0
6	SO4	A	1202	5/5	0.88	0.23	50,50,51,51	0
6	SO4	BBB	1205	5/5	0.88	0.32	42,43,44,44	0
6	SO4	B	1201	5/5	0.88	0.23	26,26,27,27	0
6	SO4	A	1201	5/5	0.89	0.29	32,33,34,34	0
6	SO4	B	1202	5/5	0.89	0.30	37,37,38,38	0
5	ZN	AAA	1203	1/1	0.98	0.08	14,14,14,14	0
5	ZN	BBB	1203	1/1	0.98	0.07	7,7,7,7	0

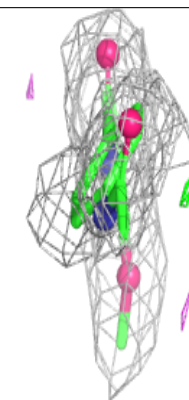
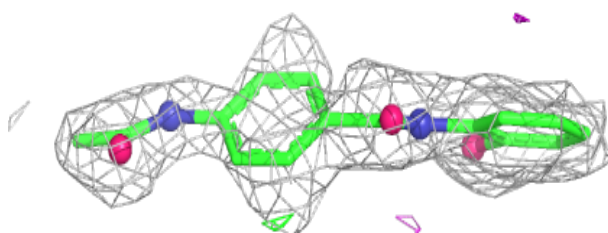
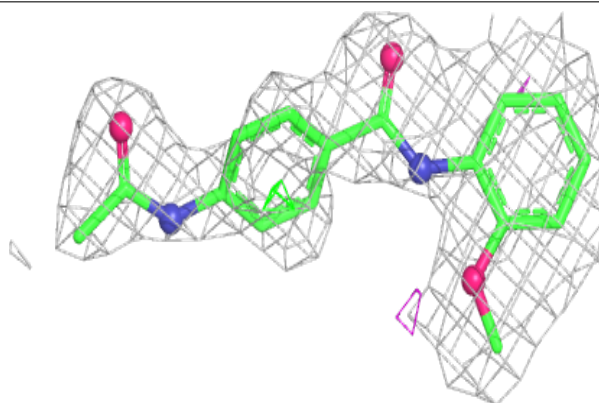
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around VGZ BBB 1202:

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

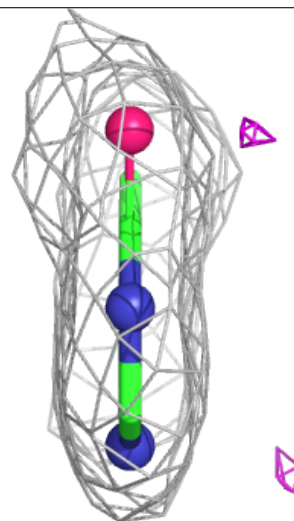
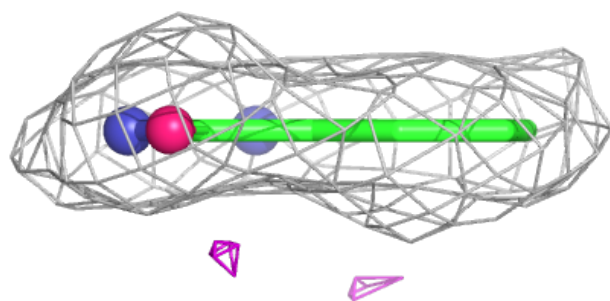
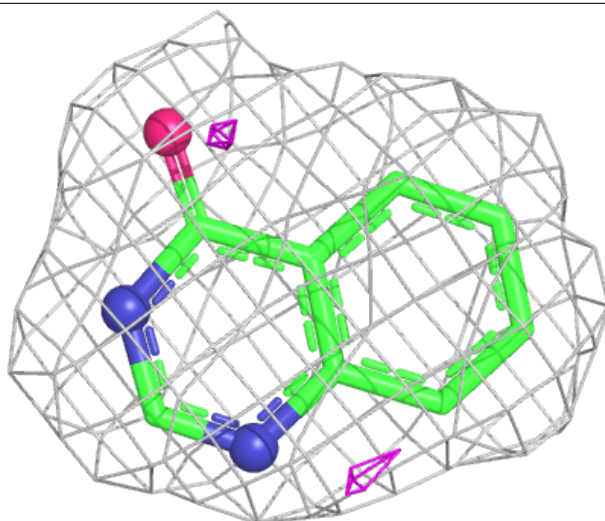
**Electron density around VGZ AAA 1202:**

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



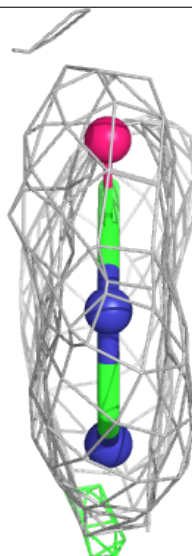
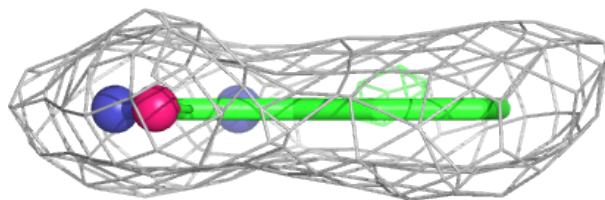
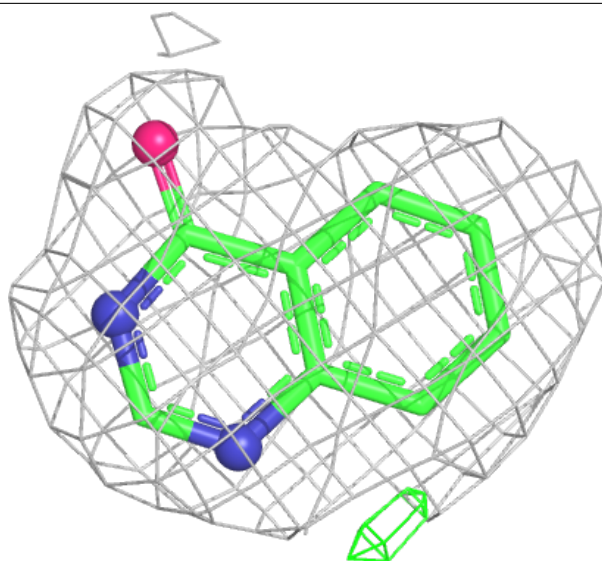
Electron density around WQG AAA 1201:

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



Electron density around WQG BBB 1201:

$2mF_o-DF_c$ (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.