



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2023 – 04:37 PM EDT

PDB ID : 8E7N
Title : Crystal structure of beluga whale Gammacoronavirus SW1 Mpro with GC-376 captured in two conformational states
Authors : Shaqra, A.M.; Schiffer, C.A.
Deposited on : 2022-08-24
Resolution : 1.65 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.32.1
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) : 2.32.1

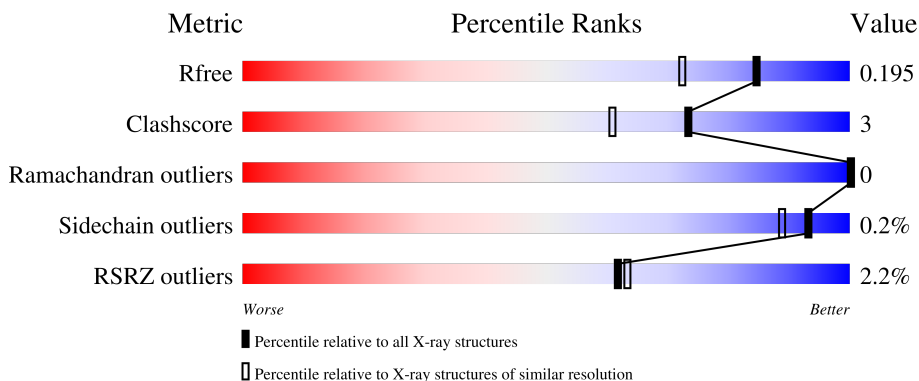
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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	1827 (1.66-1.66)
Clashscore	141614	1931 (1.66-1.66)
Ramachandran outliers	138981	1891 (1.66-1.66)
Sidechain outliers	138945	1891 (1.66-1.66)
RSRZ outliers	127900	1791 (1.66-1.66)

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	303	 3% 94% . . .
1	B	303	 2% 90% 8% .

2 Entry composition [i](#)

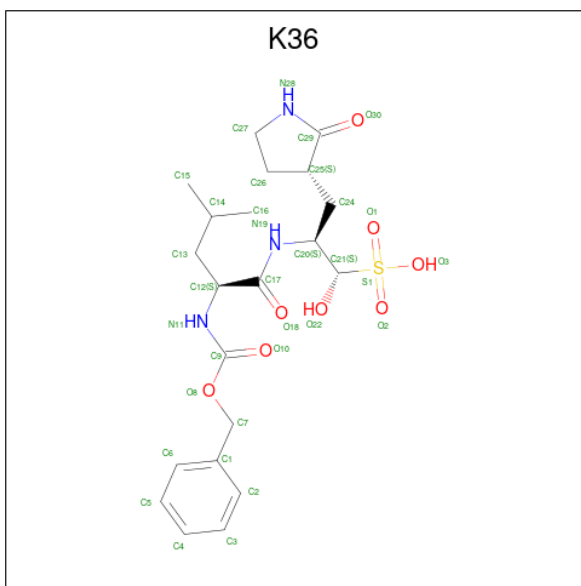
There are 5 unique types of molecules in this entry. The entry contains 5523 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 main protease.

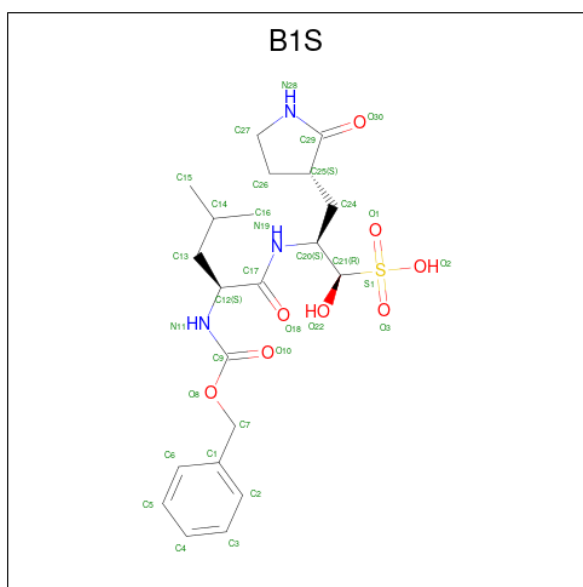
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	299	Total	C	N	O	S	0	1	0
			2301	1480	384	422	15			
1	B	298	Total	C	N	O	S	0	1	0
			2276	1463	376	422	15			

- Molecule 2 is (1S,2S)-2-({N-[(benzyloxy)carbonyl]-L-leucyl}amino)-1-hydroxy-3-[(3S)-2-oxopyrrolidin-3-yl]propane-1-sulfonic acid (three-letter code: K36) (formula: C₂₁H₃₁N₃O₈S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	Total	C	N	O	0	1
			29	21	3	5		
2	B	1	Total	C	N	O	0	1
			29	21	3	5		

- Molecule 3 is (1R,2S)-2-({N-[(benzyloxy)carbonyl]-L-leucyl}amino)-1-hydroxy-3-[(3S)-2-oxo pyrrolidin-3-yl]propane-1-sulfonic acid (three-letter code: B1S) (formula: C₂₁H₃₁N₃O₈S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
			Total	C	N			O
3	A	1	29	21	3	5	0	1
3	B	1	29	21	3	5	0	1

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	A	1	6	3	3	0	0
4	A	1	6	3	3	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		

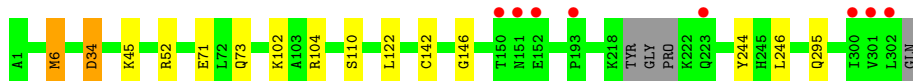
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	412	Total	O	0	0
			412	412		
5	B	382	Total	O	0	0
			382	382		

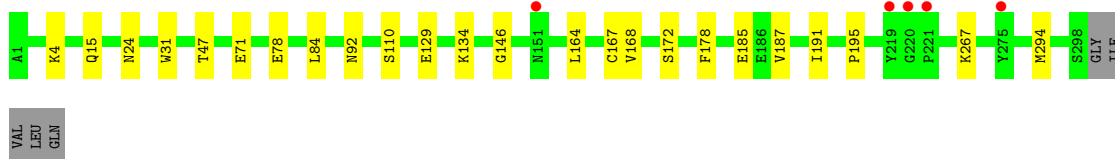
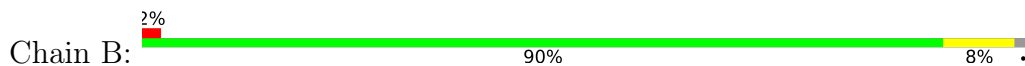
3 Residue-property plots [i](#)

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: main protease



- Molecule 1: main protease



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	63.08Å 84.16Å 68.50Å 90.00° 93.09° 90.00°	Depositor
Resolution (Å)	12.24 – 1.65 12.24 – 1.65	Depositor EDS
% Data completeness (in resolution range)	95.2 (12.24-1.65) 95.2 (12.24-1.65)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.57 (at 1.65Å)	Xtrriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.159 , 0.195 0.159 , 0.195	Depositor DCC
R_{free} test set	1999 reflections (2.45%)	wwPDB-VP
Wilson B-factor (Å ²)	13.9	Xtrriage
Anisotropy	0.426	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 61.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5523	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.47% 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: B1S, K36, GOL

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	0.88	0/2360	0.92	4/3207 (0.1%)
1	B	0.83	1/2341 (0.0%)	0.85	0/3189
All	All	0.86	1/4701 (0.0%)	0.89	4/6396 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	172	SER	CB-OG	5.43	1.49	1.42

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	6	MET	CG-SD-CE	-8.74	86.21	100.20
1	A	122	LEU	CB-CG-CD1	-6.24	100.40	111.00
1	A	34	ASP	CB-CG-OD1	5.60	123.34	118.30
1	A	142	CYS	CA-CB-SG	-5.52	104.07	114.00

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	2301	0	2204	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2276	0	2148	17	0
2	A	29	0	29	1	0
2	B	29	0	29	1	0
3	A	29	0	0	0	0
3	B	29	0	0	0	0
4	A	12	0	15	0	0
4	B	24	0	30	4	0
5	A	412	0	0	6	2
5	B	382	0	0	8	0
All	All	5523	0	4455	30	2

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 3.

All (30) 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:B:4:LYS:NZ	5:B:503:HOH:O	2.16	0.77
1:B:15:GLN:NE2	5:B:501:HOH:O	2.03	0.74
1:A:6:MET:HE3	1:A:295:GLN:NE2	2.15	0.62
1:B:71:GLU:HG2	5:B:721:HOH:O	1.99	0.62
1:B:4:LYS:NZ	5:B:502:HOH:O	2.08	0.61
1:A:34:ASP:OD2	5:A:502:HOH:O	2.17	0.58
1:A:52:ARG:NH1	5:A:501:HOH:O	2.11	0.56
1:B:178:PHE:CD2	4:B:403:GOL:H31	2.43	0.53
1:B:24:ASN:ND2	5:B:513:HOH:O	2.41	0.53
1:A:102:LYS:HE3	5:A:636:HOH:O	2.10	0.52
1:A:110:SER:O	1:A:146:GLY:HA2	2.10	0.51
4:B:403:GOL:O2	5:B:504:HOH:O	2.19	0.50
1:B:267:LYS:HE2	4:B:405:GOL:H31	1.95	0.47
4:B:403:GOL:H11	5:B:675:HOH:O	2.16	0.46
1:A:244:TYR:CZ	1:A:246:LEU:HA	2.51	0.45
1:B:164:LEU:HB2	1:B:168:VAL:HB	1.99	0.45
1:B:47:THR:HG22	1:B:185:GLU:CD	2.37	0.45
1:B:78:GLU:O	1:B:84:LEU:HD12	2.16	0.44
1:B:129:GLU:HB3	1:B:195:PRO:HD2	1.99	0.44
1:A:104:ARG:NH2	5:A:515:HOH:O	2.45	0.44
5:A:611:HOH:O	1:B:167:CYS:HB2	2.17	0.43
1:B:110:SER:O	1:B:146:GLY:HA2	2.18	0.43
1:A:104:ARG:NH1	5:A:520:HOH:O	2.51	0.42
1:A:6:MET:HE3	5:B:522:HOH:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:191:ILE:HD13	1:B:191:ILE:HG21	1.62	0.41
1:B:187:VAL:O	2:B:401[A]:K36:H28	2.20	0.41
1:A:71:GLU:OE1	1:A:73:GLN:NE2	2.54	0.41
1:B:31:TRP:CE2	1:B:92:ASN:HB2	2.56	0.41
1:B:134:LYS:HA	1:B:134:LYS:HD2	1.79	0.41
1:A:45:LYS:HD3	2:A:401[A]:K36:H14	2.04	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:582:HOH:O	5:A:835:HOH:O[2_656]	1.91	0.29
5:A:840:HOH:O	5:A:886:HOH:O[2_646]	2.16	0.04

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	296/303 (98%)	289 (98%)	7 (2%)	0	100	100
1	B	297/303 (98%)	295 (99%)	2 (1%)	0	100	100
All	All	593/606 (98%)	584 (98%)	9 (2%)	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	238/249 (96%)	238 (100%)	0	100	100
1	B	234/249 (94%)	233 (100%)	1 (0%)	91	85
All	All	472/498 (95%)	471 (100%)	1 (0%)	93	89

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	294	MET

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](#)

10 ligands are modelled in this entry.

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	GOL	B	405	-	5,5,5	0.82	0	5,5,5	1.21	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	K36	A	401[A]	1	30,30,34	7.39	17 (56%)	37,39,47	1.49	7 (18%)
4	GOL	A	404	-	5,5,5	1.00	0	5,5,5	1.29	1 (20%)
3	B1S	A	402[B]	1	30,30,34	6.45	15 (50%)	37,39,47	1.75	10 (27%)
4	GOL	B	406	-	5,5,5	1.18	1 (20%)	5,5,5	0.74	0
4	GOL	B	403	-	5,5,5	0.96	0	5,5,5	0.90	0
3	B1S	B	402[B]	1	30,30,34	7.38	17 (56%)	37,39,47	1.51	6 (16%)
2	K36	B	401[A]	1	30,30,34	7.36	17 (56%)	37,39,47	1.47	6 (16%)
4	GOL	B	404	-	5,5,5	1.41	1 (20%)	5,5,5	1.17	0
4	GOL	A	403	-	5,5,5	0.70	0	5,5,5	1.09	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
4	GOL	B	405	-	-	0/4/4/4	-
2	K36	A	401[A]	1	-	0/27/37/45	0/2/2/2
4	GOL	A	404	-	-	2/4/4/4	-
3	B1S	A	402[B]	1	-	0/27/37/45	0/2/2/2
4	GOL	B	406	-	-	0/4/4/4	-
4	GOL	B	403	-	-	4/4/4/4	-
3	B1S	B	402[B]	1	-	0/27/37/45	0/2/2/2
2	K36	B	401[A]	1	-	0/27/37/45	0/2/2/2
4	GOL	B	404	-	-	4/4/4/4	-
4	GOL	A	403	-	-	3/4/4/4	-

All (68) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401[A]	K36	C29-N28	26.42	1.61	1.33
2	B	401[A]	K36	C29-N28	25.96	1.61	1.33
3	B	402[B]	B1S	C29-N28	25.84	1.61	1.33
3	A	402[B]	B1S	C29-N28	23.94	1.59	1.33
3	B	402[B]	B1S	C25-C29	-17.83	1.30	1.52
2	B	401[A]	K36	C25-C29	-17.61	1.30	1.52
2	A	401[A]	K36	C25-C29	-17.41	1.31	1.52
3	B	402[B]	B1S	C26-C27	-15.93	1.28	1.53
2	A	401[A]	K36	C26-C27	-15.89	1.28	1.53
2	B	401[A]	K36	C26-C27	-15.86	1.28	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	402[B]	B1S	C25-C29	-12.93	1.36	1.52
3	A	402[B]	B1S	C26-C27	-12.38	1.33	1.53
2	A	401[A]	K36	C26-C25	6.64	1.72	1.54
2	B	401[A]	K36	C26-C25	6.59	1.72	1.54
3	B	402[B]	B1S	C3-C2	6.58	1.52	1.38
3	B	402[B]	B1S	C26-C25	6.55	1.72	1.54
2	B	401[A]	K36	C3-C2	6.54	1.52	1.38
2	A	401[A]	K36	C5-C6	6.52	1.52	1.38
3	B	402[B]	B1S	C2-C1	6.51	1.52	1.38
2	B	401[A]	K36	C2-C1	6.49	1.52	1.38
3	B	402[B]	B1S	C27-N28	6.48	1.59	1.46
3	B	402[B]	B1S	C5-C6	6.43	1.52	1.38
2	B	401[A]	K36	C5-C6	6.43	1.52	1.38
2	B	401[A]	K36	C27-N28	6.43	1.59	1.46
2	A	401[A]	K36	C3-C2	6.42	1.52	1.38
2	A	401[A]	K36	C6-C1	6.41	1.52	1.38
3	A	402[B]	B1S	C2-C1	6.37	1.52	1.38
3	A	402[B]	B1S	C6-C1	6.37	1.52	1.38
2	A	401[A]	K36	C2-C1	6.36	1.52	1.38
3	B	402[B]	B1S	C6-C1	6.31	1.52	1.38
2	B	401[A]	K36	C6-C1	6.31	1.52	1.38
3	A	402[B]	B1S	C5-C6	6.30	1.52	1.38
3	A	402[B]	B1S	C3-C2	6.30	1.52	1.38
2	A	401[A]	K36	C27-N28	6.29	1.59	1.46
3	A	402[B]	B1S	C27-N28	6.19	1.59	1.46
3	A	402[B]	B1S	C26-C25	5.69	1.69	1.54
3	A	402[B]	B1S	C5-C4	5.59	1.52	1.38
2	A	401[A]	K36	C5-C4	5.58	1.52	1.38
3	B	402[B]	B1S	C4-C3	5.55	1.52	1.38
2	B	401[A]	K36	C4-C3	5.55	1.52	1.38
2	A	401[A]	K36	C4-C3	5.52	1.52	1.38
2	B	401[A]	K36	C5-C4	5.50	1.52	1.38
3	B	402[B]	B1S	C5-C4	5.46	1.52	1.38
3	A	402[B]	B1S	C4-C3	5.42	1.52	1.38
3	B	402[B]	B1S	C17-N19	5.01	1.45	1.34
3	A	402[B]	B1S	C17-N19	4.86	1.44	1.34
2	A	401[A]	K36	C17-N19	4.73	1.44	1.34
2	B	401[A]	K36	C17-N19	4.65	1.44	1.34
3	B	402[B]	B1S	C9-N11	4.25	1.45	1.34
2	A	401[A]	K36	C9-N11	4.22	1.45	1.34
2	B	401[A]	K36	C9-N11	4.14	1.44	1.34
3	A	402[B]	B1S	C9-N11	3.64	1.43	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	402[B]	B1S	O8-C7	-3.15	1.39	1.45
2	B	401[A]	K36	O8-C7	-3.13	1.39	1.45
3	B	402[B]	B1S	O30-C29	-2.97	1.17	1.23
2	B	401[A]	K36	O30-C29	-2.96	1.17	1.23
2	A	401[A]	K36	O8-C7	-2.85	1.39	1.45
2	A	401[A]	K36	O30-C29	-2.64	1.18	1.23
2	A	401[A]	K36	O8-C9	2.59	1.40	1.35
2	A	401[A]	K36	O18-C17	-2.40	1.18	1.23
3	A	402[B]	B1S	O8-C9	2.39	1.39	1.35
3	B	402[B]	B1S	O8-C9	2.35	1.39	1.35
4	B	404	GOL	O2-C2	-2.34	1.36	1.43
3	B	402[B]	B1S	O18-C17	-2.32	1.18	1.23
2	B	401[A]	K36	O18-C17	-2.32	1.18	1.23
3	A	402[B]	B1S	O8-C7	-2.27	1.41	1.45
2	B	401[A]	K36	O8-C9	2.24	1.39	1.35
4	B	406	GOL	O2-C2	-2.17	1.36	1.43

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402[B]	B1S	O30-C29-C25	4.72	131.78	126.23
2	B	401[A]	K36	C27-N28-C29	-4.40	105.19	113.84
3	B	402[B]	B1S	C27-N28-C29	-4.37	105.25	113.84
2	A	401[A]	K36	C27-N28-C29	-4.24	105.51	113.84
2	A	401[A]	K36	O8-C9-N11	3.65	117.92	110.50
3	B	402[B]	B1S	O8-C9-N11	3.59	117.80	110.50
2	B	401[A]	K36	O8-C9-N11	3.51	117.63	110.50
3	A	402[B]	B1S	C27-N28-C29	-3.35	107.26	113.84
3	B	402[B]	B1S	C26-C25-C29	3.22	107.06	102.88
2	B	401[A]	K36	C26-C25-C29	2.97	106.75	102.88
3	B	402[B]	B1S	C14-C13-C12	-2.92	107.41	115.43
3	A	402[B]	B1S	C20-N19-C17	-2.87	118.62	123.20
2	B	401[A]	K36	C14-C13-C12	-2.81	107.70	115.43
2	A	401[A]	K36	C26-C25-C29	2.79	106.51	102.88
2	A	401[A]	K36	O10-C9-N11	-2.78	120.30	124.85
2	A	401[A]	K36	C20-N19-C17	-2.76	118.80	123.20
3	A	402[B]	B1S	C24-C25-C26	-2.70	107.38	117.31
3	A	402[B]	B1S	C24-C20-C21	-2.58	108.06	111.65
3	A	402[B]	B1S	C26-C25-C29	2.52	106.16	102.88
2	B	401[A]	K36	O10-C9-N11	-2.46	120.82	124.85
2	B	401[A]	K36	C21-C20-N19	-2.43	104.15	109.60
3	A	402[B]	B1S	C21-C20-N19	-2.42	104.17	109.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402[B]	B1S	O30-C29-N28	-2.42	122.18	125.54
3	B	402[B]	B1S	O10-C9-N11	-2.40	120.92	124.85
4	A	404	GOL	C3-C2-C1	-2.28	102.83	111.70
3	B	402[B]	B1S	C24-C20-C21	-2.25	108.52	111.65
3	A	402[B]	B1S	O18-C17-C12	2.21	125.11	120.45
2	A	401[A]	K36	C14-C13-C12	-2.09	109.69	115.43
2	A	401[A]	K36	C24-C25-C26	-2.05	109.76	117.31
3	A	402[B]	B1S	C13-C12-C17	-2.02	105.76	110.57

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	403	GOL	C1-C2-C3-O3
4	B	403	GOL	C1-C2-C3-O3
4	B	404	GOL	O1-C1-C2-C3
4	B	404	GOL	C1-C2-C3-O3
4	A	404	GOL	O1-C1-C2-O2
4	B	403	GOL	O2-C2-C3-O3
4	A	404	GOL	O1-C1-C2-C3
4	A	403	GOL	O2-C2-C3-O3
4	B	404	GOL	O1-C1-C2-O2
4	B	404	GOL	O2-C2-C3-O3
4	B	403	GOL	O1-C1-C2-O2
4	A	403	GOL	O1-C1-C2-C3
4	B	403	GOL	O1-C1-C2-C3

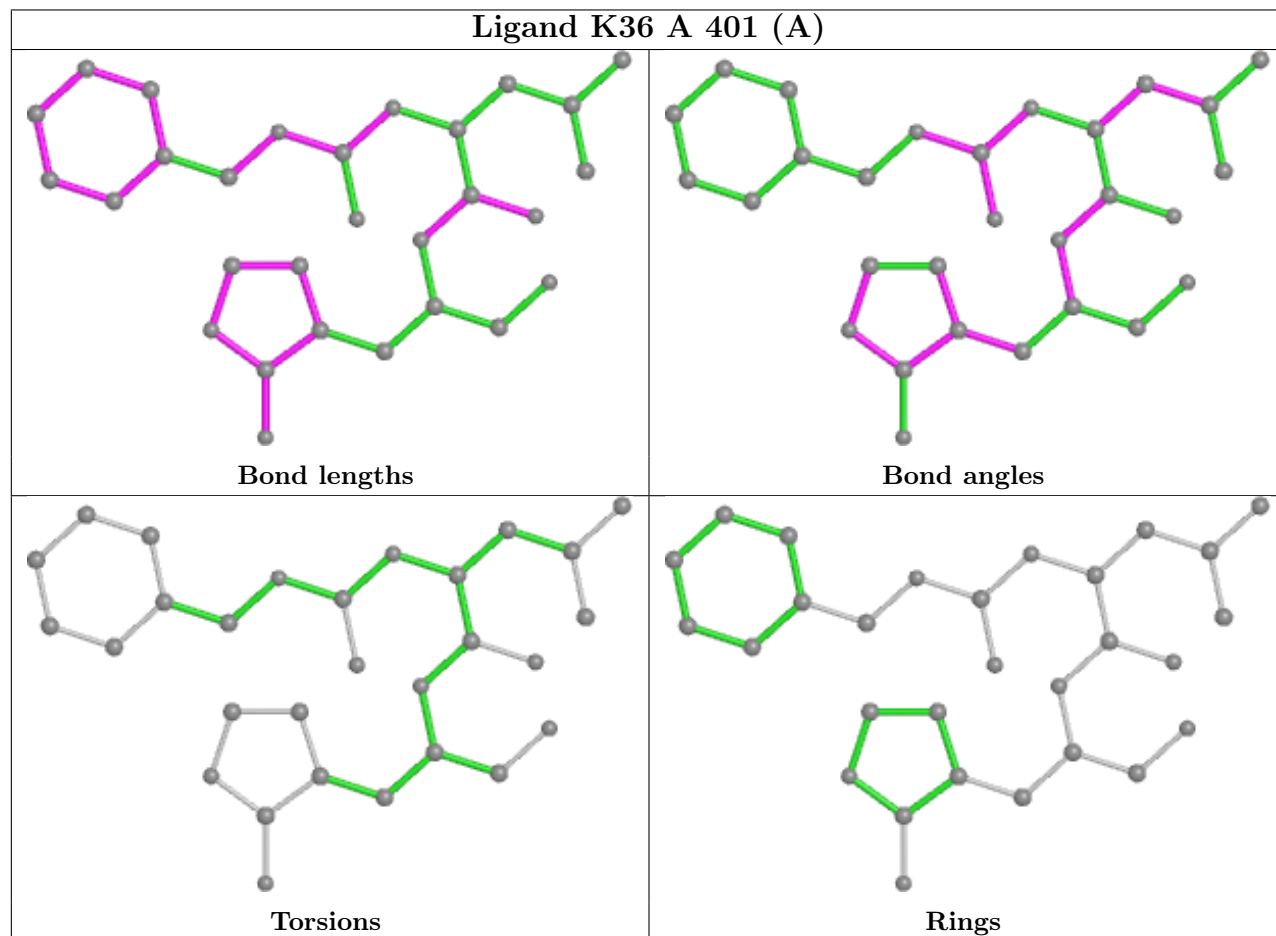
There are no ring outliers.

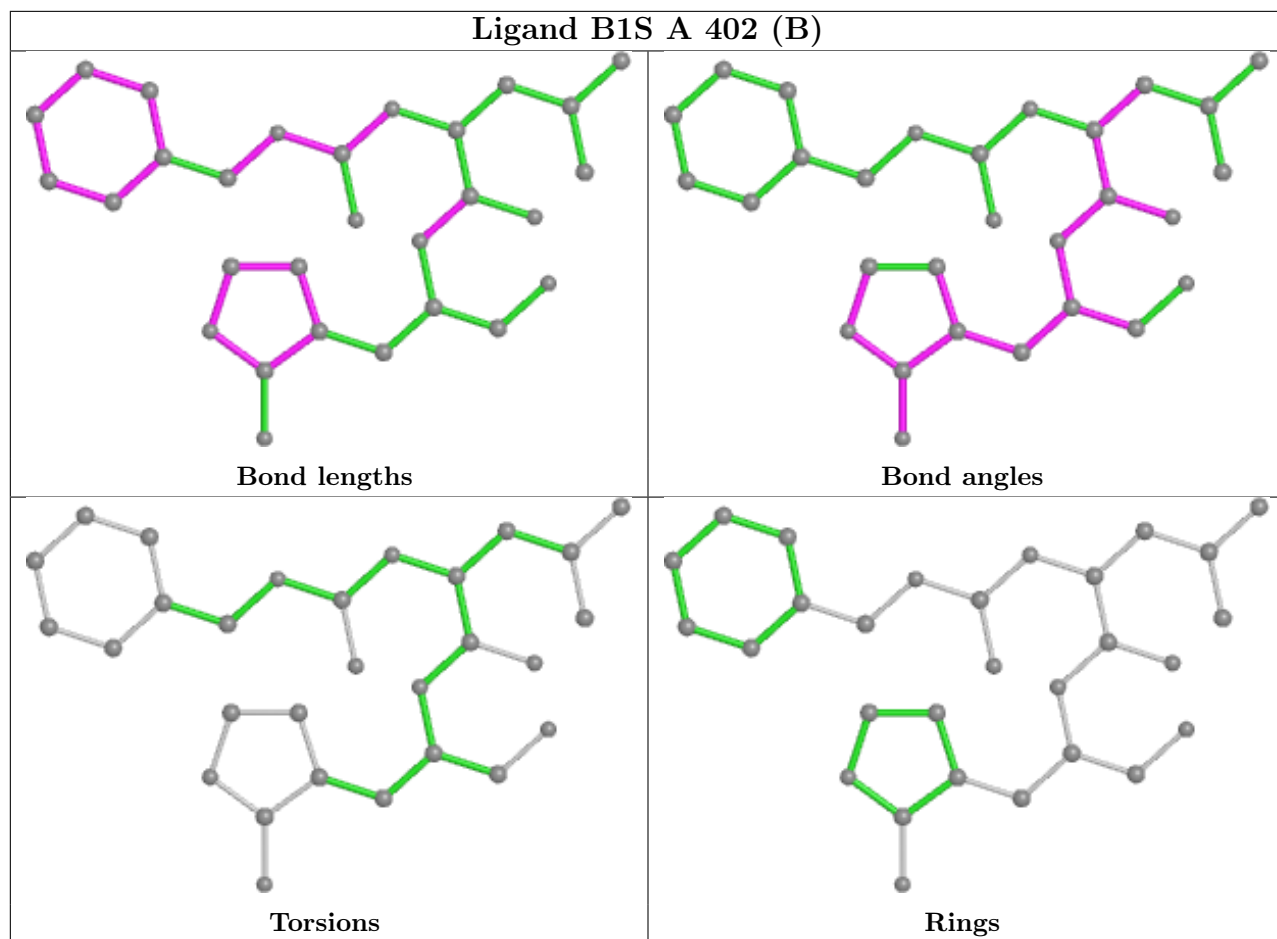
4 monomers are involved in 6 short contacts:

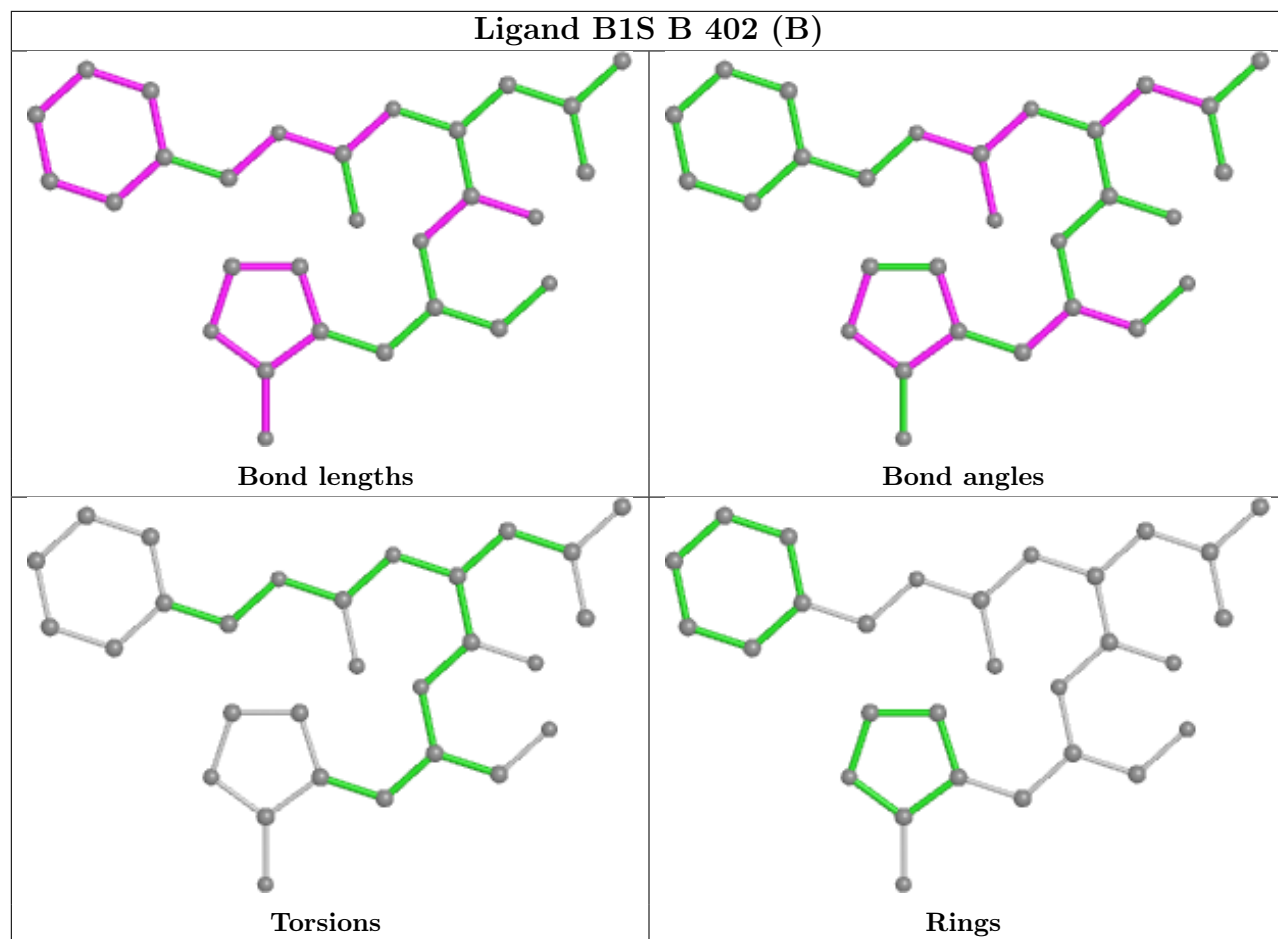
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	405	GOL	1	0
2	A	401[A]	K36	1	0
4	B	403	GOL	3	0
2	B	401[A]	K36	1	0

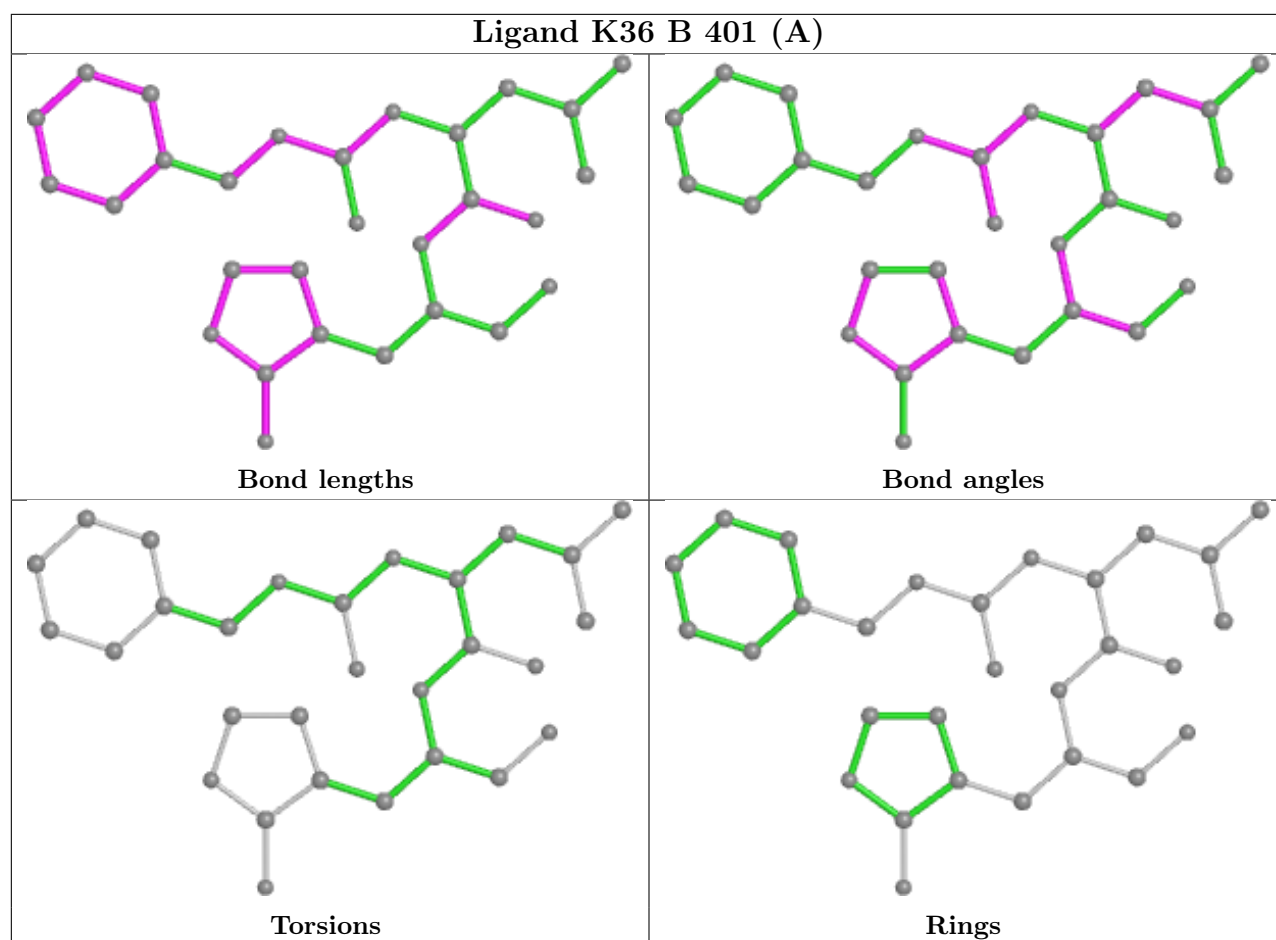
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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	299/303 (98%)	-0.37	8 (2%) 54 55	7, 15, 32, 55	0
1	B	298/303 (98%)	-0.34	5 (1%) 70 73	9, 17, 31, 49	0
All	All	597/606 (98%)	-0.36	13 (2%) 62 63	7, 16, 31, 55	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	302	LEU	9.5
1	B	220	GLY	5.2
1	A	151	ASN	4.9
1	B	219	TYR	4.8
1	A	301	VAL	4.8
1	A	152	GLU	3.5
1	A	223	GLN	3.3
1	B	151	ASN	3.1
1	A	193	PRO	2.8
1	B	275	TYR	2.5
1	B	221	PRO	2.3
1	A	300	ILE	2.2
1	A	150	THR	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 monosaccharides in this entry.

6.4 Ligands

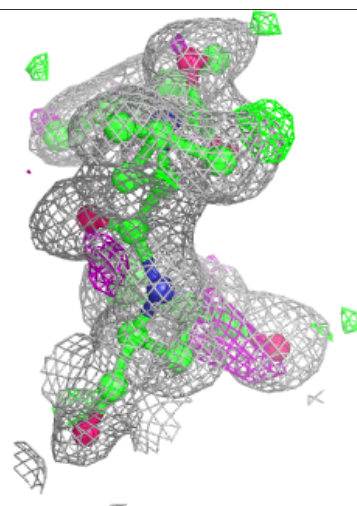
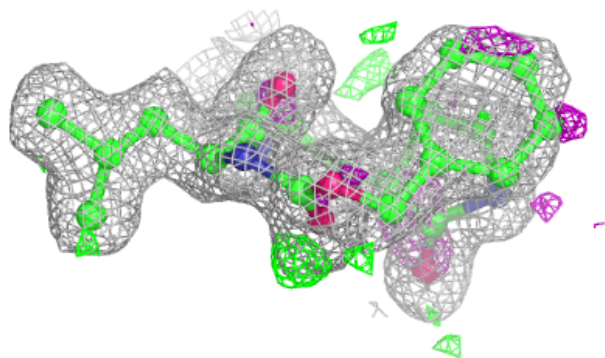
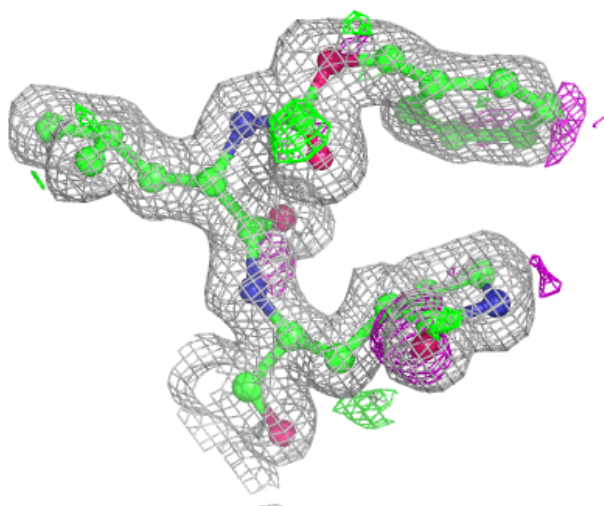
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GOL	B	405	6/6	0.84	0.25	38,40,46,51	0
4	GOL	A	404	6/6	0.85	0.23	33,38,41,43	0
4	GOL	A	403	6/6	0.86	0.33	32,38,44,45	0
4	GOL	B	406	6/6	0.88	0.19	39,42,43,44	0
4	GOL	B	404	6/6	0.90	0.21	32,35,37,41	0
2	K36	A	401[A]	29/33	0.91	0.12	9,13,23,25	29
3	B1S	B	402[B]	29/33	0.92	0.11	13,16,31,32	29
2	K36	B	401[A]	29/33	0.92	0.11	12,16,32,32	29
3	B1S	A	402[B]	29/33	0.92	0.12	9,13,24,26	29
4	GOL	B	403	6/6	0.95	0.14	18,35,40,41	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.

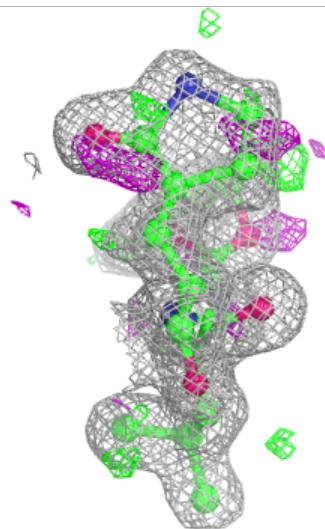
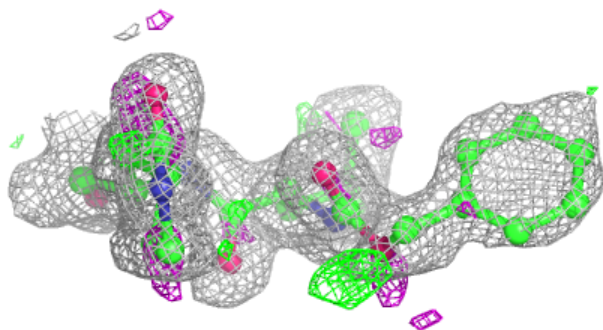
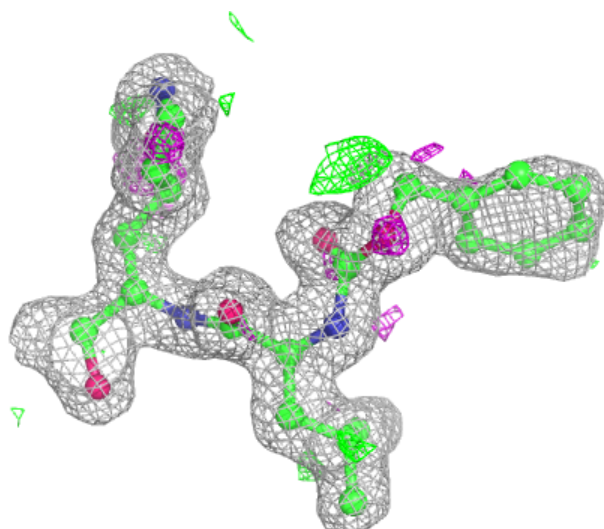
Electron density around K36 A 401 (A):

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



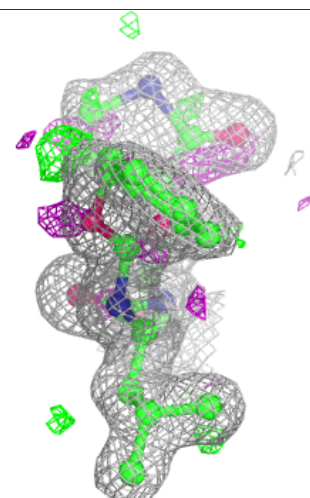
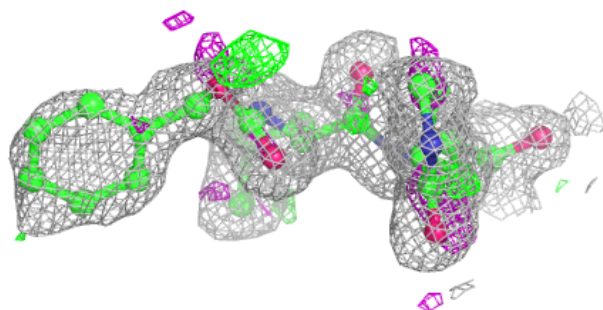
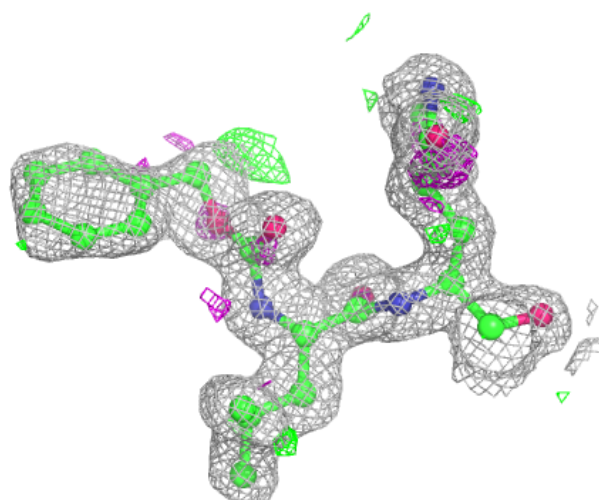
Electron density around B1S B 402 (B):

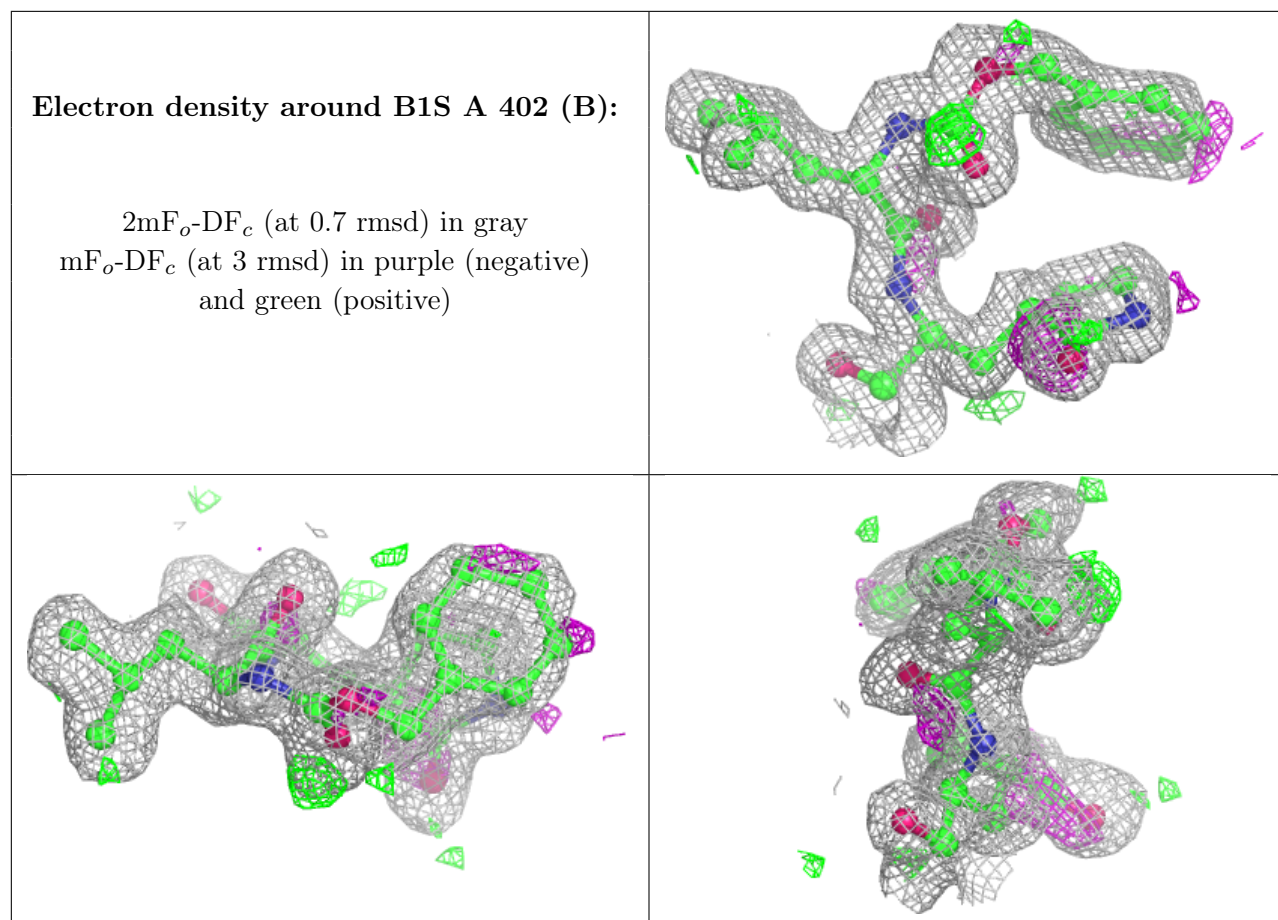
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around K36 B 401 (A):

$2mF_o-DF_c$ (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.