



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 17, 2025 – 10:11 AM EDT

PDB ID : 9BT5 / pdb_00009bt5
Title : The crystal structure of the HA1 domain of hemagglutinin from A/Shanghai/02/2013 (H7N9) bound to H7-235 Fab
Authors : Buchman, C.D.; Dong, J.; Crowe, J.E.
Deposited on : 2024-05-14
Resolution : 2.50 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 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 Phenix2.0rc1
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

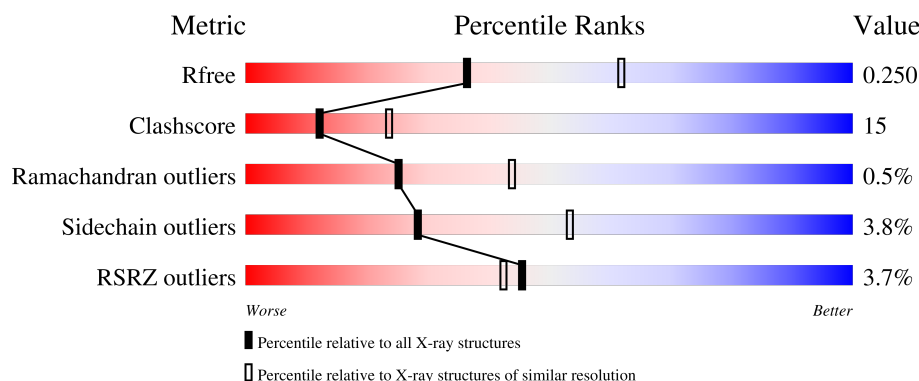
1 Overall quality at a glance

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}	164625	5504 (2.50-2.50)
Clashscore	180529	6282 (2.50-2.50)
Ramachandran outliers	177936	6191 (2.50-2.50)
Sidechain outliers	177891	6193 (2.50-2.50)
RSRZ outliers	164620	5504 (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	217	 2% 66% 33%
1	B	217	 % 75% 24%
2	C	228	 4% 63% 31% • 5%
2	E	228	 4% 71% 25% • •
3	D	219	 9% 68% 28% • •

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	F	219	<div><div></div><div>2%</div><div>64%</div><div>33%</div><div>..</div></div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10131 atoms, of which 36 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 Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	217	Total	C	N	O	S	0	0	0
			1632	1022	286	316	8			
1	B	217	Total	C	N	O	S	0	0	0
			1647	1031	290	317	9			

- Molecule 2 is a protein called Monoclonal antibody H7-235 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	217	Total	C	N	O	S	0	0	0
			1656	1049	282	318	7			
2	E	223	Total	C	N	O	S	0	0	0
			1693	1070	289	327	7			

- Molecule 3 is a protein called Monoclonal antibody H7-235 light chain.

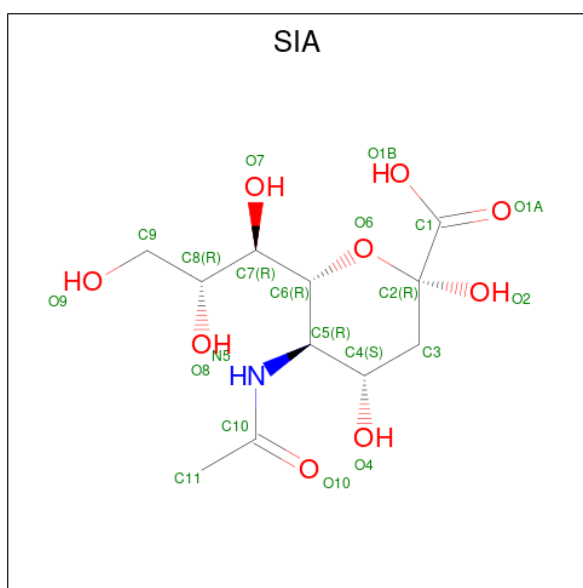
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	216	Total	C	N	O	S	0	0	0
			1601	1000	271	324	6			
3	F	216	Total	C	N	O	S	0	0	0
			1622	1018	272	326	6			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is N-acetyl-alpha-neuraminic acid (CCD ID: SIA) (formula: $C_{11}H_{19}NO_9$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	N	O	0
			39	11	18	1	9	
5	B	1	Total	C	H	N	O	0
			39	11	18	1	9	

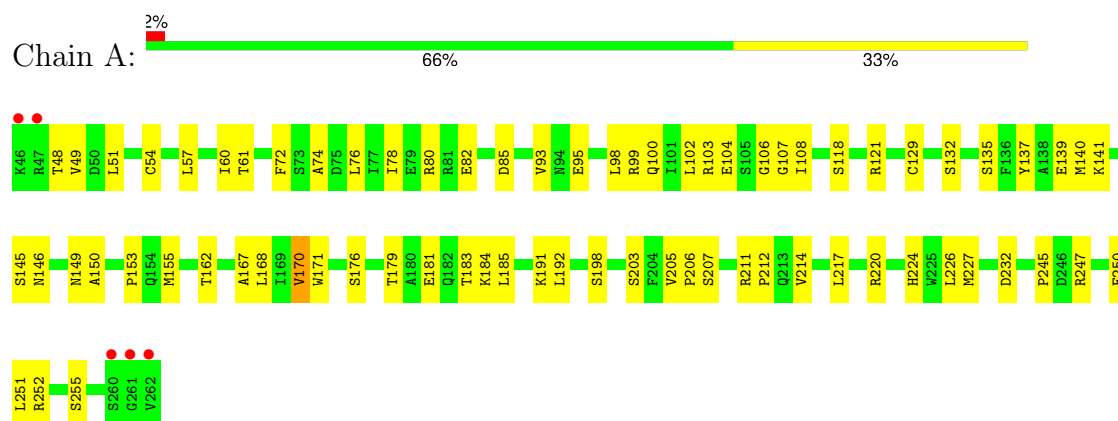
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	26	Total 26	O 26	0	0
6	C	30	Total 30	O 30	0	0
6	D	25	Total 25	O 25	0	0
6	B	34	Total 34	O 34	0	0
6	E	36	Total 36	O 36	0	0
6	F	23	Total 23	O 23	0	0

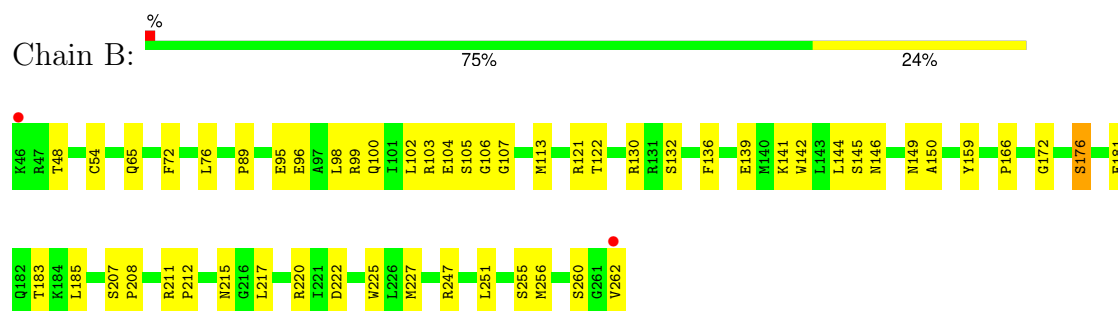
3 Residue-property plots [i](#)

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.

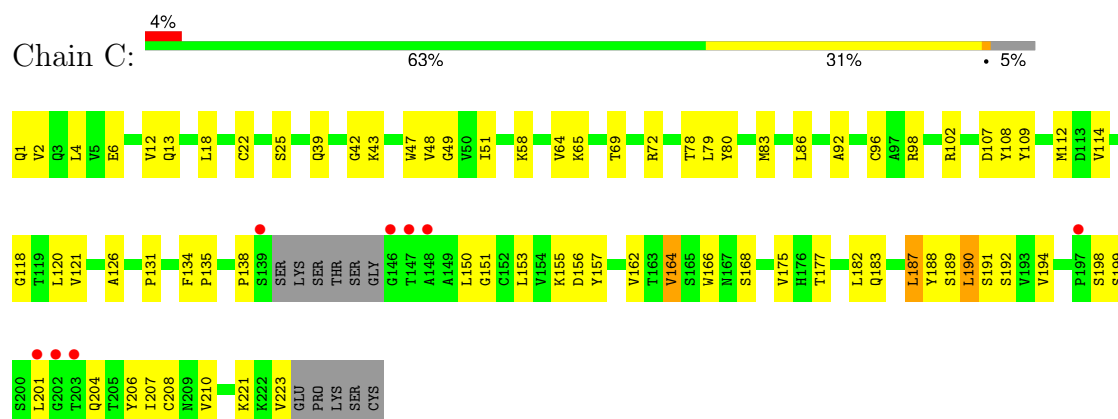
• Molecule 1: Hemagglutinin



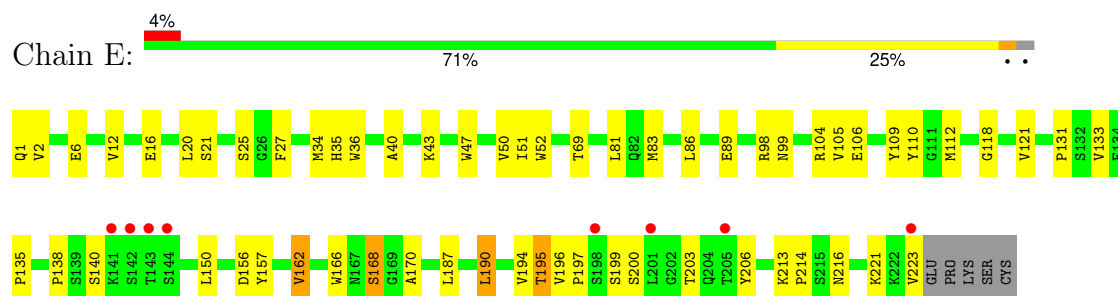
• Molecule 1: Hemagglutinin



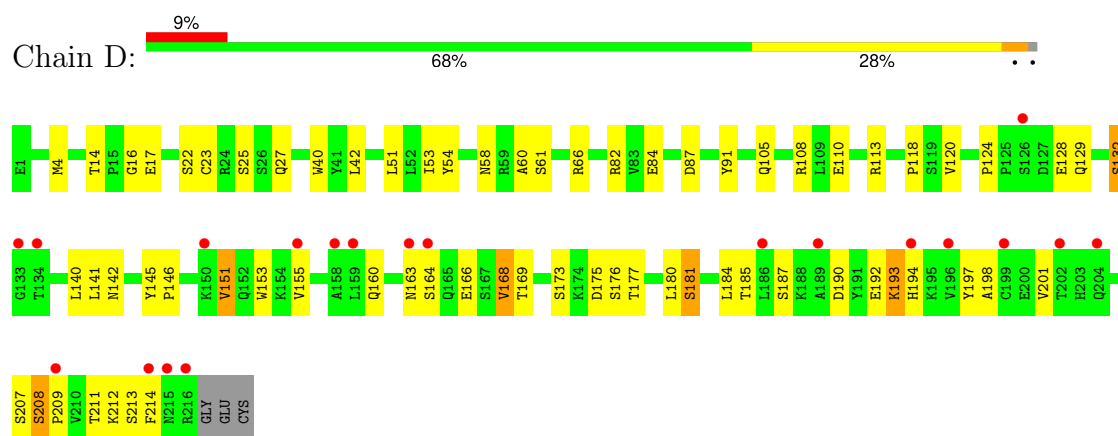
• Molecule 2: Monoclonal antibody H7-235 heavy chain



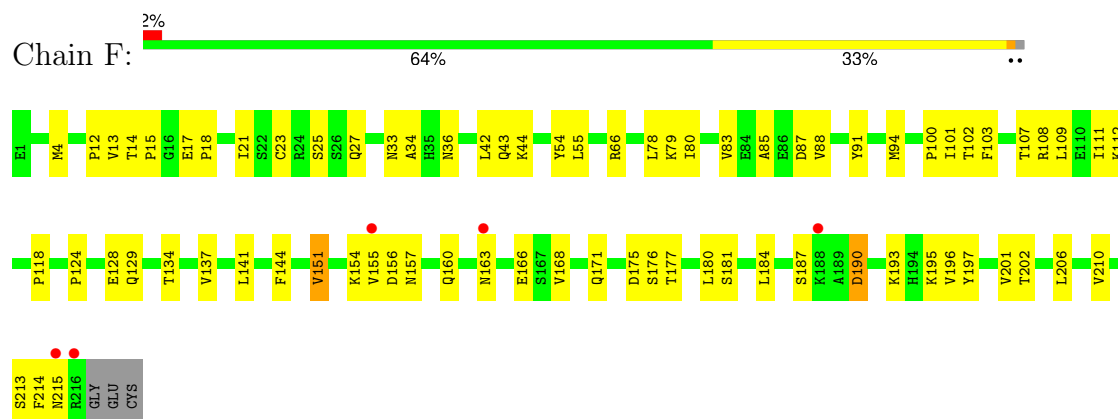
- Molecule 2: Monoclonal antibody H7-235 heavy chain



- Molecule 3: Monoclonal antibody H7-235 light chain



- Molecule 3: Monoclonal antibody H7-235 light chain



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	240.60 Å 95.05 Å 99.27 Å 90.00° 95.85° 90.00°	Depositor
Resolution (Å)	49.37 – 2.50 49.37 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.4 (49.37-2.50) 99.4 (49.37-2.50)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.75 (at 2.51 Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.195 , 0.251 0.194 , 0.250	Depositor DCC
R_{free} test set	3980 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å ²)	46.6	Xtriage
Anisotropy	0.779	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 60.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10131	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% 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: SIA, NAG

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	0.48	0/1668	0.66	0/2260
1	B	0.46	0/1683	0.63	0/2278
2	C	0.43	0/1699	0.64	0/2314
2	E	0.47	0/1737	0.65	0/2366
3	D	0.41	0/1637	0.59	0/2237
3	F	0.46	0/1658	0.65	0/2262
All	All	0.45	0/10082	0.64	0/13717

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1632	0	1550	59	1
1	B	1647	0	1581	37	1
2	C	1656	0	1585	54	0
2	E	1693	0	1621	47	0
3	D	1601	0	1481	55	0
3	F	1622	0	1541	53	0
4	A	14	0	13	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	14	0	13	0	0
5	A	21	18	18	1	0
5	B	21	18	18	2	0
6	A	26	0	0	1	0
6	B	34	0	0	1	0
6	C	30	0	0	0	0
6	D	25	0	0	2	0
6	E	36	0	0	1	0
6	F	23	0	0	2	0
All	All	10095	36	9421	296	1

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 15.

The worst 5 of 296 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:48:THR:HG23	1:A:76:LEU:HB3	1.37	1.06
2:C:135:PRO:HB3	2:C:223:VAL:HG12	1.37	1.06
3:F:21:ILE:HD12	3:F:107:THR:HG21	1.44	0.99
2:E:83:MET:HE1	2:E:121:VAL:HG21	1.43	0.97
2:E:1:GLN:OE1	2:E:1:GLN:N	1.99	0.94

All (1) 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)
1:A:211:ARG:NH1	1:B:96:GLU:OE1[2_556]	2.01	0.19

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	215/217 (99%)	205 (95%)	10 (5%)	0	100	100
1	B	215/217 (99%)	204 (95%)	11 (5%)	0	100	100
2	C	213/228 (93%)	197 (92%)	14 (7%)	2 (1%)	14	28
2	E	221/228 (97%)	210 (95%)	9 (4%)	2 (1%)	14	28
3	D	214/219 (98%)	200 (94%)	12 (6%)	2 (1%)	14	28
3	F	214/219 (98%)	205 (96%)	9 (4%)	0	100	100
All	All	1292/1328 (97%)	1221 (94%)	65 (5%)	6 (0%)	25	44

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	132	SER
3	D	193	LYS
2	E	168	SER
2	C	201	LEU
2	E	199	SER

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	172/180 (96%)	169 (98%)	3 (2%)	56	79
1	B	176/180 (98%)	173 (98%)	3 (2%)	56	79
2	C	179/191 (94%)	171 (96%)	8 (4%)	23	46
2	E	183/191 (96%)	175 (96%)	8 (4%)	24	47
3	D	172/193 (89%)	161 (94%)	11 (6%)	14	30
3	F	179/193 (93%)	172 (96%)	7 (4%)	27	52
All	All	1061/1128 (94%)	1021 (96%)	40 (4%)	28	53

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	140	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	F	151	VAL
2	E	162	VAL
2	E	203	THR
3	F	187	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	76	GLN
2	E	183	GLN
3	F	98	GLN
3	F	50	GLN
1	B	182	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	NAG	A	1001	1	14,14,15	0.29	0	17,19,21	0.56	0
5	SIA	A	1002	-	21,21,21	2.23	6 (28%)	24,31,31	3.17	12 (50%)
5	SIA	B	1002	-	21,21,21	2.14	6 (28%)	24,31,31	2.13	8 (33%)
4	NAG	B	1001	1	14,14,15	0.27	0	17,19,21	0.52	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	NAG	A	1001	1	-	2/6/23/26	0/1/1/1
5	SIA	A	1002	-	-	9/20/38/38	0/1/1/1
5	SIA	B	1002	-	-	7/20/38/38	0/1/1/1
4	NAG	B	1001	1	-	2/6/23/26	0/1/1/1

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1002	SIA	O6-C2	5.66	1.48	1.43
5	A	1002	SIA	O6-C2	4.88	1.48	1.43
5	B	1002	SIA	C2-C1	4.74	1.60	1.53
5	A	1002	SIA	C2-C1	4.42	1.60	1.53
5	A	1002	SIA	C3-C2	3.82	1.56	1.51

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1002	SIA	O1A-C1-C2	-6.73	112.62	123.85
5	A	1002	SIA	C6-C5-N5	-6.00	101.33	110.91
5	B	1002	SIA	O1A-C1-C2	-5.91	114.00	123.85
5	A	1002	SIA	O4-C4-C3	5.32	122.33	109.97
5	A	1002	SIA	O6-C6-C5	5.05	114.47	109.84

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1002	SIA	C6-C7-C8-C9
5	A	1002	SIA	C6-C7-C8-O8

Continued on next page...

Continued from previous page...

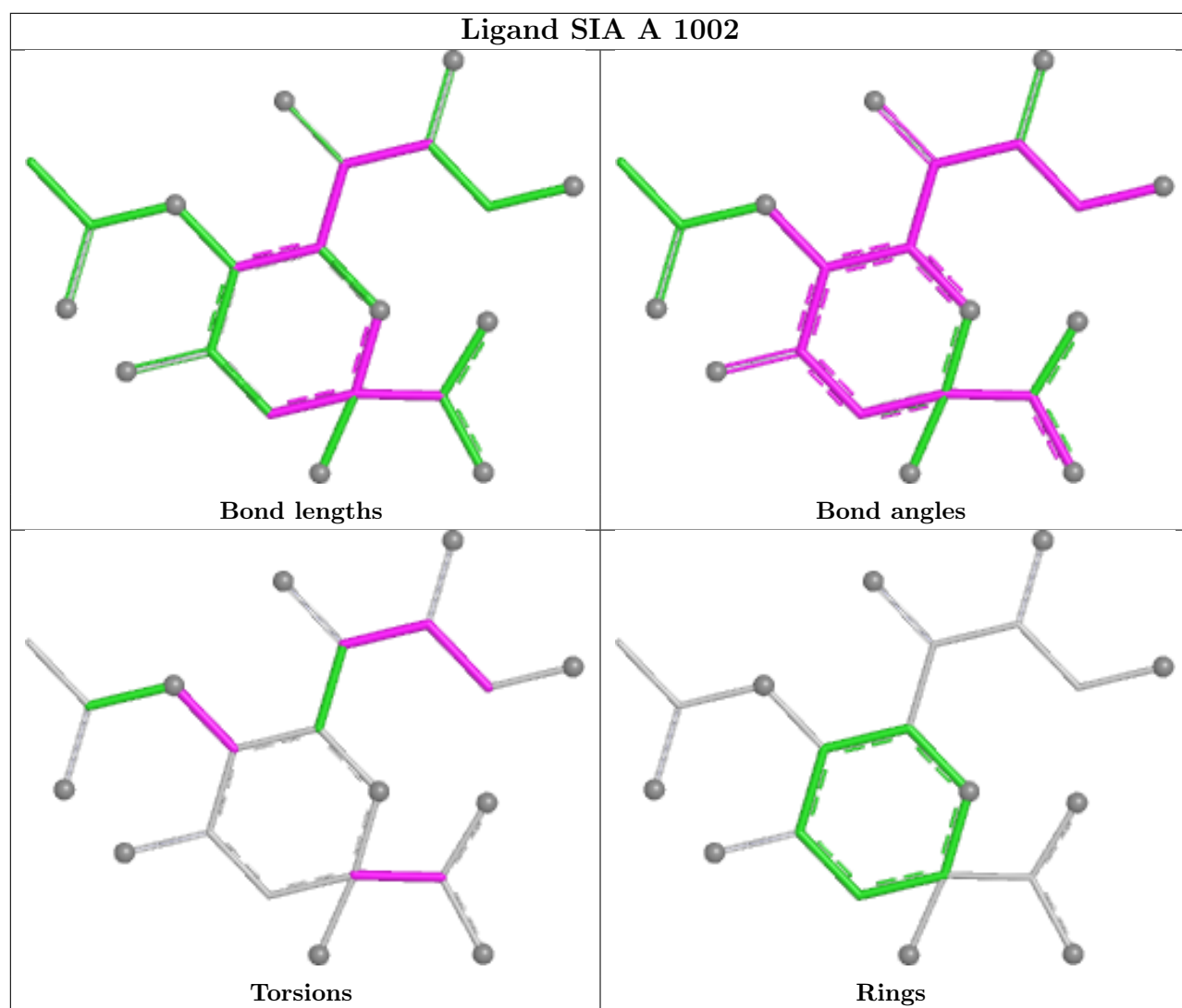
Mol	Chain	Res	Type	Atoms
5	A	1002	SIA	O7-C7-C8-C9
5	A	1002	SIA	O7-C7-C8-O8
5	B	1002	SIA	C6-C7-C8-C9

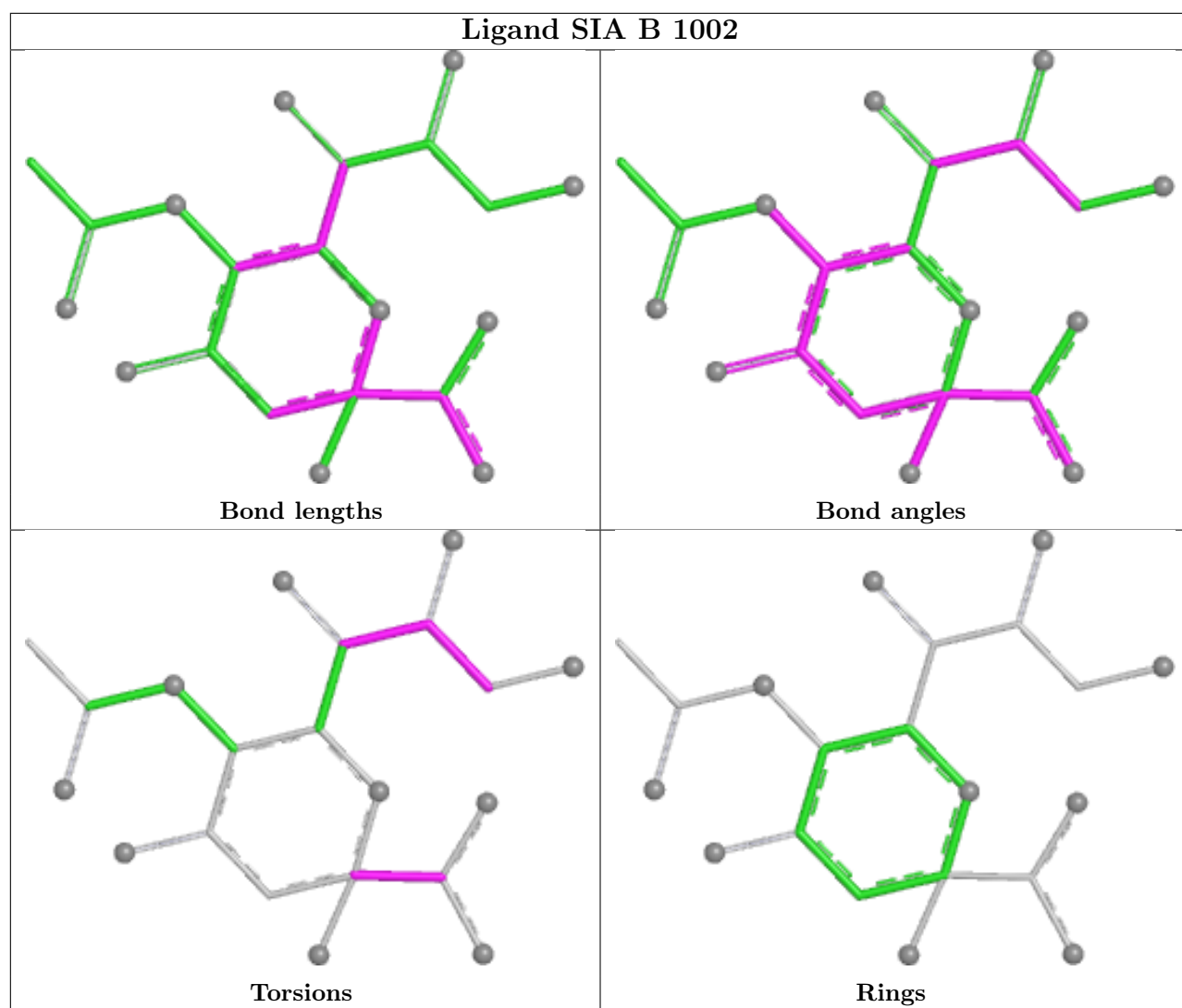
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1002	SIA	1	0
5	B	1002	SIA	2	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	217/217 (100%)	-0.06	5 (2%) 61 58	37, 57, 92, 134	0
1	B	217/217 (100%)	-0.20	2 (0%) 81 78	38, 52, 85, 111	0
2	C	217/228 (95%)	-0.01	8 (3%) 45 42	40, 58, 109, 130	0
2	E	223/228 (97%)	-0.10	8 (3%) 46 43	36, 51, 87, 119	0
3	D	216/219 (98%)	0.33	20 (9%) 16 15	38, 70, 120, 148	0
3	F	216/219 (98%)	0.02	5 (2%) 61 58	35, 58, 97, 110	0
All	All	1306/1328 (98%)	-0.00	48 (3%) 45 42	35, 56, 105, 148	0

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	262	VAL	6.6
3	D	216	ARG	4.2
2	E	142	SER	4.2
2	C	139	SER	4.0
3	D	158	ALA	3.8

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

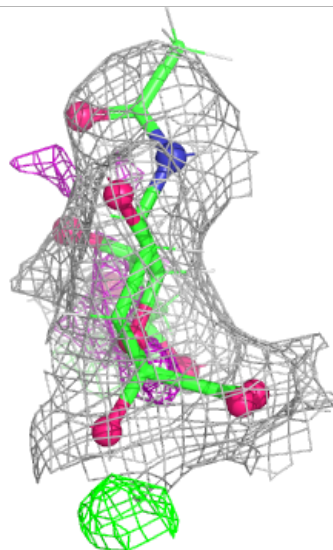
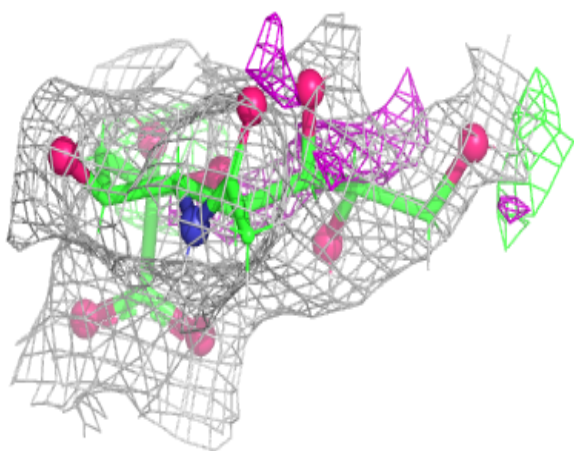
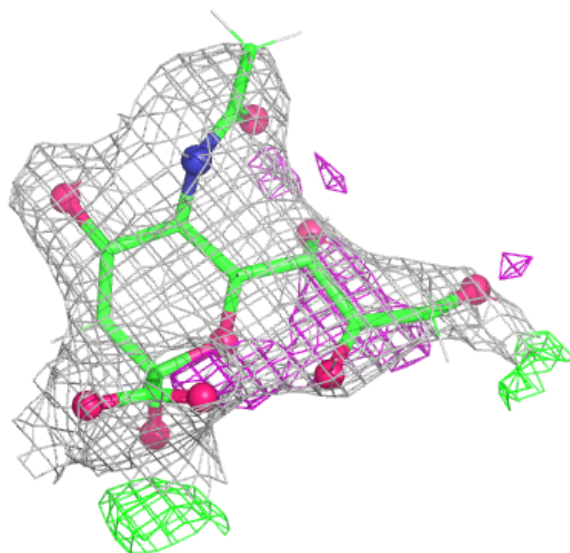
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	NAG	A	1001	14/15	0.78	0.14	85,106,112,112	0
5	SIA	B	1002	21/21	0.81	0.13	74,88,105,109	0
4	NAG	B	1001	14/15	0.83	0.13	73,88,98,100	0
5	SIA	A	1002	21/21	0.86	0.12	54,73,88,93	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.

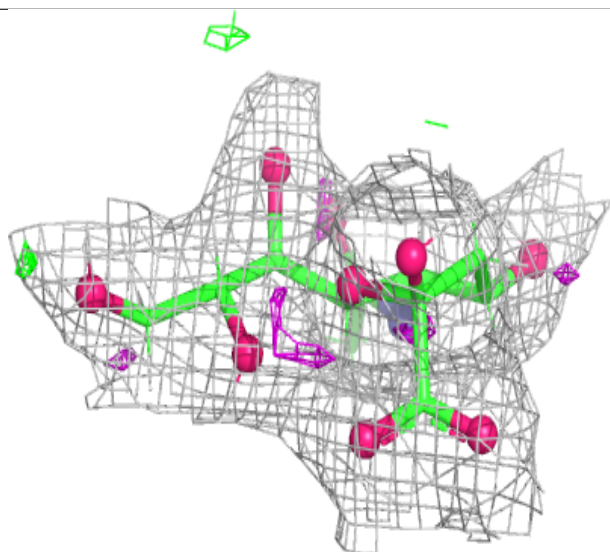
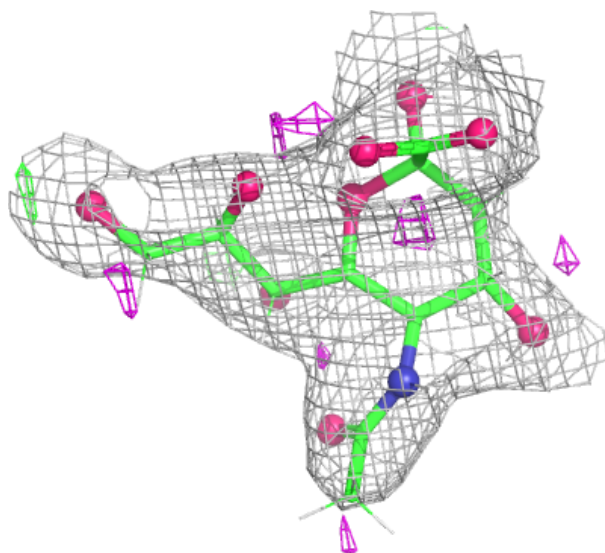
Electron density around SIA B 1002:

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



Electron density around SIA A 1002:

$2mF_o-DF_c$ (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.