



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 03:00 AM UTC

PDB ID : 8A9Q / pdb\_00008a9q  
Title : Computational design of stable mammalian serum albumins for bacterial expression  
Authors : Khersonsky, O.; Dym, O.; Fleishman, J.S.  
Deposited on : 2022-06-29  
Resolution : 2.00 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

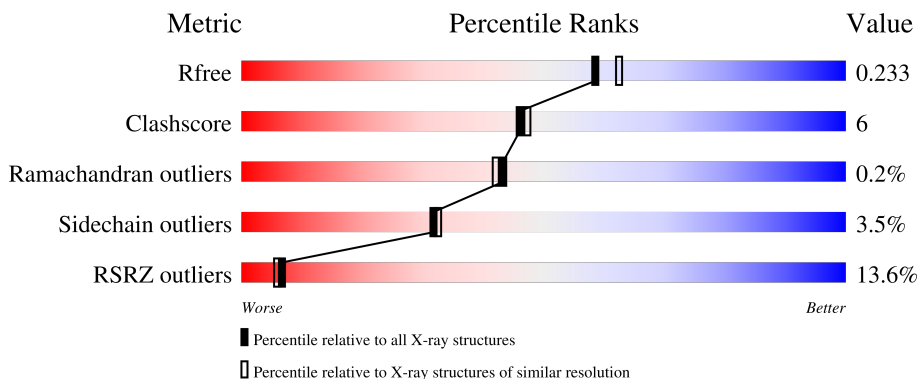
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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  $\geq 3$ , 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	585	 11% 81% 17% ..
1	B	585	 16% 82% 15% ..

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 9165 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 Albumin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	582	4458	2831	747	838	42	0	0	1
1	B	582	4444	2826	746	829	43	0	1	0

There are 32 discrepancies between the modelled and reference sequences:

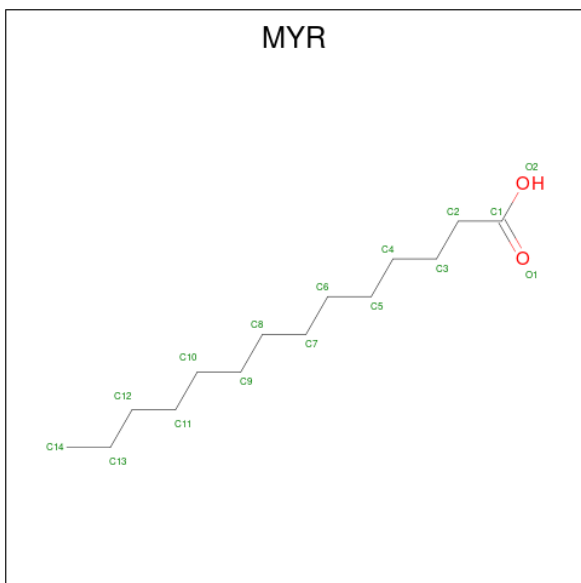
Chain	Residue	Modelled	Actual	Comment	Reference
A	39	LEU	HIS	engineered mutation	UNP P02768
A	42	MET	LEU	engineered mutation	UNP P02768
A	120	PRO	VAL	engineered mutation	UNP P02768
A	156	TYR	PHE	engineered mutation	UNP P02768
A	187	GLU	ASP	engineered mutation	UNP P02768
A	198	HIS	LEU	engineered mutation	UNP P02768
A	202	ILE	SER	engineered mutation	UNP P02768
A	310	ILE	VAL	engineered mutation	UNP P02768
A	371	SER	ALA	engineered mutation	UNP P02768
A	381	ILE	VAL	engineered mutation	UNP P02768
A	409	ILE	VAL	engineered mutation	UNP P02768
A	427	ALA	SER	engineered mutation	UNP P02768
A	455	ILE	VAL	engineered mutation	UNP P02768
A	519	GLU	LYS	engineered mutation	UNP P02768
A	552	SER	ALA	engineered mutation	UNP P02768
A	576	ILE	VAL	engineered mutation	UNP P02768
B	39	LEU	HIS	engineered mutation	UNP P02768
B	42	MET	LEU	engineered mutation	UNP P02768
B	120	PRO	VAL	engineered mutation	UNP P02768
B	156	TYR	PHE	engineered mutation	UNP P02768
B	187	GLU	ASP	engineered mutation	UNP P02768
B	198	HIS	LEU	engineered mutation	UNP P02768
B	202	ILE	SER	engineered mutation	UNP P02768
B	310	ILE	VAL	engineered mutation	UNP P02768
B	371	SER	ALA	engineered mutation	UNP P02768

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Chain	Residue	Modelled	Actual	Comment	Reference
B	381	ILE	VAL	engineered mutation	UNP P02768
B	409	ILE	VAL	engineered mutation	UNP P02768
B	427	ALA	SER	engineered mutation	UNP P02768
B	455	ILE	VAL	engineered mutation	UNP P02768
B	519	GLU	LYS	engineered mutation	UNP P02768
B	552	SER	ALA	engineered mutation	UNP P02768
B	576	ILE	VAL	engineered mutation	UNP P02768

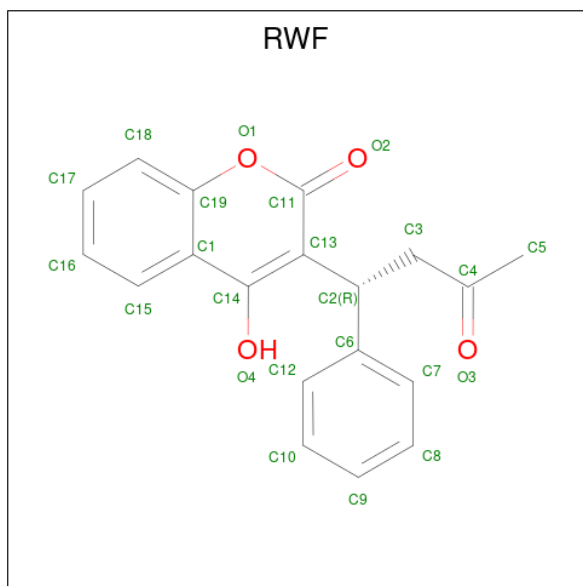
- Molecule 2 is MYRISTIC ACID (CCD ID: MYR) (formula: C<sub>14</sub>H<sub>28</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
2	A	1	Total	C	O	0	0
			16	14	2		
2	A	1	Total	C	O	0	0
			16	14	2		
2	A	1	Total	C	O	0	0
			16	14	2		
2	A	1	Total	C	O	0	0
			16	14	2		
2	B	1	Total	C	O	0	0
			16	14	2		
2	B	1	Total	C	O	0	0
			16	14	2		
2	B	1	Total	C	O	0	0
			16	14	2		

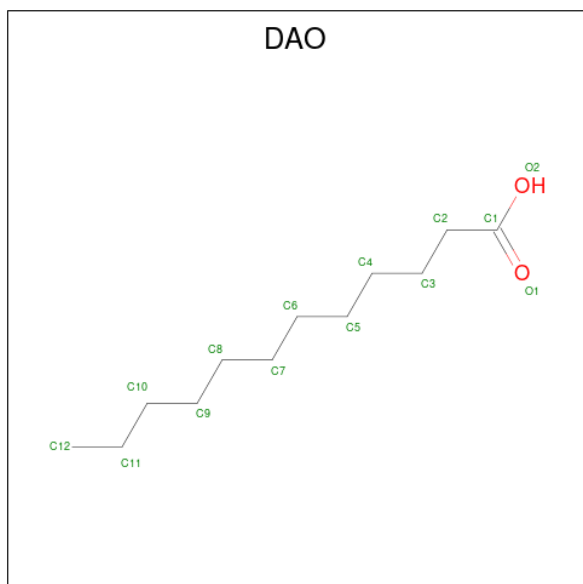
- Molecule 3 is R-WARFARIN (CCD ID: RWF) (formula: C<sub>19</sub>H<sub>16</sub>O<sub>4</sub>) (labeled as "Ligand of

Interest" by depositor).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	C O	0	0
			23	19 4		
3	B	1	Total	C O	0	0
			23	19 4		

- Molecule 4 is LAURIC ACID (CCD ID: DAO) (formula:  $C_{12}H_{24}O_2$ ).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	C O	0	0
			14	12 2		

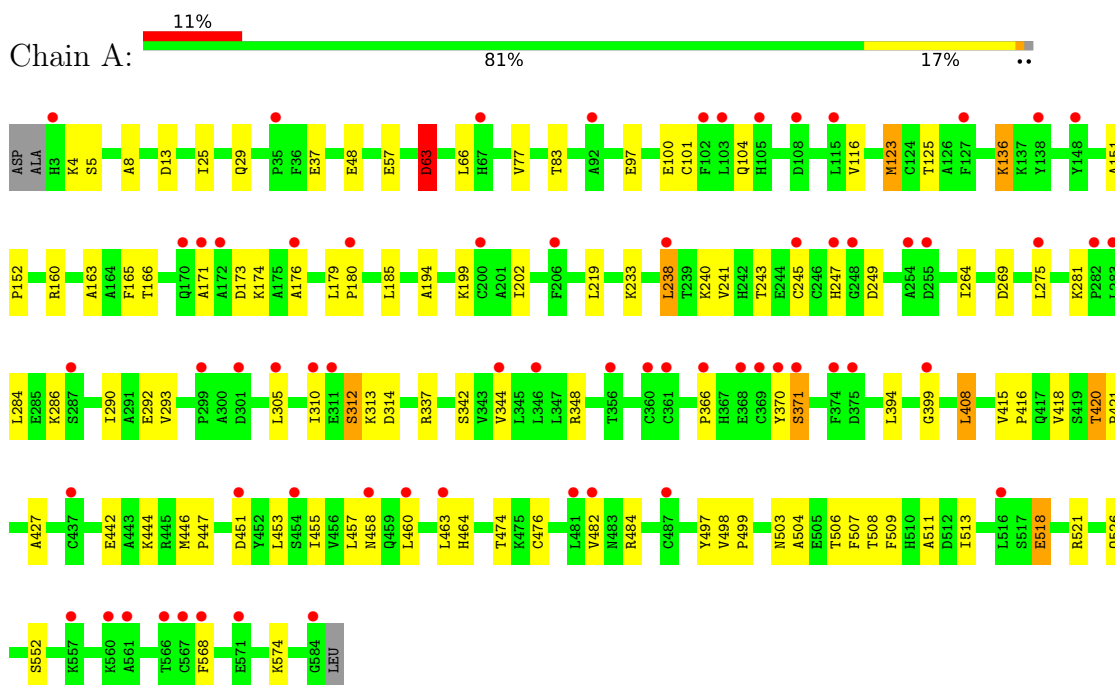
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	52	Total 52	O 52	0	0
5	B	39	Total 39	O 39	0	0

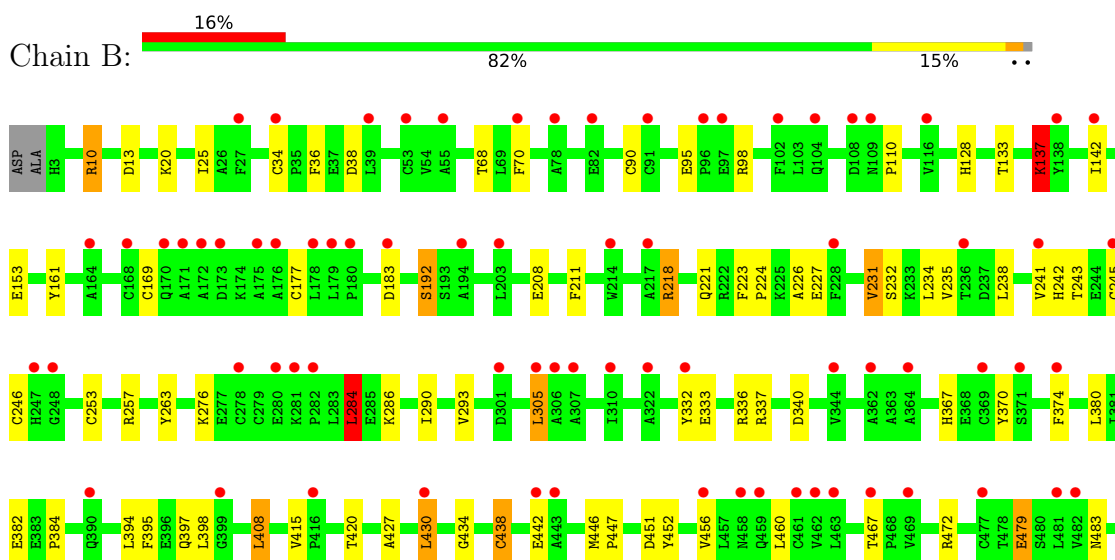
### 3 Residue-property plots

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: Albumin



#### • Molecule 1: Albumin





## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	38.26Å 92.13Å 95.55Å 74.35° 89.29° 79.98°	Depositor
Resolution (Å)	46.02 – 2.00 46.02 – 2.00	Depositor EDS
% Data completeness (in resolution range)	89.0 (46.02-2.00) 89.0 (46.02-2.00)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.38 (at 2.00Å)	Xtrriage
Refinement program	PHENIX 1.15.2	Depositor
R, $R_{free}$	0.220 , 0.271 0.236 , 0.233	Depositor DCC
$R_{free}$ test set	3603 reflections (4.31%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	41.3	Xtrriage
Anisotropy	0.290	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 25.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.36$	Xtrriage
Estimated twinning fraction	0.076 for h,h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	9165	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.02% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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: RWF, MYR, DAO

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	1.23	7/4548 (0.2%)	1.63	25/6165 (0.4%)
1	B	1.23	6/4535 (0.1%)	1.69	44/6152 (0.7%)
All	All	1.23	13/9083 (0.1%)	1.66	69/12317 (0.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	444	LYS	C-O	7.00	1.33	1.24
1	A	66	LEU	C-O	5.90	1.31	1.24
1	A	342	SER	C-O	5.82	1.31	1.23
1	A	123	MET	C-O	5.51	1.30	1.24
1	B	438	CYS	C-O	-5.47	1.17	1.24

The worst 5 of 69 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	13	ASP	CA-CB-CG	7.92	120.52	112.60
1	B	110	PRO	CA-C-N	-7.03	112.37	122.77
1	B	110	PRO	C-N-CA	-7.03	112.37	122.77
1	B	13	ASP	CA-CB-CG	7.03	119.62	112.60
1	A	420	THR	CA-CB-OG1	-7.02	99.08	109.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	312	SER	Peptide
1	A	399	GLY	Peptide

## 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	4458	0	4226	52	0
1	B	4444	0	4201	44	0
2	A	64	0	108	11	0
2	B	48	0	81	1	0
3	A	23	0	16	1	0
3	B	23	0	16	2	0
4	B	14	0	23	2	0
5	A	52	0	0	0	0
5	B	39	0	0	1	0
All	All	9165	0	8671	102	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 6.

The worst 5 of 102 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:241:VAL:O	1:A:245:CYS:SG	2.09	1.09
1:A:312:SER:OG	1:A:313:LYS:O	1.83	0.94
1:B:504:ALA:O	1:B:508:THR:HG23	1.77	0.84
1:A:504:ALA:O	1:A:508:THR:HG23	1.81	0.80
1:B:305:LEU:HD11	1:B:333:GLU:HB3	1.64	0.80

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	580/585 (99%)	553 (95%)	26 (4%)	1 (0%)	43	42
1	B	581/585 (99%)	554 (95%)	26 (4%)	1 (0%)	43	42
All	All	1161/1170 (99%)	1107 (95%)	52 (4%)	2 (0%)	43	42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	171	ALA
1	B	479	GLU

### 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	457/512 (89%)	441 (96%)	16 (4%)	32	32
1	B	451/512 (88%)	435 (96%)	16 (4%)	32	32
All	All	908/1024 (89%)	876 (96%)	32 (4%)	32	32

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	430	LEU
1	B	442	GLU
1	A	408	LEU
1	A	371	SER

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Mol	Chain	Res	Type
1	B	451	ASP

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

Mol	Chain	Res	Type
1	B	242	HIS
1	B	288	HIS
1	B	483	ASN
1	B	397	GLN
1	A	464	HIS

### 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](#)

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
2	MYR	A	601	-	15,15,15	1.19	1 (6%)	15,15,15	0.98	1 (6%)
2	MYR	A	604	-	15,15,15	0.90	1 (6%)	15,15,15	1.24	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	MYR	B	604	-	15,15,15	1.54	2 (13%)	15,15,15	0.65	0
2	MYR	A	602	-	15,15,15	0.54	0	15,15,15	1.88	4 (26%)
2	MYR	B	602	-	15,15,15	0.94	1 (6%)	15,15,15	1.06	0
3	RWF	A	605	-	25,25,25	2.92	7 (28%)	34,35,35	2.61	14 (41%)
3	RWF	B	605	-	25,25,25	2.23	7 (28%)	34,35,35	3.19	14 (41%)
4	DAO	B	603	-	13,13,13	0.60	0	13,13,13	0.63	0
2	MYR	A	603	-	15,15,15	1.72	2 (13%)	15,15,15	1.10	0
2	MYR	B	601	-	15,15,15	0.98	0	15,15,15	0.98	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
2	MYR	A	601	-	-	7/13/13/13	-
2	MYR	A	604	-	-	8/13/13/13	-
2	MYR	B	604	-	-	5/13/13/13	-
2	MYR	A	602	-	-	8/13/13/13	-
2	MYR	B	602	-	-	8/13/13/13	-
3	RWF	A	605	-	-	3/12/12/12	0/3/3/3
3	RWF	B	605	-	-	3/12/12/12	0/3/3/3
4	DAO	B	603	-	-	8/11/11/11	-
2	MYR	A	603	-	-	8/13/13/13	-
2	MYR	B	601	-	-	5/13/13/13	-

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	605	RWF	C2-C13	-7.73	1.42	1.52
3	A	605	RWF	O3-C4	6.77	1.46	1.21
3	A	605	RWF	C6-C2	-6.27	1.42	1.52
3	B	605	RWF	O3-C4	5.63	1.42	1.21
3	B	605	RWF	C6-C2	-5.59	1.43	1.52

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	605	RWF	O3-C4-C3	-11.98	102.96	121.74
3	B	605	RWF	C3-C2-C6	-6.82	94.27	111.75
3	A	605	RWF	C2-C3-C4	-5.96	106.34	114.57
3	B	605	RWF	C6-C2-C13	5.71	122.34	111.94
3	A	605	RWF	O3-C4-C3	-5.64	112.90	121.74

There are no chirality outliers.

5 of 63 torsion outliers are listed below:

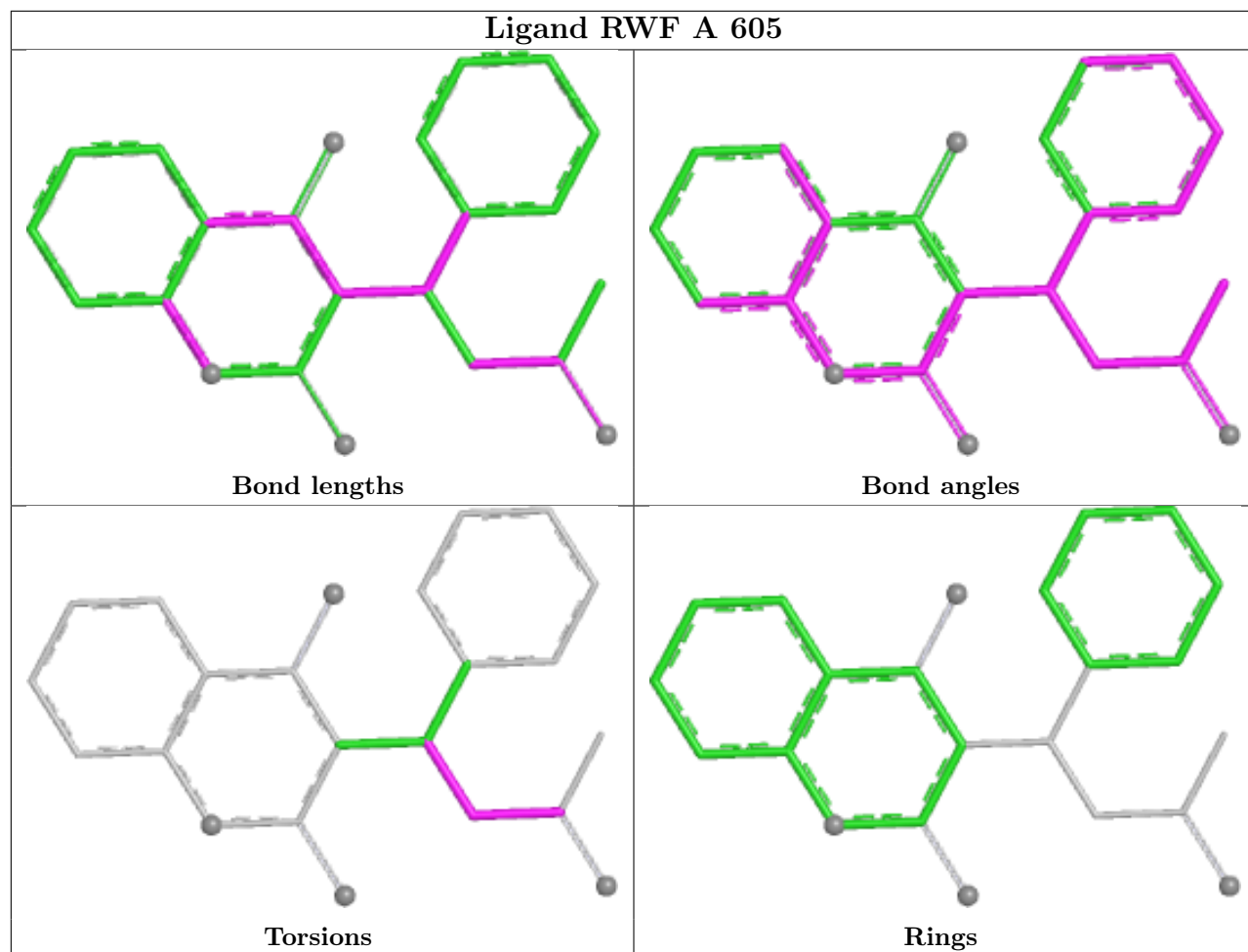
Mol	Chain	Res	Type	Atoms
2	A	601	MYR	C9-C10-C11-C12
2	A	603	MYR	C1-C2-C3-C4
3	B	605	RWF	C2-C3-C4-O3
4	B	603	DAO	C5-C6-C7-C8
4	B	603	DAO	C11-C10-C9-C8

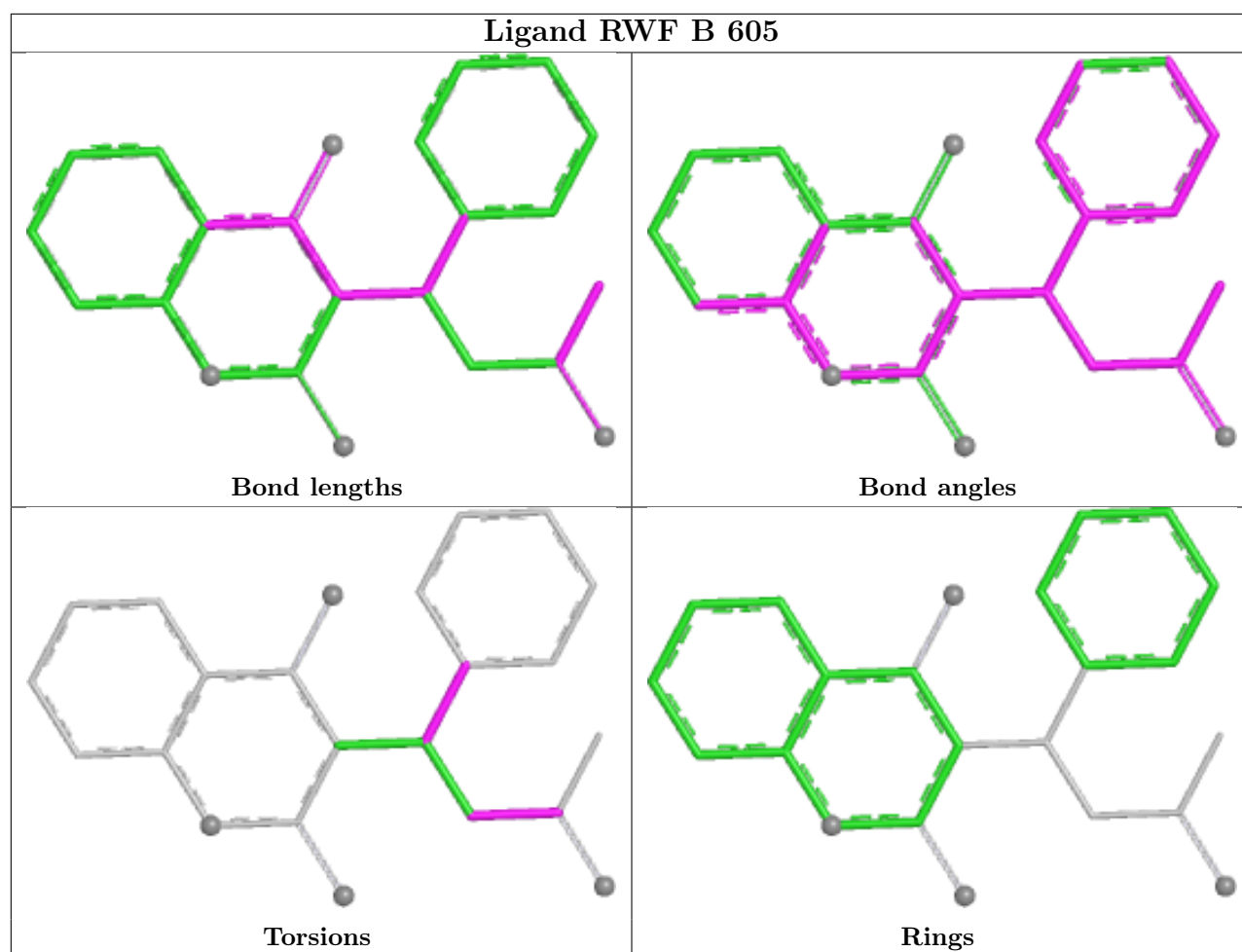
There are no ring outliers.

7 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	MYR	4	0
2	A	602	MYR	8	0
2	B	602	MYR	1	0
3	A	605	RWF	1	0
3	B	605	RWF	2	0
4	B	603	DAO	2	0
2	A	603	MYR	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	582/585 (99%)	0.91	65 (11%) 10 9	27, 41, 59, 88	0
1	B	582/585 (99%)	1.02	93 (15%) 5 4	20, 42, 59, 85	1 (0%)
All	All	1164/1170 (99%)	0.96	158 (13%) 7 6	20, 41, 60, 88	1 (0%)

The worst 5 of 158 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	168	CYS	6.7
1	B	568	PHE	5.5
1	B	248	GLY	5.3
1	B	514	CYS	5.3
1	A	172	ALA	5.1

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

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

### 6.3 Carbohydrates [i](#)

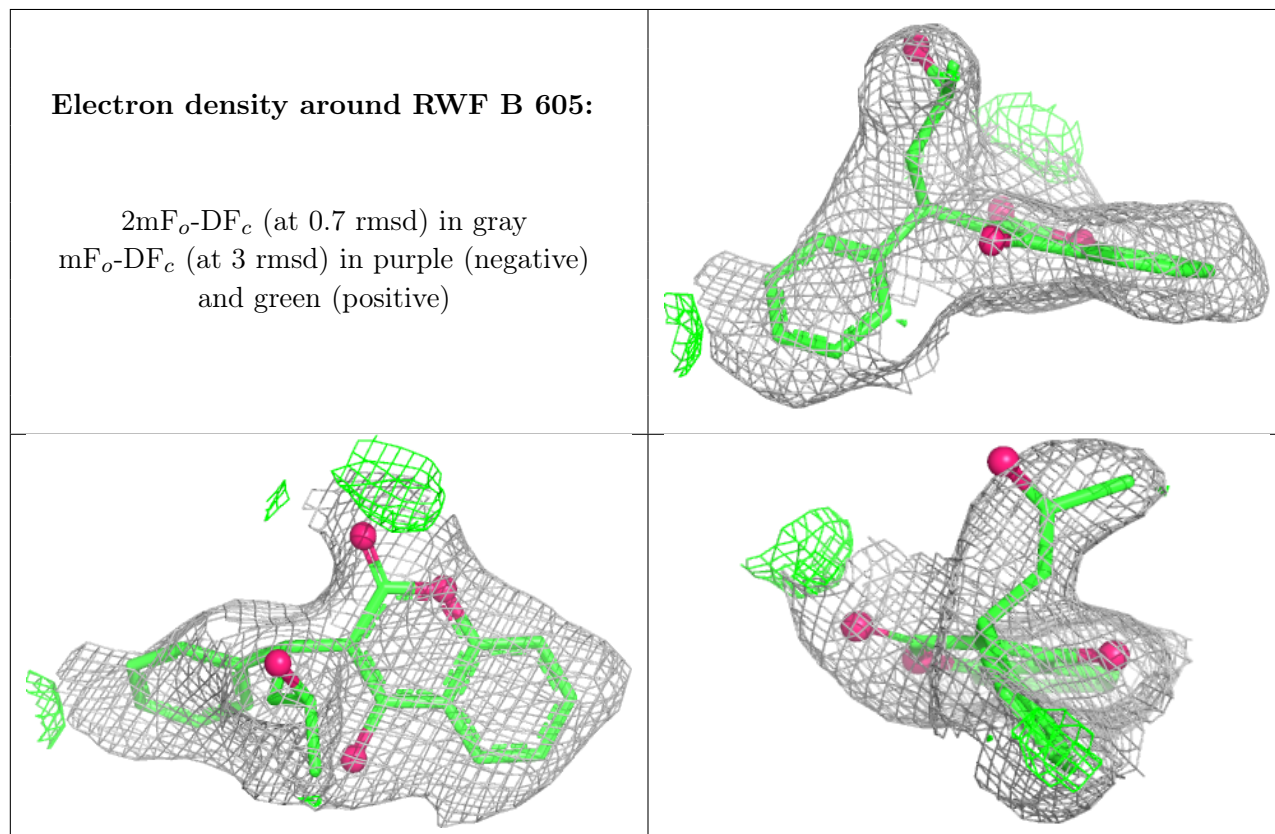
There are no oligosaccharides in this entry.

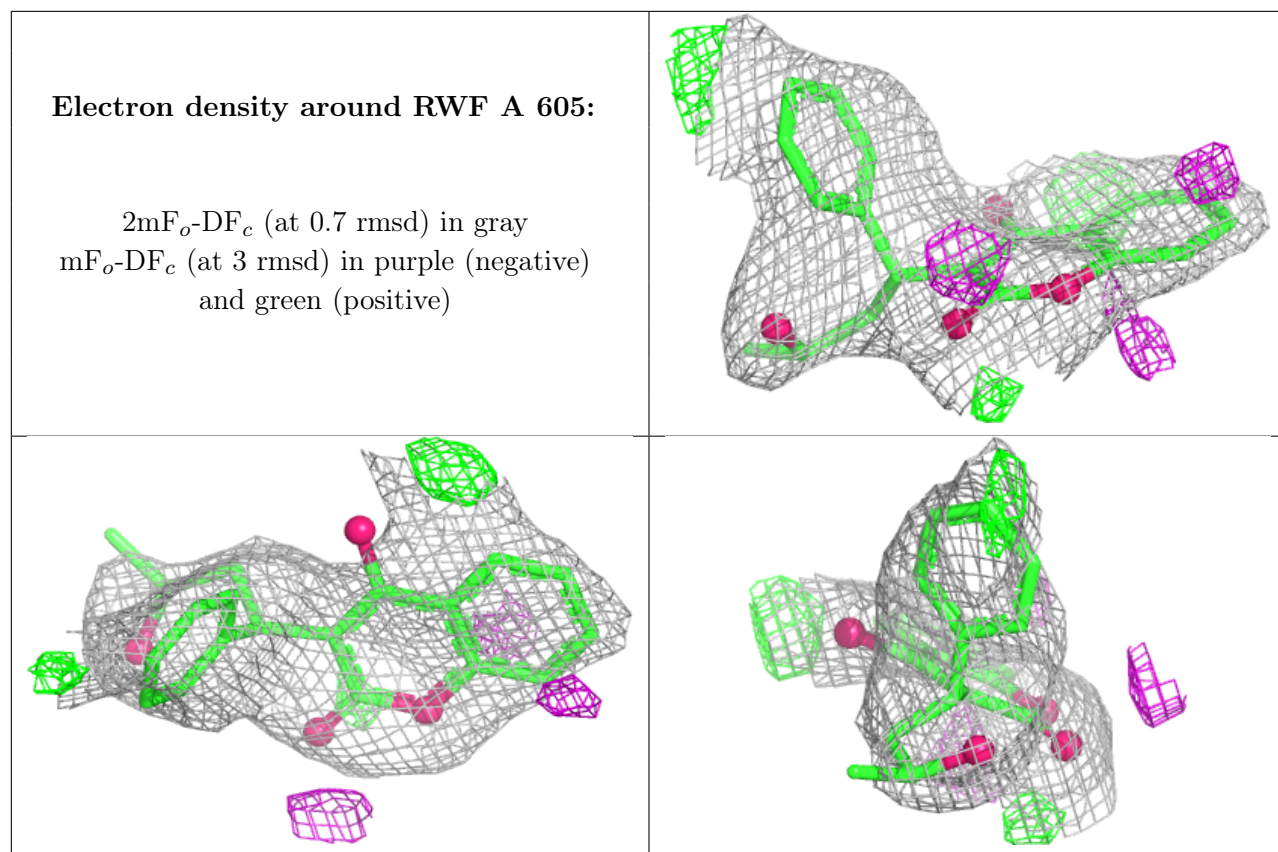
### 6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	RWF	B	605	23/23	0.76	0.18	55,66,72,76	0
3	RWF	A	605	23/23	0.82	0.21	57,66,77,82	0
2	MYR	A	603	16/16	0.82	0.15	33,39,51,57	0
2	MYR	A	604	16/16	0.85	0.17	44,54,66,72	0
2	MYR	B	602	16/16	0.85	0.18	39,47,57,57	0
4	DAO	B	603	14/14	0.85	0.19	50,56,72,74	0
2	MYR	B	601	16/16	0.87	0.19	48,57,63,64	0
2	MYR	B	604	16/16	0.88	0.10	35,43,56,57	0
2	MYR	A	602	16/16	0.88	0.18	52,64,68,68	0
2	MYR	A	601	16/16	0.91	0.15	36,47,52,53	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.





## 6.5 Other polymers [i](#)

There are no such residues in this entry.