



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:12 AM UTC

PDB ID : 5R0B / pdb_00005r0b
Title : PanDDA analysis group deposition – Aar2/RNaseH in complex with fragment F2X-Entry C05, DMSO-free
Authors : Wollenhaupt, J.; Metz, A.; Barthel, T.; Lima, G.M.A.; Heine, A.; Mueller, U.; Klebe, G.; Weiss, M.S.
Deposited on : 2020-02-12
Resolution : 1.82 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	:	4-5-2 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

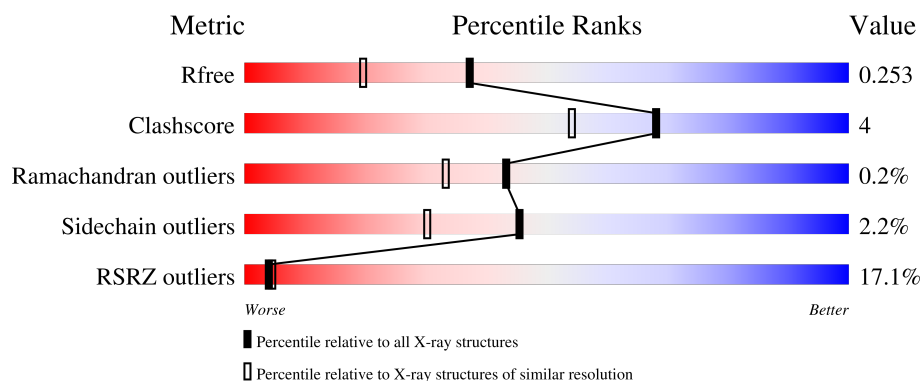
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.82 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	1112 (1.82-1.82)
Clashscore	190562	1148 (1.82-1.82)
Ramachandran outliers	187476	1140 (1.82-1.82)
Sidechain outliers	187428	1140 (1.82-1.82)
RSRZ outliers	180081	1112 (1.82-1.82)

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	258	17% 79% 10% 8%
2	B	308	16% 89% 8% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SY7	A	2501	X	-	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4694 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 Pre-mRNA-splicing factor 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	237	1994	1278	334	371	11	0	12	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1833	GLY	-	expression tag	UNP P33334
A	1834	ALA	-	expression tag	UNP P33334
A	1835	MET	-	expression tag	UNP P33334

- Molecule 2 is a protein called A1 cistron-splicing factor AAR2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	300	2580	1654	421	485	20	0	9	0

There are 20 discrepancies between the modelled and reference sequences:

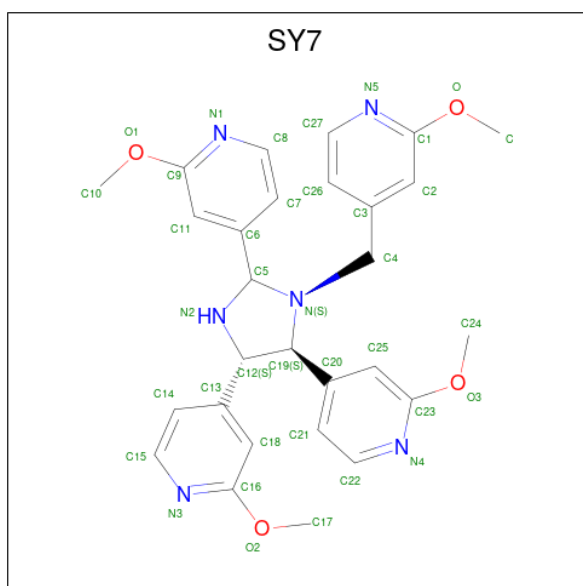
Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	expression tag	UNP P32357
B	-2	ALA	-	expression tag	UNP P32357
B	-1	MET	-	expression tag	UNP P32357
B	0	ALA	-	expression tag	UNP P32357
B	166	SER	LEU	conflict	UNP P32357
B	167	SER	LYS	conflict	UNP P32357
B	170	SER	LEU	conflict	UNP P32357
B	?	-	GLN	deletion	UNP P32357
B	?	-	LYS	deletion	UNP P32357
B	?	-	ALA	deletion	UNP P32357
B	?	-	GLY	deletion	UNP P32357
B	?	-	SER	deletion	UNP P32357
B	?	-	LYS	deletion	UNP P32357

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	MET	deletion	UNP P32357
B	?	-	GLU	deletion	UNP P32357
B	?	-	ALA	deletion	UNP P32357
B	?	-	LYS	deletion	UNP P32357
B	?	-	ASN	deletion	UNP P32357
B	?	-	GLU	deletion	UNP P32357
B	?	-	ASP	deletion	UNP P32357

- Molecule 3 is 2-methoxy-4-[[[(4 {S},5 {S})-2,4,5-tris(2-methoxypyridin-4-yl)imidazolidin-1-yl]methyl]pyridine (CCD ID: SY7) (formula: C₂₈H₃₀N₆O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			38	28	6	4		

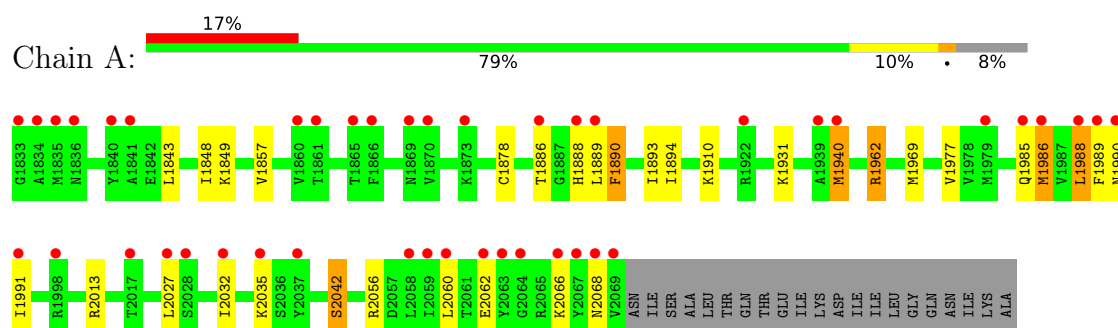
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	42	Total	O	0	0
			42	42		
4	B	40	Total	O	0	0
			40	40		

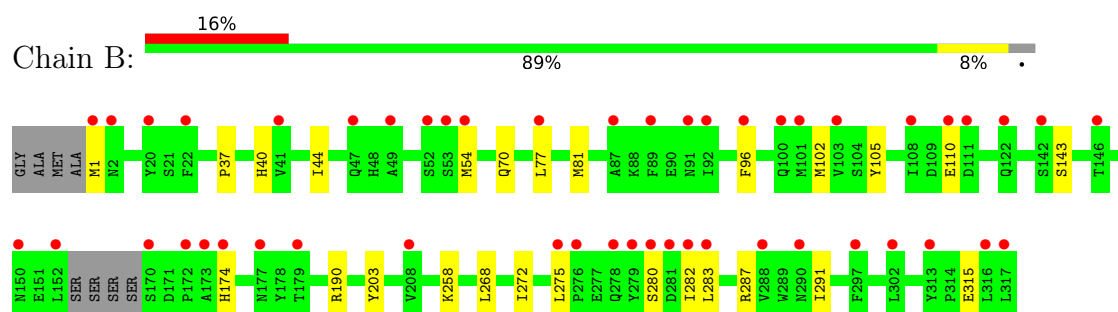
3 Residue-property plots

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: Pre-mRNA-splicing factor 8



• Molecule 2: A1 cistron-splicing factor AAR2



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	87.83Å 82.01Å 93.33Å 90.00° 108.52° 90.00°	Depositor
Resolution (Å)	21.88 – 1.82 21.88 – 1.82	Depositor EDS
% Data completeness (in resolution range)	99.5 (21.88-1.82) 99.8 (21.88-1.82)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.01 (at 1.82Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.227 , 0.264 (Not available) , 0.253	Depositor DCC
R_{free} test set	2101 reflections (3.72%)	wwPDB-VP
Wilson B-factor (Å ²)	42.5	Xtriage
Anisotropy	0.393	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 52.0	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	4694	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.42% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SY7

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	0.71	5/2041 (0.2%)	0.82	3/2765 (0.1%)
2	B	0.57	0/2651	0.66	0/3581
All	All	0.64	5/4692 (0.1%)	0.73	3/6346 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1990	ASN	C-O	7.31	1.32	1.23
1	A	1886	THR	C-O	-5.74	1.16	1.24
1	A	1940	MET	SD-CE	-5.54	1.65	1.79
1	A	1888	HIS	C-O	-5.07	1.17	1.23
1	A	1890	PHE	C-O	-5.02	1.17	1.24

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1989	PHE	CA-CB-CG	5.30	119.10	113.80
1	A	2035	LYS	CB-CA-C	5.14	118.45	109.65
1	A	1988	LEU	CA-C-O	-5.11	115.11	120.58

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	1994	0	2020	18	0
2	B	2580	0	2450	14	0
3	A	38	0	0	1	0
4	A	42	0	0	0	0
4	B	40	0	0	2	0
All	All	4694	0	4470	33	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 4.

All (33) 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:1890:PHE:HD2	1:A:1986:MET:HE1	1.40	0.87
1:A:1962:ARG:O	1:A:2013:ARG:NH1	2.12	0.81
1:A:1890:PHE:HD2	1:A:1986:MET:CE	1.94	0.81
2:B:96:PHE:HB2	2:B:102:MET:HE3	1.67	0.76
2:B:1:MET:N	4:B:401:HOH:O	2.25	0.69
1:A:1890:PHE:CD2	1:A:1986:MET:HE1	2.30	0.62
2:B:70:GLN:HB3	2:B:81:MET:CE	2.30	0.61
1:A:1890:PHE:CD2	1:A:1986:MET:CE	2.82	0.60
2:B:287:ARG:O	2:B:291:ILE:HD13	2.02	0.59
2:B:96:PHE:CB	2:B:102:MET:HE3	2.33	0.57
1:A:1843:LEU:HA	1:A:1849:LYS:HD2	1.86	0.57
2:B:44[A]:ILE:O	2:B:44[A]:ILE:HG23	2.08	0.54
1:A:2062:GLU:O	1:A:2066:LYS:HG2	2.08	0.54
2:B:70:GLN:HB3	2:B:81:MET:HE2	1.91	0.53
2:B:258:LYS:HD2	2:B:258:LYS:H	1.73	0.52
2:B:275:LEU:HD21	2:B:283:LEU:HD13	1.92	0.51
1:A:1910:LYS:O	1:A:1940:MET:HE1	2.11	0.50
1:A:1848:ILE:H	1:A:1931[A]:LYS:HZ2	1.57	0.50
1:A:1878:CYS:SG	1:A:1969:MET:HE3	2.53	0.49
1:A:2032:ILE:HG23	1:A:2042:SER:O	2.12	0.49
1:A:1893:ILE:HD11	1:A:1977:VAL:HG22	1.96	0.47
1:A:1890:PHE:CD2	1:A:1986:MET:HE2	2.49	0.46
3:A:2501:SY7:C4	3:A:2501:SY7:C21	2.93	0.46
2:B:54[B]:MET:HE1	2:B:143:SER:HB3	1.96	0.46
1:A:2056[B]:ARG:O	1:A:2060:LEU:HG	2.17	0.44
2:B:190:ARG:HG3	2:B:203[B]:TYR:CZ	2.53	0.43
1:A:1889:LEU:HD22	1:A:1991:ILE:HD12	2.00	0.43
1:A:1890:PHE:CD2	1:A:1988:LEU:HD23	2.54	0.43
2:B:268:LEU:O	2:B:272:ILE:HG12	2.19	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:37:PRO:HD3	2:B:105:TYR:CD1	2.55	0.42
1:A:1857:VAL:HG13	1:A:1894:ILE:HG13	2.02	0.41
2:B:40:HIS:HD2	4:B:416:HOH:O	2.03	0.41
1:A:2062:GLU:HB3	1:A:2066:LYS:HE3	2.02	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	A	247/258 (96%)	240 (97%)	6 (2%)	1 (0%)	30	19
2	B	306/308 (99%)	297 (97%)	9 (3%)	0	100	100
All	All	553/566 (98%)	537 (97%)	15 (3%)	1 (0%)	43	33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2068	ASN

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	225/233 (97%)	220 (98%)	5 (2%)	45	30

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	287/284 (101%)	281 (98%)	6 (2%)	47	32
All	All	512/517 (99%)	501 (98%)	11 (2%)	45	32

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1962	ARG
1	A	1985	GLN
1	A	1986	MET
1	A	2027	LEU
1	A	2042	SER
2	B	77	LEU
2	B	110	GLU
2	B	174	HIS
2	B	280	SER
2	B	282	ILE
2	B	315	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1863	HIS
2	B	40	HIS
2	B	45	HIS
2	B	47	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

1 ligand is 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
3	SY7	A	2501	-	41,42,42	3.28	9 (21%)	54,58,58	3.42	14 (25%)

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
3	SY7	A	2501	-	1/1/4/5	12/24/40/40	0/5/5/5

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	2501	SY7	C5-N2	-18.23	1.21	1.46
3	A	2501	SY7	C4-N	-4.91	1.40	1.47
3	A	2501	SY7	C20-C19	3.49	1.56	1.51
3	A	2501	SY7	C13-C12	-3.23	1.47	1.52
3	A	2501	SY7	C4-C3	-3.13	1.45	1.51
3	A	2501	SY7	C26-C3	-2.50	1.34	1.38
3	A	2501	SY7	C26-C27	-2.43	1.33	1.38
3	A	2501	SY7	O2-C16	-2.18	1.31	1.35
3	A	2501	SY7	C7-C8	-2.08	1.34	1.38

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2501	SY7	C6-C5-N	15.37	137.37	113.11
3	A	2501	SY7	C12-C19-N	-10.08	87.00	101.25
3	A	2501	SY7	O3-C23-N4	-9.81	101.80	119.68
3	A	2501	SY7	O1-C9-N1	-5.39	109.85	119.68

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2501	SY7	O3-C23-C25	5.05	133.83	118.04
3	A	2501	SY7	C20-C19-N	4.70	118.94	112.61
3	A	2501	SY7	C5-N2-C12	-4.68	98.40	106.97
3	A	2501	SY7	C4-N-C19	4.23	123.95	113.83
3	A	2501	SY7	C4-C3-C26	-4.20	113.02	120.75
3	A	2501	SY7	C20-C19-C12	3.81	121.37	112.35
3	A	2501	SY7	C21-C20-C25	-3.24	114.98	118.74
3	A	2501	SY7	O1-C9-C11	2.51	125.88	118.04
3	A	2501	SY7	C4-C3-C2	2.49	124.97	120.27
3	A	2501	SY7	C13-C12-N2	-2.15	109.57	112.98

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	2501	SY7	C5

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	2501	SY7	N4-C23-O3-C24
3	A	2501	SY7	C25-C23-O3-C24
3	A	2501	SY7	C3-C4-N-C19
3	A	2501	SY7	N2-C12-C13-C14
3	A	2501	SY7	N2-C12-C13-C18
3	A	2501	SY7	N2-C5-C6-C11
3	A	2501	SY7	C19-C12-C13-C14
3	A	2501	SY7	C19-C12-C13-C18
3	A	2501	SY7	N1-C9-O1-C10
3	A	2501	SY7	N-C19-C20-C21
3	A	2501	SY7	C3-C4-N-C5
3	A	2501	SY7	N2-C5-C6-C7

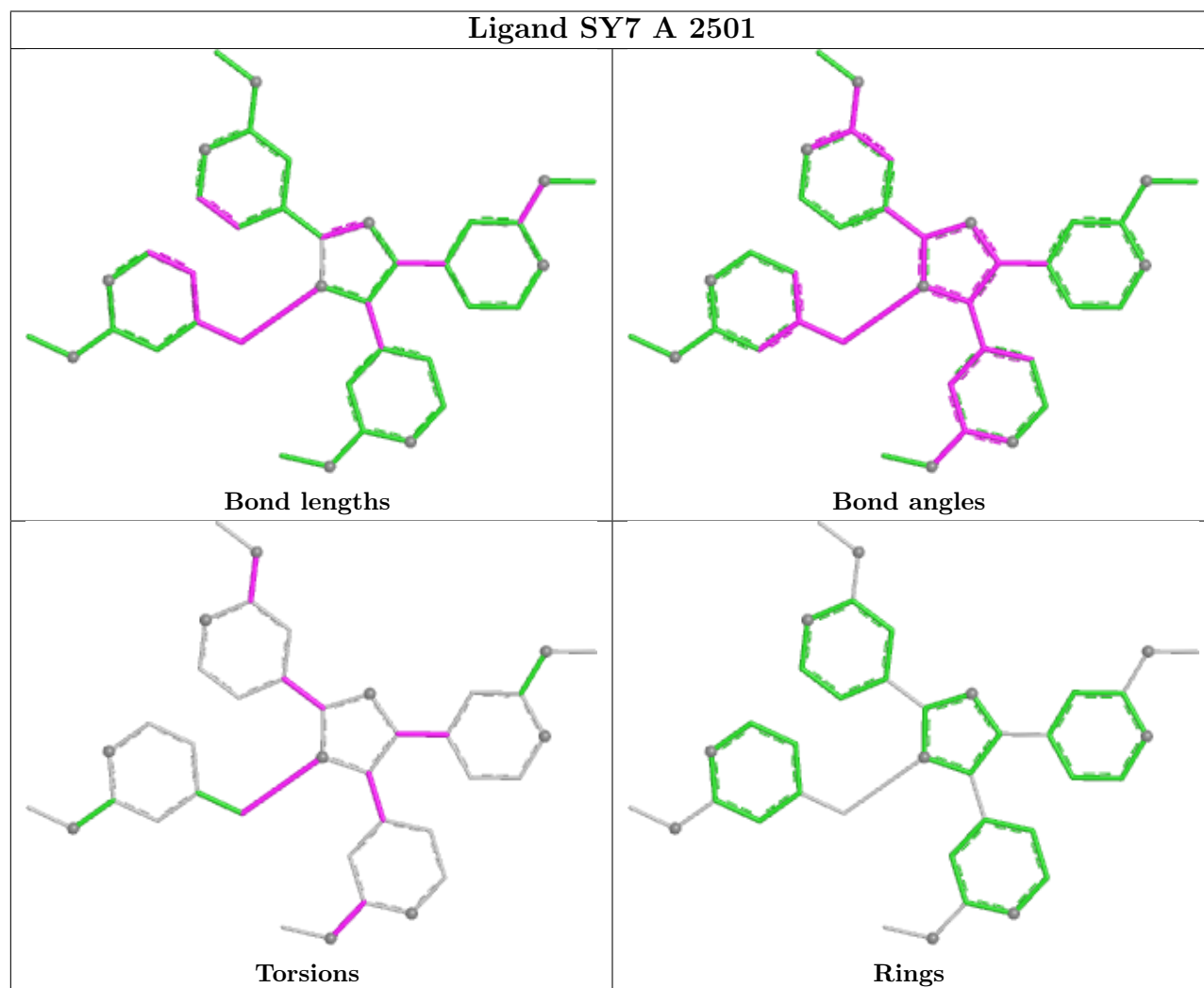
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2501	SY7	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1923:SER	C	1924:LEU	N	1.18

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	A	237/258 (91%)	0.98	43 (18%) 3 4	21, 54, 107, 144	12 (5%)
2	B	300/308 (97%)	0.95	49 (16%) 4 5	17, 56, 111, 265	9 (3%)
All	All	537/566 (94%)	0.97	92 (17%) 4 4	17, 55, 111, 265	21 (3%)

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2037	TYR	5.7
2	B	54[A]	MET	5.7
2	B	22	PHE	5.5
1	A	1840	TYR	5.0
2	B	101	MET	5.0
1	A	2069	VAL	4.9
2	B	316	LEU	4.8
2	B	170	SER	4.6
1	A	1988	LEU	4.4
1	A	1986	MET	4.4
1	A	1886	THR	4.2
1	A	1979[A]	MET	4.1
2	B	108	ILE	4.0
1	A	1989	PHE	4.0
1	A	1861	THR	3.8
2	B	52	SER	3.7
2	B	53	SER	3.7
1	A	2067	TYR	3.6
2	B	283	LEU	3.5
2	B	1	MET	3.4
1	A	2035	LYS	3.3
2	B	275	LEU	3.3
2	B	280	SER	3.3
2	B	281	ASP	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	2060	LEU	3.3
2	B	92	ILE	3.2
2	B	2	ASN	3.1
2	B	279	TYR	3.1
1	A	2066	LYS	3.1
1	A	1866	PHE	3.1
1	A	2068	ASN	3.0
1	A	1991	ILE	2.9
1	A	1836	ASN	2.8
1	A	2063	TYR	2.7
1	A	1834	ALA	2.7
2	B	100	GLN	2.7
2	B	122[A]	GLN	2.7
2	B	96	PHE	2.6
2	B	179	THR	2.6
2	B	91	ASN	2.6
1	A	2064	GLY	2.6
2	B	87	ALA	2.6
2	B	208	VAL	2.6
1	A	1835	MET	2.6
2	B	20	TYR	2.5
1	A	2027	LEU	2.5
2	B	173	ALA	2.5
1	A	2017[A]	THR	2.5
2	B	172	PRO	2.5
2	B	77	LEU	2.5
1	A	1940	MET	2.5
1	A	1873	LYS	2.5
1	A	1870	VAL	2.4
2	B	174	HIS	2.4
2	B	317	LEU	2.4
2	B	89	PHE	2.4
1	A	1998	ARG	2.4
1	A	2059	ILE	2.4
2	B	47	GLN	2.4
2	B	297	PHE	2.3
1	A	1888	HIS	2.3
2	B	41[A]	VAL	2.3
2	B	103	VAL	2.3
2	B	142	SER	2.3
1	A	1860	VAL	2.3
1	A	2058	LEU	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	1841	ALA	2.2
1	A	2028	SER	2.2
2	B	278	GLN	2.2
2	B	49	ALA	2.2
2	B	282	ILE	2.2
1	A	1869	ASN	2.2
2	B	302	LEU	2.2
2	B	146	THR	2.2
1	A	1939	ALA	2.2
1	A	1922	ARG	2.2
2	B	290	ASN	2.1
1	A	1985	GLN	2.1
2	B	111	ASP	2.1
2	B	288	VAL	2.1
2	B	276	PRO	2.1
1	A	2062	GLU	2.1
1	A	1889	LEU	2.1
1	A	1990	ASN	2.1
1	A	2032	ILE	2.1
2	B	313	TYR	2.1
1	A	1865	THR	2.1
2	B	110	GLU	2.1
1	A	1833	GLY	2.1
2	B	152	LEU	2.1
2	B	150	ASN	2.0
2	B	177[A]	ASN	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](#)

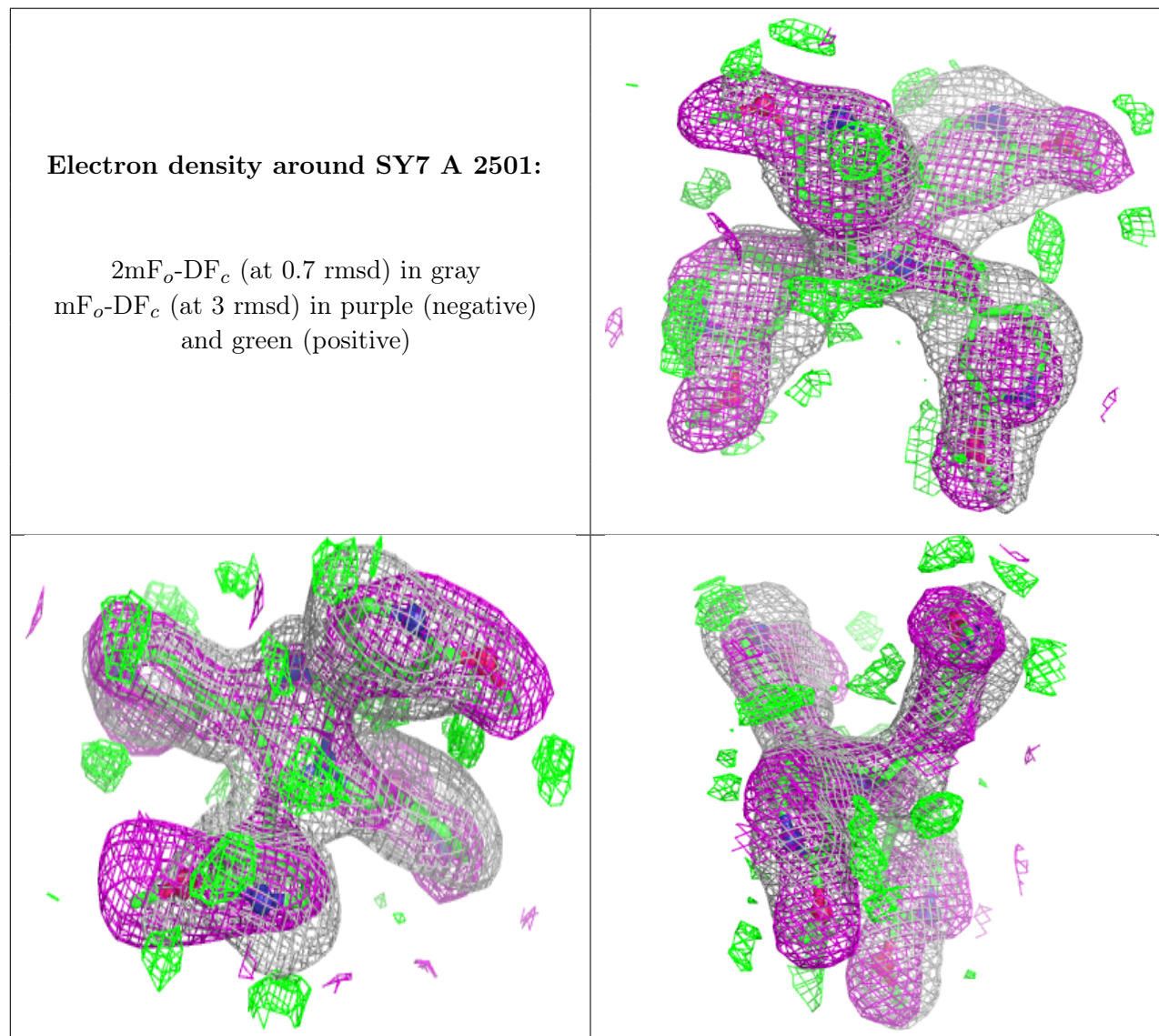
There are no oligosaccharides in this entry.

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, 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($\text{\AA}^2$)	Q<0.9
3	SY7	A	2501	38/38	0.67	0.15	30,30,30,30	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 ⓘ

There are no such residues in this entry.