



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:42 AM UTC

PDB ID : 7FOP / pdb_00007fop
Title : PanDDA analysis group deposition – Aar2/RNaseH in complex with fragment P08C08 from the F2X-Universal Library
Authors : Barthel, T.; Wollenhaupt, J.; Lima, G.M.A.; Wahl, M.C.; Weiss, M.S.
Deposited on : 2022-08-26
Resolution : 1.66 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
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

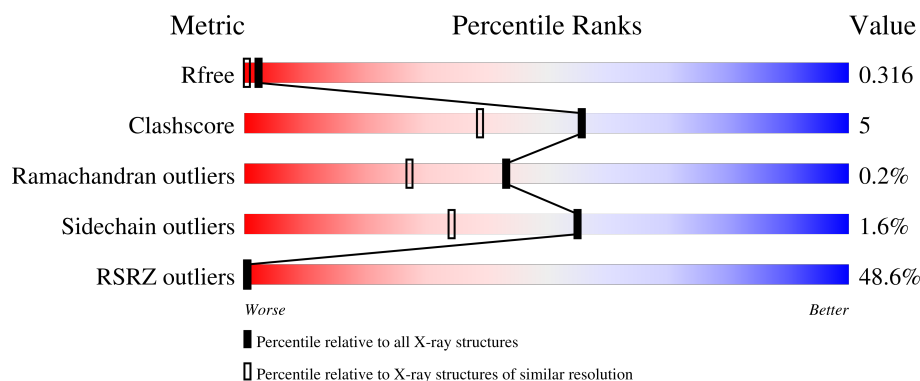
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.66 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	2563 (1.66-1.66)
Clashscore	190562	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)
RSRZ outliers	180081	2564 (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	258	47% 82% 9% 8%
2	B	308	46% 84% 12% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9228 atoms, of which 4524 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	H	N	O	S			
1	A	237	4068	1287	2060	336	373	12	0	21	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	H	N	O	S			
2	B	300	5044	1654	2464	421	485	20	22	17	0

There are 20 discrepancies between the modelled and reference sequences:

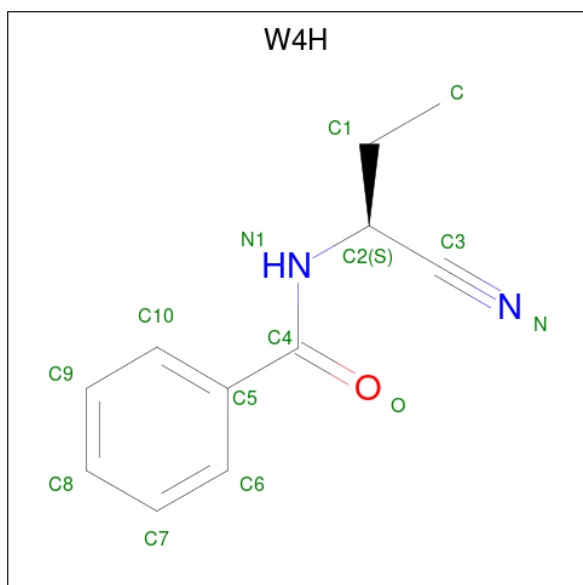
Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	expression tag	UNP P32357
B	-2	ALA	-	expression tag	UNP P32357
B	-1	MET	-	expression tag	UNP P32357
B	0	ALA	-	expression tag	UNP P32357
B	166	SER	LEU	conflict	UNP P32357
B	167	SER	LYS	conflict	UNP P32357
B	?	-	LEU	deletion	UNP P32357
B	?	-	GLN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

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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	170	SER	ASP	conflict	UNP P32357

- Molecule 3 is N-[(1S)-1-cyanopropyl]benzamide (CCD ID: W4H) (formula: C₁₁H₁₂N₂O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			14	11	2	1		

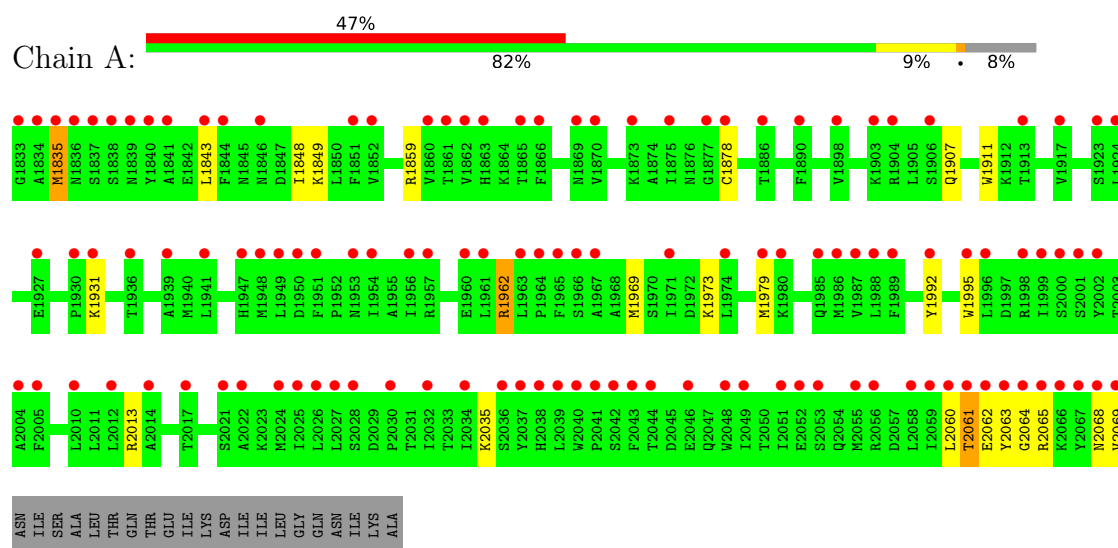
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	48	Total	O	0	0
			48	48		
4	B	54	Total	O	0	0
			54	54		

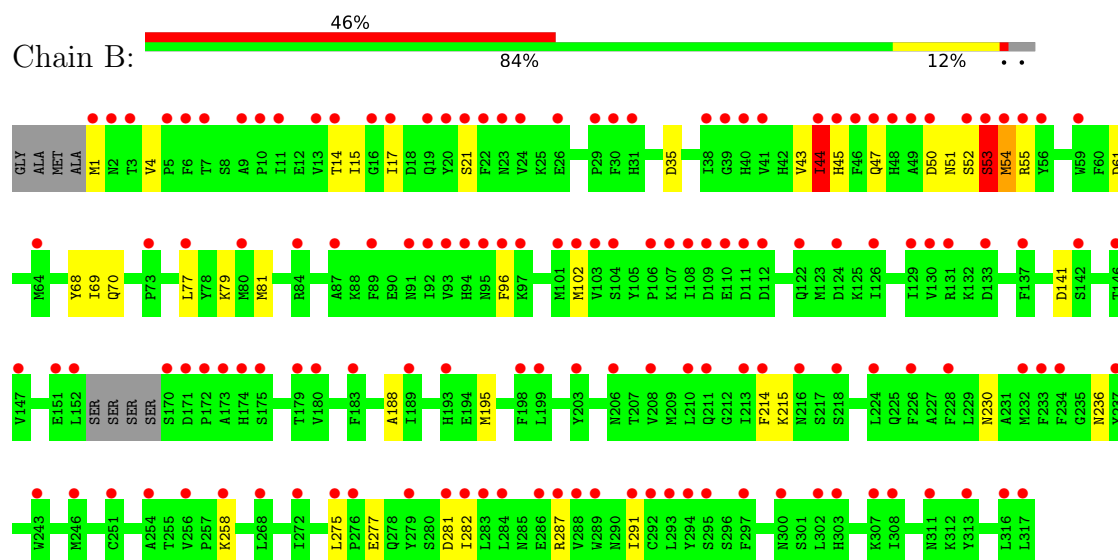
3 Residue-property plots

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	88.58Å 81.69Å 92.87Å 90.00° 108.23° 90.00°	Depositor
Resolution (Å)	44.10 – 1.66 44.10 – 1.66	Depositor EDS
% Data completeness (in resolution range)	98.9 (44.10-1.66) 99.0 (44.10-1.66)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.96 (at 1.66Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.268 , 0.304 0.278 , 0.316	Depositor DCC
R_{free} test set	2100 reflections (2.88%)	wwPDB-VP
Wilson B-factor (Å ²)	41.3	Xtriage
Anisotropy	0.322	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 46.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9228	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.06% 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: W4H

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	0.64	0/2149	0.78	0/2911
2	B	0.86	8/2739 (0.3%)	1.03	21/3699 (0.6%)
All	All	0.77	8/4888 (0.2%)	0.93	21/6610 (0.3%)

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
2	B	0	6

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	44[A]	ILE	C-N	-9.72	1.21	1.33
2	B	44[B]	ILE	C-N	-9.72	1.21	1.33
2	B	230[A]	ASN	C-O	7.91	1.33	1.24
2	B	230[B]	ASN	C-O	7.91	1.33	1.24
2	B	54[A]	MET	C-N	6.40	1.42	1.33
2	B	54[B]	MET	C-N	6.40	1.42	1.33
2	B	55[A]	ARG	N-CA	6.36	1.54	1.45
2	B	55[B]	ARG	N-CA	6.36	1.54	1.45

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	230[A]	ASN	CA-C-O	10.44	131.61	120.55
2	B	230[B]	ASN	CA-C-O	10.44	131.61	120.55
2	B	54[A]	MET	CA-C-N	-9.12	106.25	121.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	54[A]	MET	C-N-CA	-9.12	106.25	121.39
2	B	54[B]	MET	CA-C-N	-9.12	106.25	121.39
2	B	54[B]	MET	C-N-CA	-9.12	106.25	121.39
2	B	44[A]	ILE	O-C-N	-7.25	113.55	122.61
2	B	44[B]	ILE	O-C-N	-7.25	113.55	122.61
2	B	53	SER	CA-C-O	-6.50	114.33	121.87
2	B	47	GLN	CB-CA-C	-6.35	102.22	111.23
2	B	230[A]	ASN	O-C-N	-6.09	115.66	122.12
2	B	230[B]	ASN	O-C-N	-6.09	115.66	122.12
2	B	14	THR	CB-CA-C	5.64	119.33	110.19
2	B	230[A]	ASN	N-CA-C	5.53	117.31	111.28
2	B	230[B]	ASN	N-CA-C	5.53	117.31	111.28
2	B	141	ASP	CA-C-N	5.45	127.85	120.38
2	B	141	ASP	C-N-CA	5.45	127.85	120.38
2	B	44[A]	ILE	N-CA-C	-5.34	100.69	109.12
2	B	44[B]	ILE	N-CA-C	-5.34	100.69	109.12
2	B	236	ASN	N-CA-CB	5.31	118.53	109.87
2	B	277	GLU	CB-CA-C	-5.13	102.27	110.79

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	44[A]	ILE	Mainchain
2	B	44[B]	ILE	Mainchain
2	B	53	SER	Mainchain
2	B	54[A]	MET	Mainchain
2	B	54[B]	MET	Mainchain

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	2008	2060	1974	18	1
2	B	2580	2464	2398	26	1
3	B	14	0	0	1	0
4	A	48	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	54	0	0	1	0
All	All	4704	4524	4372	42	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 5.

All (42) 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:1962:ARG:O	1:A:2013:ARG:NH1	2.08	0.87
2:B:70:GLN:HB3	2:B:81:MET:HE2	1.61	0.82
1:A:1848:ILE:H	1:A:1931[A]:LYS:HZ2	1.31	0.75
2:B:50:ASP:OD1	2:B:51:ASN:N	2.21	0.73
2:B:68:TYR:CE2	2:B:81:MET:HE3	2.24	0.73
2:B:96:PHE:HB2	2:B:102:MET:HE3	1.72	0.71
2:B:1:MET:N	4:B:501:HOH:O	2.26	0.69
1:A:2064:GLY:O	1:A:2068:ASN:N	2.29	0.66
2:B:96:PHE:CB	2:B:102:MET:HE3	2.26	0.66
1:A:2061:THR:O	1:A:2064:GLY:N	2.29	0.65
2:B:44[A]:ILE:HD13	2:B:69:ILE:HD11	1.82	0.61
2:B:287:ARG:O	2:B:291:ILE:HD13	2.02	0.60
1:A:1979[B]:MET:HA	1:A:1979[B]:MET:HE2	1.86	0.57
1:A:1843:LEU:HA	1:A:1849:LYS:HD2	1.91	0.53
2:B:43:VAL:HG13	2:B:43:VAL:O	2.11	0.50
2:B:258:LYS:HD2	2:B:258:LYS:H	1.76	0.50
2:B:77:LEU:HD21	2:B:79:LYS:HE3	1.94	0.49
2:B:15:ILE:O	2:B:21:SER:HA	2.12	0.48
1:A:1911:TRP:CD1	2:B:195:MET:HE3	2.49	0.48
2:B:70:GLN:CB	2:B:81:MET:HE2	2.36	0.48
1:A:1878:CYS:SG	1:A:1969:MET:HE3	2.54	0.47
2:B:282:ILE:HD11	3:B:401:W4H:C	2.45	0.47
1:A:2062:GLU:OE1	1:A:2065:ARG:NH1	2.49	0.46
2:B:44[A]:ILE:HD11	2:B:69:ILE:HG13	1.96	0.46
2:B:70:GLN:HB3	2:B:81:MET:CE	2.41	0.44
1:A:2060:LEU:O	1:A:2063:TYR:HB3	2.18	0.44
1:A:1992:TYR:O	1:A:1995:TRP:CG	2.71	0.44
1:A:2035:LYS:HA	1:A:2035:LYS:HD3	1.88	0.44
2:B:1:MET:HB3	2:B:35:ASP:HA	1.98	0.43
2:B:4:VAL:HG11	2:B:44[B]:ILE:CD1	2.48	0.43
2:B:214:PHE:O	2:B:215:LYS:HB2	2.18	0.43
1:A:1973:LYS:NZ	4:A:2103:HOH:O	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1962:ARG:HD3	1:A:1962:ARG:H	1.84	0.42
1:A:1859:ARG:NH1	1:A:1979[B]:MET:HE3	2.34	0.42
2:B:17:ILE:O	2:B:17:ILE:HG23	2.21	0.41
1:A:1907:GLN:HG2	2:B:195:MET:CE	2.51	0.41
2:B:1:MET:HE3	2:B:35:ASP:O	2.21	0.40
2:B:44[A]:ILE:CD1	2:B:69:ILE:HG13	2.50	0.40

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:2069:VAL:O	2:B:53:SER:OG[2_655]	2.03	0.17

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	258/258 (100%)	248 (96%)	9 (4%)	1 (0%)	30	15
2	B	315/308 (102%)	306 (97%)	9 (3%)	0	100	100
All	All	573/566 (101%)	554 (97%)	18 (3%)	1 (0%)	43	27

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2061	THR

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	237/233 (102%)	235 (99%)	2 (1%)	73	60
2	B	294/284 (104%)	286 (97%)	8 (3%)	39	16
All	All	531/517 (103%)	521 (98%)	10 (2%)	55	28

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1835	MET
1	A	1962	ARG
2	B	44[A]	ILE
2	B	44[B]	ILE
2	B	45[A]	HIS
2	B	45[B]	HIS
2	B	52	SER
2	B	53	SER
2	B	275	LEU
2	B	281	ASP

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
1	A	2038	HIS
2	B	135	ASN
2	B	206	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

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	W4H	B	401	-	12,14,14	1.36	2 (16%)	13,17,17	1.52	3 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	W4H	B	401	-	-	2/10/12/12	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	401	W4H	O-C4	-2.80	1.16	1.23
3	B	401	W4H	C2-C3	-2.13	1.46	1.48

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	401	W4H	C2-C3-N	-3.28	173.55	178.01
3	B	401	W4H	C-C1-C2	-2.50	107.14	113.33
3	B	401	W4H	C5-C4-N1	-2.28	112.81	117.04

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	401	W4H	C-C1-C2-N1
3	B	401	W4H	C3-C2-N1-C4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	401	W4H	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	237/258 (91%)	2.54	120 (50%) 0 0	23, 65, 137, 228	12 (5%)
2	B	300/308 (97%)	2.14	141 (47%) 0 0	24, 67, 123, 194	9 (3%)
All	All	537/566 (94%)	2.32	261 (48%) 0 0	23, 66, 133, 228	21 (3%)

All (261) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1979[A]	MET	30.6
1	A	2039	LEU	11.0
2	B	275	LEU	9.7
1	A	2040	TRP	9.7
1	A	2058	LEU	8.8
1	A	2069	VAL	8.6
1	A	2060	LEU	8.6
1	A	2061	THR	7.4
2	B	54[A]	MET	7.3
1	A	1878	CYS	7.3
2	B	122[A]	GLN	7.3
1	A	2026	LEU	7.0
2	B	152	LEU	6.8
1	A	2059	ILE	6.4
1	A	2063	TYR	6.1
2	B	1	MET	6.1
2	B	316	LEU	6.1
1	A	2037	TYR	5.9
2	B	279	TYR	5.8
1	A	2067	TYR	5.6
1	A	2064	GLY	5.6
2	B	276	PRO	5.6
1	A	1840	TYR	5.6
2	B	246	MET	5.4

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Mol	Chain	Res	Type	RSRZ
1	A	2010	LEU	5.1
2	B	170	SER	5.1
2	B	108	ILE	5.0
1	A	1841	ALA	5.0
1	A	1866	PHE	4.9
2	B	93	VAL	4.9
1	A	2068	ASN	4.9
1	A	2038	HIS	4.8
1	A	2065	ARG	4.8
1	A	2048	TRP	4.8
2	B	172	PRO	4.7
2	B	101	MET	4.6
2	B	44[A]	ILE	4.5
1	A	1833	GLY	4.5
1	A	2005	PHE	4.4
2	B	317	LEU	4.4
1	A	1927	GLU	4.4
2	B	272	ILE	4.4
2	B	80	MET	4.3
1	A	1954	ILE	4.3
2	B	308	ILE	4.3
1	A	2043	PHE	4.3
1	A	2025	ILE	4.3
2	B	146	THR	4.2
1	A	1996	LEU	4.2
2	B	302	LEU	4.2
2	B	22	PHE	4.2
2	B	258	LYS	4.2
2	B	286	GLU	4.2
2	B	291	ILE	4.2
2	B	49	ALA	4.2
2	B	281	ASP	4.1
1	A	1965	PHE	4.1
2	B	19	GLN	4.1
1	A	2027	LEU	4.0
2	B	183	PHE	4.0
2	B	203[A]	TYR	4.0
2	B	45[A]	HIS	3.9
1	A	1834	ALA	3.9
1	A	2066	LYS	3.9
2	B	199	LEU	3.9
1	A	2030	PRO	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	2052	GLU	3.8
1	A	2028	SER	3.8
2	B	55[A]	ARG	3.8
1	A	2032	ILE	3.8
2	B	137	PHE	3.8
1	A	1860	VAL	3.8
1	A	1862	VAL	3.7
1	A	1951	PHE	3.7
2	B	103	VAL	3.7
1	A	1995	TRP	3.7
1	A	2053[A]	SER	3.7
2	B	282	ILE	3.6
1	A	2017[A]	THR	3.6
2	B	92	ILE	3.6
2	B	21	SER	3.6
2	B	193	HIS	3.6
1	A	2051	ILE	3.5
2	B	173	ALA	3.5
1	A	1980[A]	LYS	3.5
2	B	10	PRO	3.5
2	B	30	PHE	3.5
2	B	96	PHE	3.5
2	B	2	ASN	3.5
2	B	297	PHE	3.4
2	B	313	TYR	3.4
1	A	2034	ILE	3.4
2	B	106	PRO	3.4
1	A	2049	ILE	3.3
1	A	1949	LEU	3.3
1	A	2001[A]	SER	3.3
2	B	133	ASP	3.3
1	A	1931[A]	LYS	3.3
2	B	20	TYR	3.3
2	B	287	ARG	3.3
2	B	11	ILE	3.2
1	A	1835	MET	3.2
1	A	2036	SER	3.2
2	B	40	HIS	3.2
1	A	2055	MET	3.2
2	B	174	HIS	3.2
2	B	294	TYR	3.2
2	B	107	LYS	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	1957	ARG	3.1
2	B	38	ILE	3.1
2	B	295	SER	3.1
2	B	87	ALA	3.1
2	B	64[A]	MET	3.1
1	A	1964	PRO	3.1
2	B	48	HIS	3.1
1	A	2022	ALA	3.1
1	A	1865	THR	3.1
1	A	1870	VAL	3.0
2	B	47	GLN	3.0
2	B	131	ARG	3.0
2	B	24	VAL	3.0
2	B	7	THR	3.0
2	B	77	LEU	3.0
1	A	1898[A]	VAL	3.0
2	B	256	VAL	3.0
1	A	1837	SER	3.0
1	A	1863	HIS	3.0
2	B	214	PHE	3.0
2	B	111	ASP	2.9
2	B	124	ASP	2.9
1	A	1873	LYS	2.9
2	B	9	ALA	2.9
1	A	1877	GLY	2.9
2	B	6	PHE	2.9
1	A	1999	ILE	2.9
2	B	102	MET	2.9
1	A	1906	SER	2.9
2	B	228	PHE	2.9
1	A	1913	THR	2.9
2	B	268	LEU	2.9
1	A	1971	ILE	2.9
2	B	142	SER	2.9
1	A	1953	ASN	2.9
1	A	2046	GLU	2.8
1	A	1963	LEU	2.8
1	A	2012	LEU	2.8
2	B	29	PRO	2.8
2	B	94	HIS	2.8
1	A	1956	ILE	2.8
2	B	206	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
2	B	13	VAL	2.8
2	B	52	SER	2.8
2	B	293	LEU	2.8
2	B	50	ASP	2.8
2	B	95	ASN	2.8
1	A	1966	SER	2.8
1	A	1939	ALA	2.7
1	A	1989	PHE	2.7
2	B	130	VAL	2.7
2	B	284	LEU	2.7
1	A	1875	ILE	2.7
1	A	1987	VAL	2.7
2	B	110	GLU	2.7
1	A	1836	ASN	2.7
1	A	1967	ALA	2.7
1	A	1890	PHE	2.7
2	B	189	ILE	2.7
2	B	237	TYR	2.6
1	A	1936	THR	2.6
1	A	1998	ARG	2.6
2	B	56	TYR	2.6
2	B	109	ASP	2.6
1	A	1992	TYR	2.6
2	B	147	VAL	2.6
1	A	1930	PRO	2.6
2	B	73	PRO	2.6
2	B	289	TRP	2.6
2	B	46	PHE	2.5
2	B	53	SER	2.5
2	B	210	LEU	2.5
2	B	234	PHE	2.5
1	A	2056[A]	ARG	2.5
1	A	1985	GLN	2.5
1	A	2014	ALA	2.5
2	B	39	GLY	2.5
1	A	1838	SER	2.5
1	A	1974	LEU	2.4
2	B	307	LYS	2.4
1	A	1904	ARG	2.4
1	A	1917	VAL	2.4
1	A	2021	SER	2.4
1	A	2044	THR	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	1960[A]	GLU	2.4
2	B	26	GLU	2.4
1	A	2024[A]	MET	2.4
1	A	1961[A]	LEU	2.4
2	B	16	GLY	2.4
2	B	283	LEU	2.4
1	A	2002[A]	TYR	2.4
2	B	151	GLU	2.4
2	B	251	CYS	2.4
1	A	1941	LEU	2.4
2	B	3	THR	2.4
2	B	59	TRP	2.4
2	B	97	LYS	2.4
2	B	126	ILE	2.4
2	B	23	ASN	2.3
2	B	216	ASN	2.3
2	B	300	ASN	2.3
2	B	5	PRO	2.3
1	A	2062	GLU	2.3
2	B	84	ARG	2.3
2	B	171	ASP	2.3
1	A	1869	ASN	2.3
1	A	1988	LEU	2.3
2	B	224	LEU	2.3
2	B	213	ILE	2.3
2	B	175	SER	2.3
1	A	1986	MET	2.3
1	A	1843	LEU	2.3
2	B	311	ASN	2.3
2	B	180	VAL	2.3
2	B	31	HIS	2.2
2	B	211[A]	GLN	2.2
2	B	218	SER	2.2
2	B	129	ILE	2.2
2	B	208	VAL	2.2
2	B	14	THR	2.2
2	B	179	THR	2.2
1	A	1923	SER	2.2
2	B	89	PHE	2.2
1	A	1839	ASN	2.2
1	A	1846	ASN	2.2
2	B	91	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	1924	LEU	2.2
2	B	198	PHE	2.2
2	B	233	PHE	2.2
1	A	2041	PRO	2.2
2	B	232	MET	2.1
2	B	288	VAL	2.1
1	A	1948	MET	2.1
1	A	1861	THR	2.1
1	A	1886	THR	2.1
2	B	17	ILE	2.1
1	A	1852	VAL	2.1
1	A	2004	ALA	2.1
1	A	2042	SER	2.1
2	B	104	SER	2.1
2	B	303	HIS	2.1
2	B	254	ALA	2.1
2	B	292	CYS	2.1
1	A	1947	HIS	2.1
2	B	243	TRP	2.1
1	A	1903	LYS	2.1
1	A	1844	PHE	2.1
1	A	1851	PHE	2.1
2	B	226	PHE	2.1
1	A	2000	SER	2.0
1	A	1950	ASP	2.0
2	B	112	ASP	2.0
2	B	41[A]	VAL	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	W4H	B	401	14/14	0.66	0.19	20,20,20,20	14

6.5 Other polymers [i](#)

There are no such residues in this entry.