



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:05 PM UTC

PDB ID : 7OG0 / pdb_00007og0
Title : Nontypeable Haemophilus influenzae SapA in open and closed conformations, in complex with double stranded RNA
Authors : Lukacik, P.; Owen, C.D.; Nettleship, J.E.; Bird, L.E.; Owens, R.J.; Walsh, M.A.
Deposited on : 2021-05-05
Resolution : 2.61 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
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

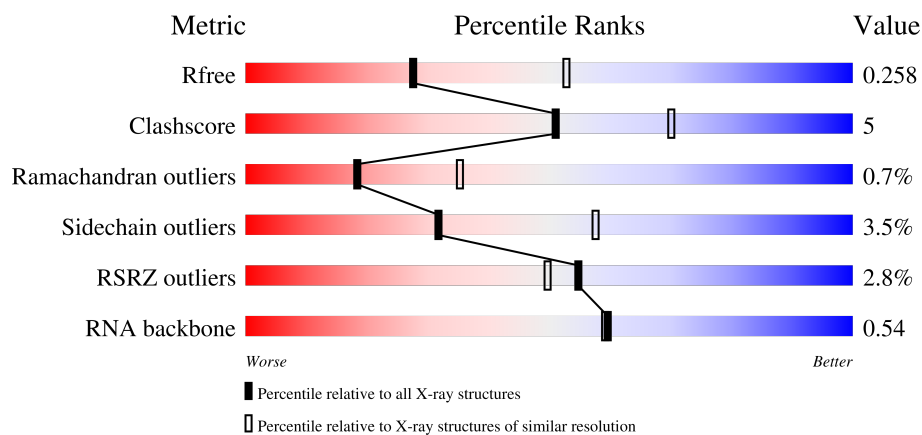
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 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	4951 (2.64-2.60)
Clashscore	190562	5303 (2.64-2.60)
Ramachandran outliers	187476	5217 (2.64-2.60)
Sidechain outliers	187428	5217 (2.64-2.60)
RSRZ outliers	180081	4950 (2.64-2.60)
RNA backbone	3983	1035 (2.86-2.38)

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	527	83% 11% 6%
1	B	527	3% 79% 14% 6%
2	D	17	24% 88% 12%
2	E	17	41% 82% 18%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8917 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 ABC-type transport system, periplasmic component, involved in antimicrobial peptide resistance.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	497	Total	C	N	O	S	0	1	0
			4011	2565	684	748	14			
1	B	498	Total	C	N	O	S	0	1	0
			4019	2570	683	752	14			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	153	LYS	ARG	conflict	UNP Q4QL73
B	153	LYS	ARG	conflict	UNP Q4QL73

- Molecule 2 is a RNA chain called RNA (5'-R(P*CP*CP*CP*CP*CP*CP*CP*CP*CP*GP*GP*GP*GP*GP*GP*GP*GP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	17	Total	C	N	O	P	0	0	0
			364	161	67	119	17			
2	E	17	Total	C	N	O	P	0	0	0
			364	161	67	119	17			

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca	0	0
			1	1		
3	B	1	Total	Ca	0	0
			1	1		

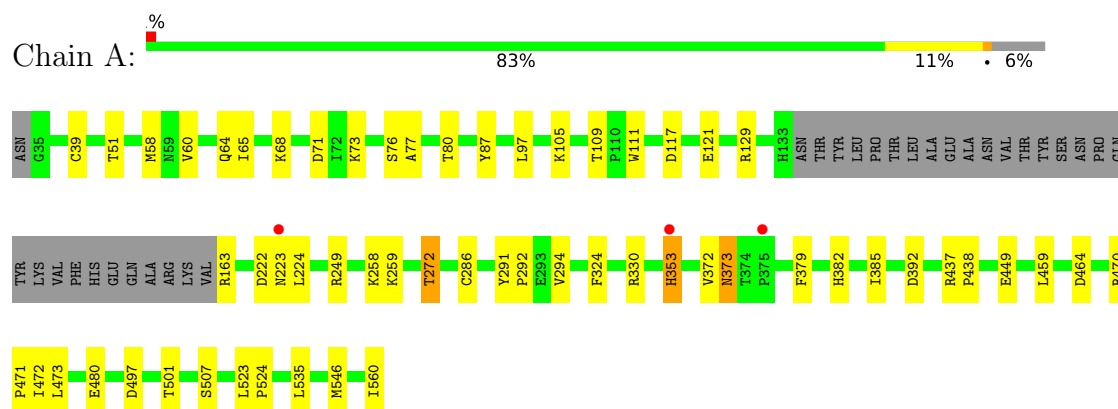
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	77	Total 77	O 77	0	0
4	B	74	Total 74	O 74	0	0
4	D	3	Total 3	O 3	0	0
4	E	3	Total 3	O 3	0	0

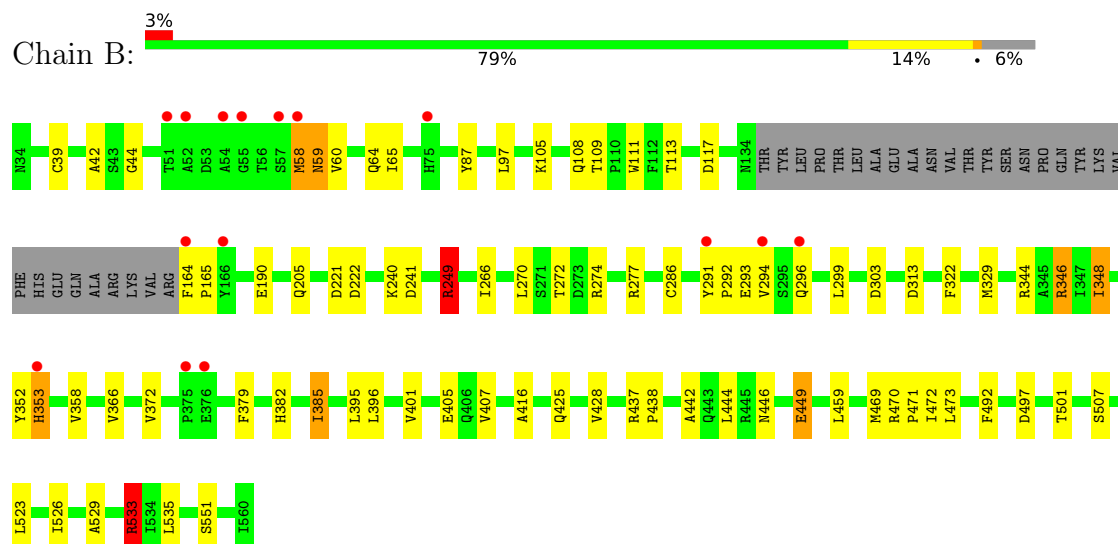
3 Residue-property plots

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: ABC-type transport system, periplasmic component, involved in antimicrobial peptide resistance

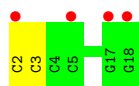


- Molecule 1: ABC-type transport system, periplasmic component, involved in antimicrobial peptide resistance

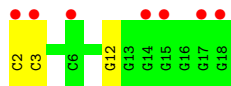
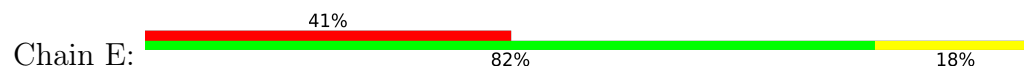


- Molecule 2: RNA (5'-R(P*CP*CP*CP*CP*CP*CP*CP*CP*CP*GP*GP*GP*GP*GP*G P*GP*GP*G)-3')





- Molecule 2: RNA (5'-R(P*CP*CP*CP*CP*CP*CP*CP*CP*CP*GP*GP*GP*GP*GP*GP*GP*GP*G)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	143.26Å 147.97Å 59.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	65.74 – 2.61 65.74 – 2.61	Depositor EDS
% Data completeness (in resolution range)	96.9 (65.74-2.61) 96.9 (65.74-2.61)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.11 (at 2.62Å)	Xtriage
Refinement program	REFMAC 5.8.0230	Depositor
R, R_{free}	0.197 , 0.249 0.205 , 0.258	Depositor DCC
R_{free} test set	1870 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	48.4	Xtriage
Anisotropy	0.166	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 40.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.029 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8917	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 3.68% 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: CA

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	0/4107	0.95	1/5575 (0.0%)
1	B	0.70	0/4116	0.95	0/5590
2	D	0.40	0/405	0.74	0/630
2	E	0.60	0/405	0.80	0/630
All	All	0.69	0/9033	0.93	1/12425 (0.0%)

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	1
1	B	0	3
All	All	0	4

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	464	ASP	CA-CB-CG	5.45	118.05	112.60

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	330	ARG	Sidechain
1	B	249	ARG	Sidechain
1	B	346	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	B	533	ARG	Sidechain

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	4011	0	3954	28	0
1	B	4019	0	3949	53	0
2	D	364	0	188	7	0
2	E	364	0	188	2	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	77	0	0	0	0
4	B	74	0	0	1	0
4	D	3	0	0	0	0
4	E	3	0	0	0	0
All	All	8917	0	8279	88	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 5.

All (88) 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)
2:D:2:C:O2'	2:D:3:C:H5'	1.57	1.02
1:B:407:VAL:HG11	1:B:533:ARG:NH2	1.75	1.02
1:B:296:GLN:OE1	1:B:299:LEU:HD22	1.74	0.86
1:B:444:LEU:HD23	1:B:449:GLU:HG2	1.60	0.83
1:B:407:VAL:HG11	1:B:533:ARG:HH22	1.47	0.79
1:B:407:VAL:CG1	1:B:533:ARG:NH2	2.49	0.75
1:B:407:VAL:CG1	1:B:533:ARG:HH21	2.03	0.72
1:B:39:CYS:HG	1:B:286:CYS:HG	1.38	0.71
1:A:472:ILE:HG22	1:A:473:LEU:HG	1.75	0.67
1:A:259:LYS:HE3	2:E:12:G:OP1	1.96	0.66
1:B:313:ASP:HB2	1:B:366:VAL:HG13	1.80	0.62
2:D:2:C:C2'	2:D:3:C:H5'	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:THR:O	1:A:163:ARG:NH1	2.32	0.62
1:B:274:ARG:HH21	1:B:294:VAL:HG23	1.64	0.61
1:B:396:LEU:C	1:B:396:LEU:HD13	2.26	0.61
1:B:294:VAL:HG12	1:B:353:HIS:ND1	2.16	0.60
2:D:2:C:H2'	2:D:3:C:C5'	2.33	0.59
1:A:294:VAL:HG12	1:A:353:HIS:ND1	2.18	0.59
1:B:39:CYS:HB3	1:B:277:ARG:HG2	1.85	0.58
2:D:2:C:C2'	2:D:3:C:C5'	2.82	0.57
1:A:105:LYS:HE2	1:A:117:ASP:OD1	2.05	0.56
1:B:105:LYS:HE2	1:B:117:ASP:OD1	2.06	0.56
1:B:472:ILE:HG22	1:B:473:LEU:HG	1.87	0.55
2:D:2:C:H2'	2:D:3:C:O4'	2.07	0.54
1:B:108:GLN:NE2	1:B:113:THR:HG23	2.23	0.53
2:E:2:C:O2'	2:E:3:C:H5'	2.08	0.53
1:B:241:ASP:OD1	1:B:249:ARG:HD3	2.10	0.52
1:B:437:ARG:HB3	1:B:438:PRO:HD3	1.91	0.52
1:B:322:PHE:HD1	1:B:329:MET:HE3	1.74	0.52
1:B:497:ASP:O	1:B:501:THR:HG23	2.10	0.52
1:B:348:ILE:HD11	1:B:529:ALA:HB2	1.93	0.51
1:A:76:SER:O	1:A:77:ALA:HB3	2.11	0.51
1:A:437:ARG:HB3	1:A:438:PRO:HD3	1.93	0.50
1:B:401:VAL:HG21	1:B:416:ALA:HB2	1.95	0.49
1:A:39:CYS:SG	1:A:286:CYS:SG	3.10	0.49
1:A:535:LEU:C	1:A:535:LEU:HD12	2.37	0.49
1:B:442:ALA:O	1:B:446:ASN:ND2	2.46	0.49
1:A:109:THR:HG1	1:A:111:TRP:CD1	2.32	0.48
1:B:108:GLN:HE21	1:B:113:THR:HG23	1.78	0.48
1:B:533:ARG:HH11	1:B:533:ARG:HG3	1.78	0.48
1:A:291:TYR:N	1:A:292:PRO:HD3	2.28	0.48
1:B:313:ASP:HB2	1:B:366:VAL:CG1	2.44	0.48
1:B:58:MET:SD	1:B:551:SER:HB2	2.53	0.47
1:B:109:THR:HG1	1:B:111:TRP:CD1	2.32	0.47
1:A:379:PHE:CD2	1:A:523:LEU:HD11	2.49	0.47
1:B:58:MET:HG2	1:B:205:GLN:OE1	2.14	0.47
1:B:535:LEU:HD12	1:B:535:LEU:C	2.38	0.47
2:D:2:C:H2'	2:D:3:C:O5'	2.14	0.47
1:A:470:ARG:HB3	1:A:471:PRO:HD3	1.97	0.47
1:A:39:CYS:SG	1:A:286:CYS:HB3	2.55	0.46
1:B:164:PHE:N	1:B:165:PRO:CD	2.79	0.46
1:B:395:LEU:HB2	1:B:428:VAL:HG13	1.98	0.46
1:B:382:HIS:CD2	1:B:385:ILE:HG13	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:272:THR:HG21	1:B:299:LEU:HD21	1.99	0.45
1:A:372:VAL:O	1:A:373:ASN:HB2	2.16	0.45
1:B:296:GLN:CD	1:B:299:LEU:HD22	2.39	0.45
1:B:313:ASP:O	1:B:366:VAL:HG11	2.17	0.45
1:B:533:ARG:HA	1:B:533:ARG:HD2	1.73	0.44
1:A:68:LYS:HE3	1:A:71:ASP:OD1	2.18	0.44
1:B:164:PHE:N	1:B:165:PRO:HD2	2.32	0.44
1:B:459:LEU:C	1:B:459:LEU:HD12	2.43	0.44
1:A:382:HIS:CE1	1:A:385:ILE:HG12	2.53	0.44
2:D:2:C:C2'	2:D:3:C:O5'	2.66	0.44
1:A:497:ASP:O	1:A:501:THR:HG23	2.18	0.43
1:B:348:ILE:HG12	1:B:358:VAL:HG22	2.00	0.43
1:B:221:ASP:O	1:B:222:ASP:C	2.62	0.43
1:B:291:TYR:N	1:B:292:PRO:HD3	2.33	0.43
1:A:73[A]:LYS:NZ	1:A:80:THR:HG21	2.33	0.43
1:B:87:TYR:HA	1:B:97:LEU:O	2.18	0.43
1:A:449:GLU:O	1:A:449:GLU:HG2	2.17	0.43
1:B:60:VAL:O	1:B:64:GLN:HG2	2.19	0.43
1:A:109:THR:HG1	1:A:111:TRP:CG	2.36	0.42
1:B:396:LEU:C	1:B:396:LEU:CD1	2.91	0.42
1:B:109:THR:HG1	1:B:111:TRP:CG	2.37	0.42
1:B:42:ALA:HB2	1:B:270:LEU:O	2.19	0.42
1:B:313:ASP:CB	1:B:366:VAL:HG13	2.47	0.42
1:A:324:PHE:HE1	1:A:524:PRO:HA	1.85	0.42
1:A:60:VAL:O	1:A:64:GLN:HG2	2.20	0.42
1:B:470:ARG:HB3	1:B:471:PRO:HD3	2.02	0.42
1:A:58:MET:HG2	1:A:459:LEU:HD21	2.02	0.41
1:B:379:PHE:CD2	1:B:523:LEU:HD11	2.55	0.41
1:A:258:LYS:O	1:A:259:LYS:C	2.63	0.41
1:B:348:ILE:HD12	1:B:352:TYR:CD2	2.56	0.41
1:A:87:TYR:HA	1:A:97:LEU:O	2.20	0.41
1:B:58:MET:CE	4:B:736:HOH:O	2.68	0.40
1:B:322:PHE:HZ	1:B:526:ILE:HD11	1.87	0.40
1:B:469:MET:HE2	1:B:492:PHE:CE1	2.57	0.40
1:A:39:CYS:SG	1:A:286:CYS:CB	3.10	0.40

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	494/527 (94%)	480 (97%)	11 (2%)	3 (1%)	21	39
1	B	495/527 (94%)	480 (97%)	11 (2%)	4 (1%)	16	31
All	All	989/1054 (94%)	960 (97%)	22 (2%)	7 (1%)	18	35

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	223	ASN
1	B	44	GLY
1	A	353	HIS
1	B	59	ASN
1	B	353	HIS
1	A	373	ASN
1	B	372	VAL

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	441/467 (94%)	429 (97%)	12 (3%)	39	65
1	B	442/467 (95%)	423 (96%)	19 (4%)	26	49
All	All	883/934 (94%)	852 (96%)	31 (4%)	32	57

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	ILE
1	A	121	GLU
1	A	129	ARG
1	A	222	ASP
1	A	224	LEU
1	A	249	ARG
1	A	272	THR
1	A	392	ASP
1	A	480	GLU
1	A	507	SER
1	A	546	MET
1	A	560	ILE
1	B	58	MET
1	B	59	ASN
1	B	65	ILE
1	B	190	GLU
1	B	240	LYS
1	B	249	ARG
1	B	266	ILE
1	B	272	THR
1	B	293	GLU
1	B	303	ASP
1	B	344	ARG
1	B	346	ARG
1	B	348	ILE
1	B	385	ILE
1	B	405	GLU
1	B	425	GLN
1	B	449	GLU
1	B	507	SER
1	B	533	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	ASN
1	A	75	HIS
1	A	99	ASN
1	A	186	GLN
1	A	223	ASN
1	A	246	GLN
1	A	265	HIS
1	A	340	GLN

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Mol	Chain	Res	Type
1	A	361	ASN
1	A	443	GLN
1	A	446	ASN
1	A	530	ASN
1	B	34	ASN
1	B	99	ASN
1	B	108	GLN
1	B	186	GLN
1	B	245	ASN
1	B	265	HIS
1	B	361	ASN
1	B	443	GLN
1	B	504	HIS
1	B	513	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	D	16/17 (94%)	0	0
2	E	16/17 (94%)	0	0
All	All	32/34 (94%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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 ⓘ

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	497/527 (94%)	-0.07	3 (0%) 85 83	19, 49, 82, 105	1 (0%)
1	B	498/527 (94%)	0.11	15 (3%) 52 47	24, 53, 95, 131	1 (0%)
2	D	17/17 (100%)	1.48	4 (23%) 2 1	47, 106, 207, 225	0
2	E	17/17 (100%)	1.56	7 (41%) 0 0	45, 107, 213, 227	0
All	All	1029/1088 (94%)	0.07	29 (2%) 55 50	19, 52, 96, 227	2 (0%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	296	GLN	5.1
1	B	55	GLY	4.8
2	E	18	G	4.0
2	D	2	C	3.7
2	D	18	G	3.6
1	B	291	TYR	3.6
1	B	164	PHE	3.4
1	B	166[A]	TYR	3.2
2	E	2	C	3.2
1	B	294	VAL	2.9
2	D	17	G	2.8
2	D	5	C	2.6
1	B	54	ALA	2.6
1	B	375	PRO	2.5
2	E	17	G	2.5
1	A	353	HIS	2.4
1	B	353	HIS	2.4
1	B	58	MET	2.4
2	E	14	G	2.4
1	A	375	PRO	2.3
2	E	6	C	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	52	ALA	2.3
1	B	51	THR	2.2
2	E	3	C	2.2
1	B	57	SER	2.2
2	E	15	G	2.1
1	B	376	GLU	2.1
1	B	75	HIS	2.1
1	A	223	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	CA	A	601	1/1	0.91	0.08	68,68,68,68	0
3	CA	B	601	1/1	0.99	0.04	41,41,41,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.