



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:25 PM UTC

PDB ID : 2R05 / pdb_00002r05
Title : Crystal Structure of ALIX/AIP1 in complex with the HIV-1 YPLASL Late Domain
Authors : Hill, C.P.; Zhai, Q.; Fisher, R.D.
Deposited on : 2007-08-17
Resolution : 2.55 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

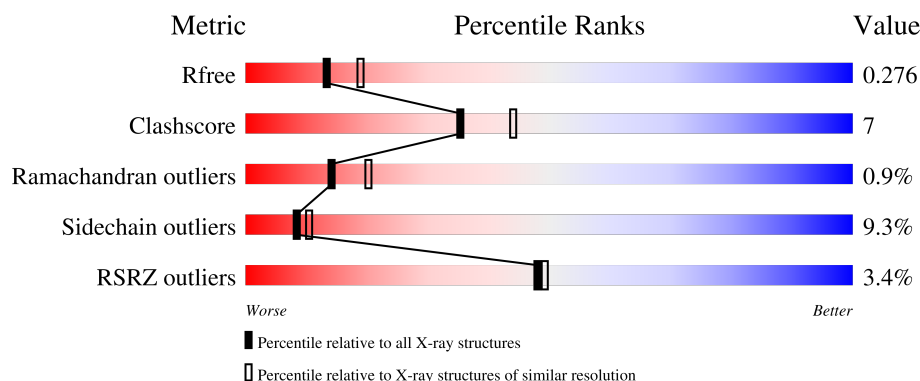
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

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	697	3% 78% 19% .
2	B	11	18% 82% 9% 9%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5591 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 Programmed cell death 6-interacting protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	697	Total	C	N	O	S	0	0	0
			5486	3461	938	1069	18			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	268	TYR	LYS	engineered mutation	UNP Q8WUM4
A	269	TYR	LYS	engineered mutation	UNP Q8WUM4

- Molecule 2 is a protein called p6-Gag.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	11	Total	C	N	O	0	0	0
			88	58	14	16			

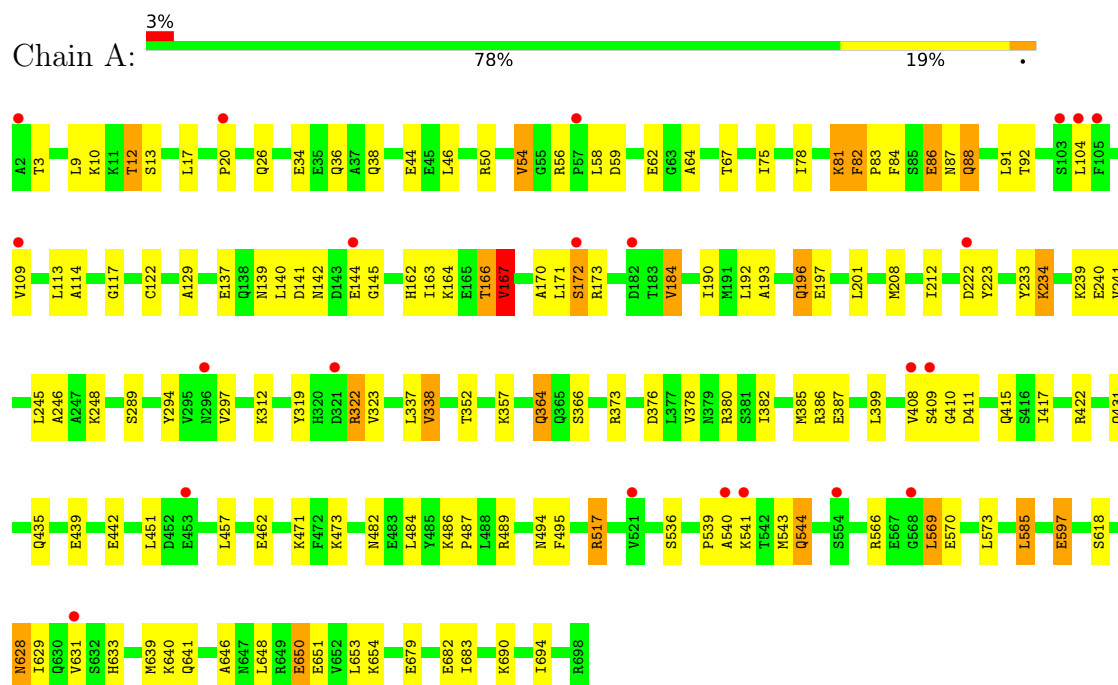
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	17	Total	O	0	0
			17	17		

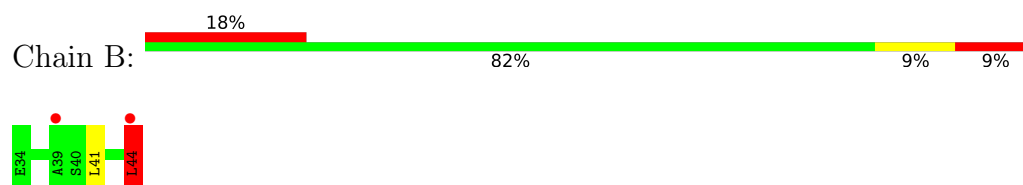
3 Residue-property plots

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: Programmed cell death 6-interacting protein



- Molecule 2: p6-Gag



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	146.09Å 99.44Å 73.54Å 90.00° 107.29° 90.00°	Depositor
Resolution (Å)	27.90 – 2.55 27.90 – 2.55	Depositor EDS
% Data completeness (in resolution range)	98.7 (27.90-2.55) 98.6 (27.90-2.55)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.37 (at 2.53Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.225 , 0.280 0.221 , 0.276	Depositor DCC
R_{free} test set	1622 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	69.1	Xtriage
Anisotropy	0.355	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 54.0	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	5591	wwPDB-VP
Average B, all atoms (Å ²)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.43% 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](#)

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	0.70	1/5570 (0.0%)	0.95	5/7523 (0.1%)
2	B	2.24	1/89 (1.1%)	0.88	0/120
All	All	0.75	2/5659 (0.0%)	0.95	5/7643 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	44	LEU	C-O	20.66	1.64	1.23
1	A	246	ALA	CA-CB	6.47	1.63	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	641	GLN	N-CA-C	7.79	119.85	110.19
1	A	196	GLN	N-CA-C	-6.00	104.65	111.07
1	A	167	VAL	N-CA-C	5.61	116.25	110.36
1	A	319	TYR	N-CA-C	5.49	118.02	111.71
1	A	222	ASP	N-CA-C	-5.24	105.47	111.07

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	5486	0	5532	82	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	88	0	93	2	0
3	A	17	0	0	0	0
All	All	5591	0	5625	83	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 7.

All (83) 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:B:44:LEU:O	2:B:44:LEU:C	1.64	1.40
1:A:486:LYS:HG3	1:A:487:PRO:HD3	1.45	0.97
1:A:382:ILE:HD12	1:A:570:GLU:HG3	1.46	0.94
1:A:517:ARG:HH11	1:A:517:ARG:HG3	1.39	0.87
1:A:92:THR:HG22	1:A:114:ALA:HB2	1.60	0.84
1:A:646:ALA:O	1:A:650:GLU:HB2	1.86	0.75
1:A:376:ASP:O	1:A:380:ARG:HB2	1.90	0.72
1:A:385:MET:HE1	1:A:569:LEU:HB3	1.75	0.69
1:A:486:LYS:HG3	1:A:487:PRO:CD	2.23	0.68
1:A:517:ARG:HH11	1:A:517:ARG:CG	2.08	0.66
1:A:117:GLY:HA3	1:A:170:ALA:HB1	1.80	0.64
1:A:113:LEU:HD11	1:A:173:ARG:HG3	1.83	0.60
1:A:192:LEU:CD1	1:A:338:VAL:HG13	2.32	0.59
1:A:415:GLN:HE22	1:A:422:ARG:NH2	2.01	0.59
1:A:386:ARG:NH2	1:A:570:GLU:OE2	2.35	0.58
1:A:142:ASN:HD22	1:A:145:GLY:H	1.50	0.58
1:A:410:GLY:O	1:A:536:SER:HA	2.04	0.58
1:A:26:GLN:HG2	1:A:36:GLN:HE21	1.69	0.57
1:A:3:THR:HG21	1:A:294:TYR:O	2.04	0.57
1:A:385:MET:HE1	1:A:569:LEU:CB	2.35	0.56
1:A:172:SER:O	1:A:173:ARG:HG2	2.06	0.56
1:A:517:ARG:CG	1:A:517:ARG:NH1	2.69	0.55
1:A:628:ASN:C	1:A:628:ASN:HD22	2.15	0.55
1:A:56:ARG:HD3	1:A:58:LEU:HD12	1.89	0.54
1:A:462:GLU:OE1	1:A:482:ASN:ND2	2.40	0.54
1:A:679:GLU:HB3	2:B:41:LEU:HD21	1.90	0.54
1:A:190:ILE:HG12	1:A:245:LEU:HD21	1.88	0.54
1:A:12:THR:HG21	1:A:50:ARG:HH22	1.72	0.53
1:A:540:ALA:HB3	1:A:640:LYS:HG2	1.90	0.53
1:A:639:MET:HB2	1:A:640:LYS:HD2	1.91	0.52
1:A:208:MET:HE2	1:A:212:ILE:HD13	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:364:GLN:C	1:A:366:SER:H	2.17	0.52
1:A:17:LEU:HD13	1:A:46:LEU:HG	1.92	0.52
1:A:164:LYS:HB2	1:A:184:VAL:HG13	1.94	0.50
1:A:192:LEU:HD12	1:A:338:VAL:HG13	1.92	0.50
1:A:163:ILE:O	1:A:167:VAL:HG22	2.11	0.49
1:A:690:LYS:O	1:A:694:ILE:HG12	2.13	0.49
1:A:3:THR:O	1:A:248:LYS:HE2	2.14	0.48
1:A:10:LYS:HE2	1:A:122:CYS:SG	2.54	0.47
1:A:233:TYR:O	1:A:234:LYS:HG2	2.14	0.47
1:A:139:ASN:OD1	1:A:141:ASP:HB2	2.15	0.47
1:A:164:LYS:HB2	1:A:184:VAL:CG1	2.44	0.47
1:A:17:LEU:HD23	1:A:91:LEU:HD21	1.97	0.46
1:A:431:GLN:NE2	1:A:435:GLN:HE21	2.13	0.46
1:A:142:ASN:ND2	1:A:145:GLY:H	2.13	0.46
1:A:373:ARG:NH2	1:A:597:GLU:HG2	2.31	0.46
1:A:462:GLU:OE1	1:A:482:ASN:CG	2.59	0.46
1:A:439:GLU:HA	1:A:442:GLU:OE2	2.15	0.45
1:A:451:LEU:HD12	1:A:495:PHE:HB3	1.97	0.45
1:A:385:MET:HE2	1:A:566:ARG:CB	2.46	0.45
1:A:9:LEU:HD23	1:A:129:ALA:HB3	1.98	0.45
1:A:399:LEU:HD22	1:A:633:HIS:CD2	2.51	0.45
1:A:378:VAL:O	1:A:382:ILE:HG12	2.17	0.45
1:A:196:GLN:O	1:A:197:GLU:C	2.59	0.45
1:A:409:SER:OG	1:A:411:ASP:HB2	2.17	0.45
1:A:34:GLU:C	1:A:36:GLN:H	2.25	0.44
1:A:193:ALA:HB2	1:A:223:TYR:HB3	1.98	0.44
1:A:59:ASP:HB3	1:A:64:ALA:HB2	2.00	0.44
1:A:486:LYS:CG	1:A:487:PRO:HD3	2.32	0.44
1:A:162:HIS:O	1:A:166:THR:HB	2.18	0.44
1:A:240:GLU:O	1:A:241:VAL:C	2.60	0.44
1:A:386:ARG:HG2	1:A:386:ARG:HH11	1.83	0.44
1:A:322:ARG:NH1	1:A:323:VAL:O	2.51	0.43
1:A:462:GLU:CD	1:A:489:ARG:HH12	2.26	0.42
1:A:233:TYR:O	1:A:234:LYS:CG	2.67	0.42
1:A:81:LYS:O	1:A:82:PHE:C	2.62	0.42
1:A:541:LYS:C	1:A:543:MET:H	2.28	0.42
1:A:385:MET:CE	1:A:566:ARG:HA	2.50	0.42
1:A:385:MET:HE2	1:A:566:ARG:HG2	2.01	0.41
1:A:679:GLU:O	1:A:683:ILE:HG12	2.20	0.41
1:A:540:ALA:HB3	1:A:640:LYS:CG	2.50	0.41
1:A:20:PRO:HG3	1:A:91:LEU:HD13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:409:SER:OG	1:A:411:ASP:CB	2.68	0.41
1:A:56:ARG:HD2	1:A:56:ARG:O	2.21	0.41
1:A:171:LEU:HD23	1:A:173:ARG:HB2	2.02	0.41
1:A:192:LEU:HD11	1:A:338:VAL:HG13	2.01	0.41
1:A:208:MET:HE2	1:A:212:ILE:HG21	2.02	0.41
1:A:84:PHE:C	1:A:86:GLU:H	2.28	0.41
1:A:197:GLU:OE2	1:A:248:LYS:NZ	2.53	0.41
1:A:208:MET:CE	1:A:212:ILE:HD13	2.50	0.40
1:A:409:SER:HA	1:A:539:PRO:HB3	2.03	0.40
1:A:585:LEU:HD12	1:A:585:LEU:HA	1.91	0.40
1:A:82:PHE:HA	1:A:83:PRO:HD3	1.93	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	695/697 (100%)	651 (94%)	38 (6%)	6 (1%)	14	20
2	B	9/11 (82%)	8 (89%)	1 (11%)	0	100	100
All	All	704/708 (99%)	659 (94%)	39 (6%)	6 (1%)	14	20

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	81	LYS
1	A	544	GLN
1	A	87	ASN
1	A	88	GLN
1	A	82	PHE
1	A	54	VAL

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	600/600 (100%)	544 (91%)	56 (9%)	8	10
2	B	10/10 (100%)	9 (90%)	1 (10%)	7	9
All	All	610/610 (100%)	553 (91%)	57 (9%)	8	10

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	THR
1	A	13	SER
1	A	38	GLN
1	A	44	GLU
1	A	54	VAL
1	A	62	GLU
1	A	67	THR
1	A	75	ILE
1	A	78	ILE
1	A	86	GLU
1	A	88	GLN
1	A	104	LEU
1	A	109	VAL
1	A	137	GLU
1	A	140	LEU
1	A	144	GLU
1	A	166	THR
1	A	167	VAL
1	A	172	SER
1	A	184	VAL
1	A	201	LEU
1	A	234	LYS
1	A	239	LYS
1	A	289	SER
1	A	297	VAL
1	A	312	LYS
1	A	322	ARG

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Mol	Chain	Res	Type
1	A	337	LEU
1	A	338	VAL
1	A	352	THR
1	A	357	LYS
1	A	364	GLN
1	A	387	GLU
1	A	408	VAL
1	A	417	ILE
1	A	457	LEU
1	A	471	LYS
1	A	473	LYS
1	A	484	LEU
1	A	494	ASN
1	A	517	ARG
1	A	544	GLN
1	A	569	LEU
1	A	573	LEU
1	A	585	LEU
1	A	597	GLU
1	A	618	SER
1	A	628	ASN
1	A	629	ILE
1	A	631	VAL
1	A	648	LEU
1	A	650	GLU
1	A	651	GLU
1	A	653	LEU
1	A	654	LYS
1	A	682	GLU
2	B	44	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	GLN
1	A	61	HIS
1	A	133	GLN
1	A	142	ASN
1	A	162	HIS
1	A	219	GLN
1	A	249	HIS
1	A	253	GLN

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Mol	Chain	Res	Type
1	A	267	GLN
1	A	364	GLN
1	A	415	GLN
1	A	427	GLN
1	A	435	GLN
1	A	447	ASN
1	A	482	ASN
1	A	516	HIS
1	A	544	GLN
1	A	571	ASN
1	A	628	ASN
1	A	633	HIS
1	A	647	ASN
1	A	662	ASN
1	A	689	ASN

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](#)

There are no ligands in this entry.

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	697/697 (100%)	0.42	22 (3%)	50	51	40, 93, 142, 190	2 (0%)
2	B	11/11 (100%)	1.17	2 (18%)	3	3	102, 121, 173, 182	0
All	All	708/708 (100%)	0.44	24 (3%)	48	49	40, 94, 144, 190	2 (0%)

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	104	LEU	5.9
1	A	453	GLU	3.4
1	A	109	VAL	3.1
1	A	103	SER	3.1
1	A	408	VAL	3.0
1	A	409	SER	2.9
1	A	554	SER	2.9
1	A	144	GLU	2.9
1	A	2	ALA	2.8
1	A	172	SER	2.7
1	A	540	ALA	2.5
1	A	57	PRO	2.5
1	A	631	VAL	2.4
1	A	521	VAL	2.4
1	A	20	PRO	2.3
1	A	222	ASP	2.3
1	A	541	LYS	2.3
1	A	105	PHE	2.3
2	B	39	ALA	2.2
1	A	568	GLY	2.2
1	A	182	ASP	2.1
1	A	296	ASN	2.1
2	B	44	LEU	2.1
1	A	321	ASP	2.1

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.