



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:33 PM UTC

PDB ID : 8ERI / pdb_00008eri
Title : HTLV-1 capsid protein full-length
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Deposited on : 2022-10-11
Resolution : 2.25 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

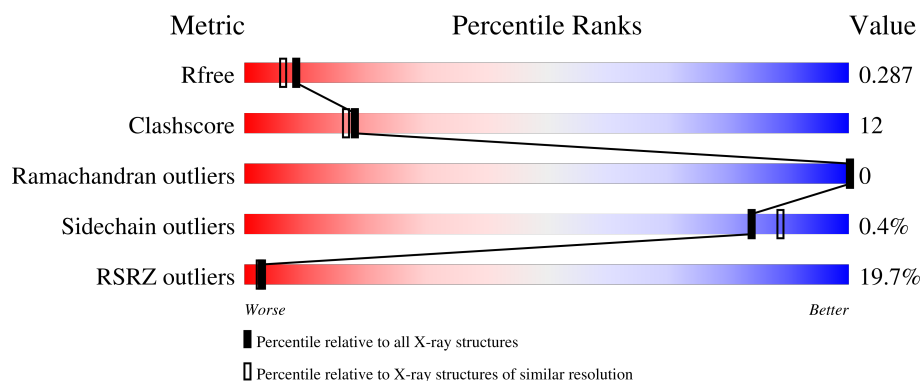
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	214	24% 73% 23% .
1	B	214	15% 80% 16% .
1	C	214	18% 73% 22% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9690 atoms, of which 4763 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 capsid protein p24.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	206	Total	C	H	N	O	S	0	0	0
			3195	1011	1586	291	300	7			
1	B	206	Total	C	H	N	O	S	0	0	0
			3195	1011	1586	291	300	7			
1	C	206	Total	C	H	N	O	S	0	0	0
			3203	1014	1591	291	300	7			

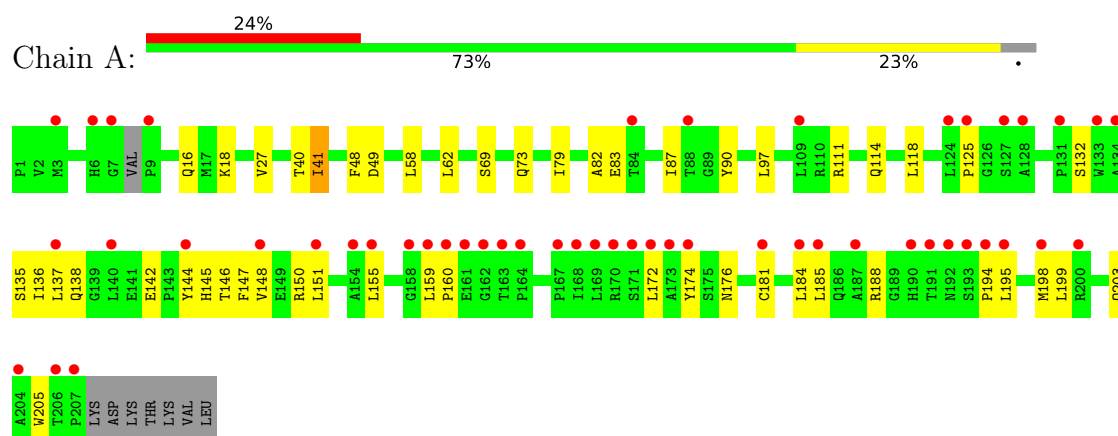
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	29	Total	O	0	0
			29	29		
2	B	35	Total	O	0	0
			35	35		
2	C	33	Total	O	0	0
			33	33		

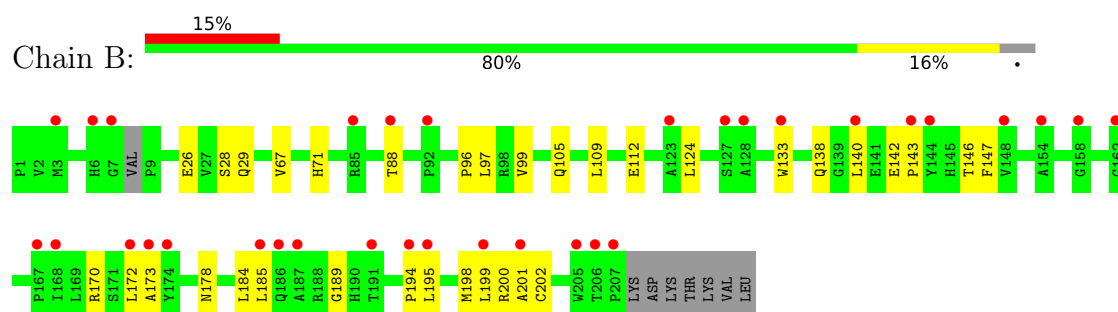
3 Residue-property plots [i](#)

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.

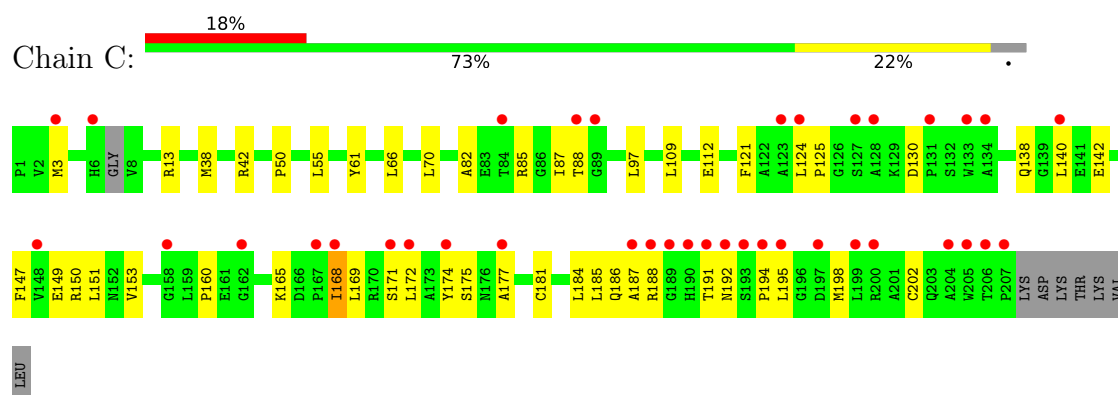
• Molecule 1: capsid protein p24



• Molecule 1: capsid protein p24



• Molecule 1: capsid protein p24



4 Data and refinement statistics

Property	Value	Source
Space group	F 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	74.08Å 128.66Å 297.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.63 – 2.25 43.63 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.3 (43.63-2.25) 91.8 (43.63-2.25)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.28 (at 2.24Å)	Xtriage
Refinement program	PHENIX 1.20.1	Depositor
R, R_{free}	0.251 , 0.288 0.251 , 0.287	Depositor DCC
R_{free} test set	1773 reflections (5.22%)	wwPDB-VP
Wilson B-factor (Å ²)	38.7	Xtriage
Anisotropy	0.878	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 82.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9690	wwPDB-VP
Average B, all atoms (Å ²)	118.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.33% 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

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	0.18	0/1650	0.31	0/2246
1	B	0.17	0/1650	0.32	0/2246
1	C	0.17	0/1653	0.34	0/2252
All	All	0.17	0/4953	0.32	0/6744

There are no bond length outliers.

There are no bond angle outliers.

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	1609	1586	1586	43	0
1	B	1609	1586	1586	29	0
1	C	1612	1591	1591	45	0
2	A	29	0	0	0	0
2	B	35	0	0	0	0
2	C	33	0	0	1	0
All	All	4927	4763	4763	116	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 12.

All (116) 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:B:88:THR:HG23	1:B:112:GLU:OE2	1.75	0.86
1:C:185:LEU:HB3	1:C:188:ARG:HG2	1.59	0.85
1:B:105:GLN:N	1:B:105:GLN:OE1	2.15	0.80
1:A:16:GLN:OE1	1:A:18:LYS:NZ	2.16	0.79
1:A:185:LEU:O	1:A:188:ARG:NH1	2.16	0.78
1:B:198:MET:SD	1:B:201:ALA:HB3	2.25	0.76
1:B:185:LEU:HD12	1:B:201:ALA:HB1	1.66	0.76
1:B:140:LEU:O	1:B:178:ASN:ND2	2.22	0.73
1:A:181:CYS:HG	1:A:205:TRP:CD1	2.09	0.71
1:B:97:LEU:HD21	1:B:109:LEU:HD11	1.73	0.70
1:B:198:MET:O	1:B:201:ALA:N	2.25	0.69
1:C:194:PRO:C	1:C:198:MET:HE1	2.20	0.67
1:C:150:ARG:HA	1:C:150:ARG:NE	2.09	0.66
1:A:137:LEU:HD12	1:A:176:ASN:O	1.96	0.66
1:B:142:GLU:OE2	1:B:146:THR:HG23	1.95	0.66
1:C:165:LYS:O	1:C:169:LEU:N	2.25	0.66
1:C:198:MET:N	1:C:198:MET:SD	2.69	0.65
1:A:199:LEU:O	1:A:203:GLN:N	2.30	0.65
1:C:97:LEU:HD11	1:C:109:LEU:HD11	1.80	0.64
1:C:191:THR:HG22	1:C:192:ASN:H	1.64	0.63
1:C:97:LEU:CD1	1:C:109:LEU:HD11	2.30	0.61
1:A:181:CYS:SG	1:A:205:TRP:CE2	2.95	0.60
1:C:195:LEU:HA	1:C:198:MET:SD	2.42	0.60
1:B:97:LEU:HD21	1:B:109:LEU:CD1	2.32	0.59
1:A:111:ARG:HD3	1:A:114:GLN:HE22	1.67	0.58
1:B:143:PRO:O	1:B:146:THR:HG22	2.03	0.58
1:B:67:VAL:HG13	1:B:124:LEU:HD12	1.85	0.58
1:B:142:GLU:OE2	1:B:146:THR:CG2	2.51	0.58
1:C:150:ARG:NH2	1:C:153:VAL:HG11	2.19	0.58
1:B:185:LEU:HD12	1:B:201:ALA:CB	2.35	0.57
1:A:155:LEU:HD22	1:A:159:LEU:HD11	1.87	0.56
1:A:41:ILE:HD12	1:A:118:LEU:CD2	2.34	0.56
1:A:79:ILE:O	1:A:83:GLU:HG3	2.06	0.56
1:C:172:LEU:O	1:C:175:SER:OG	2.24	0.56
1:C:185:LEU:HB3	1:C:188:ARG:CG	2.32	0.56
1:C:185:LEU:O	1:C:188:ARG:HG2	2.06	0.55
1:C:88:THR:HG22	1:C:112:GLU:OE2	2.07	0.55
1:A:125:PRO:HB2	1:A:160:PRO:HG3	1.90	0.54
1:C:130:ASP:OD2	1:C:130:ASP:N	2.38	0.54
1:C:124:LEU:HB2	1:C:125:PRO:HD3	1.90	0.53
1:A:194:PRO:CB	1:A:198:MET:HE1	2.38	0.53
1:B:184:LEU:HD23	1:B:202:CYS:SG	2.48	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:185:LEU:HD11	1:C:198:MET:HA	1.90	0.53
1:A:58:LEU:HD11	1:A:62:LEU:HD11	1.89	0.53
1:A:132:SER:O	1:A:135:SER:OG	2.25	0.53
1:A:194:PRO:HB2	1:A:198:MET:HE1	1.92	0.51
1:A:184:LEU:O	1:A:185:LEU:HD23	2.10	0.51
1:C:82:ALA:CB	1:C:87:ILE:HD11	2.40	0.51
1:A:125:PRO:CB	1:A:160:PRO:HG3	2.40	0.51
1:B:28:SER:OG	1:B:29:GLN:N	2.42	0.51
1:C:85:ARG:NH2	2:C:302:HOH:O	2.44	0.50
1:B:97:LEU:CD2	1:B:109:LEU:HD11	2.40	0.50
1:A:195:LEU:HA	1:A:198:MET:SD	2.52	0.49
1:A:142:GLU:OE1	1:A:147:PHE:CD2	2.65	0.49
1:A:69:SER:O	1:A:73:GLN:HG2	2.13	0.49
1:C:194:PRO:CB	1:C:198:MET:HE1	2.42	0.49
1:C:50:PRO:HG2	1:C:55:LEU:HD21	1.94	0.48
1:A:27:VAL:HG23	1:A:40:THR:HG21	1.95	0.48
1:B:26:GLU:OE2	1:C:61:TYR:OH	2.30	0.48
1:C:171:SER:HA	1:C:174:TYR:CE2	2.49	0.48
1:A:41:ILE:CD1	1:A:118:LEU:CD2	2.92	0.47
1:C:3:MET:HG3	1:C:13:ARG:HD2	1.95	0.47
1:B:138:GLN:HB2	1:B:147:PHE:CD2	2.48	0.47
1:C:184:LEU:HD22	1:C:202:CYS:SG	2.55	0.47
1:A:138:GLN:N	1:A:147:PHE:CZ	2.82	0.47
1:A:184:LEU:C	1:A:185:LEU:HD23	2.40	0.47
1:B:147:PHE:CZ	1:B:173:ALA:HA	2.50	0.46
1:A:185:LEU:HB3	1:A:188:ARG:HH11	1.81	0.46
1:A:142:GLU:OE2	1:A:150:ARG:NE	2.48	0.46
1:C:195:LEU:CA	1:C:198:MET:SD	3.03	0.46
1:B:170:ARG:HG2	1:B:195:LEU:HB2	1.97	0.46
1:B:195:LEU:HA	1:B:198:MET:HB3	1.96	0.46
1:C:186:GLN:O	1:C:187:ALA:HB3	2.16	0.45
1:A:174:TYR:CD2	1:A:185:LEU:HD13	2.51	0.45
1:C:125:PRO:HB2	1:C:160:PRO:HG3	1.98	0.45
1:A:82:ALA:HB1	1:A:87:ILE:HD11	1.99	0.45
1:C:150:ARG:HA	1:C:150:ARG:HE	1.81	0.44
1:A:41:ILE:HD12	1:A:118:LEU:HD21	1.99	0.44
1:A:111:ARG:HD3	1:A:114:GLN:NE2	2.32	0.44
1:B:185:LEU:CD1	1:B:201:ALA:HB1	2.41	0.44
1:A:136:ILE:HG23	1:A:150:ARG:NH2	2.32	0.44
1:A:181:CYS:SG	1:A:205:TRP:CD1	3.10	0.44
1:C:194:PRO:O	1:C:198:MET:SD	2.75	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:TYR:O	1:A:148:VAL:HG23	2.17	0.44
1:A:151:LEU:HD13	1:A:172:LEU:HB3	1.98	0.44
1:C:138:GLN:CG	1:C:142:GLU:HB2	2.48	0.44
1:A:181:CYS:SG	1:A:205:TRP:CD2	3.11	0.44
1:C:38:MET:O	1:C:42:ARG:HG3	2.17	0.44
1:C:185:LEU:O	1:C:188:ARG:CG	2.65	0.43
1:A:90:TYR:CD1	1:A:97:LEU:HD12	2.53	0.43
1:B:189:GLY:O	1:B:194:PRO:HA	2.18	0.43
1:C:66:LEU:O	1:C:70:LEU:HD22	2.19	0.43
1:C:195:LEU:C	1:C:198:MET:SD	3.03	0.42
1:A:155:LEU:HD22	1:A:159:LEU:CD1	2.48	0.42
1:C:82:ALA:HB1	1:C:87:ILE:HD11	1.99	0.42
1:A:181:CYS:SG	1:A:205:TRP:NE1	2.92	0.42
1:B:133:TRP:CE3	1:B:172:LEU:HD21	2.55	0.42
1:B:198:MET:O	1:B:199:LEU:C	2.63	0.42
1:B:200:ARG:HG3	1:B:200:ARG:HH11	1.85	0.42
1:C:121:PHE:CD1	1:C:124:LEU:HD12	2.55	0.42
1:C:151:LEU:HD21	1:C:172:LEU:HB3	2.01	0.42
1:A:82:ALA:CB	1:A:87:ILE:HD11	2.49	0.41
1:B:71:HIS:HA	1:B:124:LEU:HD21	2.02	0.41
1:C:165:LYS:O	1:C:168:ILE:N	2.53	0.41
1:A:145:HIS:NE2	1:A:146:THR:HG23	2.35	0.41
1:B:185:LEU:CD1	1:B:201:ALA:CB	2.98	0.41
1:A:194:PRO:C	1:A:198:MET:HE1	2.45	0.41
1:C:147:PHE:CD1	1:C:147:PHE:C	2.99	0.41
1:C:185:LEU:CD1	1:C:198:MET:HB3	2.51	0.41
1:A:48:PHE:O	1:A:49:ASP:C	2.63	0.41
1:C:140:LEU:N	1:C:140:LEU:HD23	2.35	0.41
1:C:149:GLU:O	1:C:153:VAL:HG12	2.21	0.41
1:C:177:ALA:HB1	1:C:181:CYS:HB2	2.02	0.41
1:A:147:PHE:HE2	1:A:150:ARG:HH21	1.69	0.40
1:B:96:PRO:O	1:B:99:VAL:HG12	2.21	0.40
1:C:195:LEU:O	1:C:198:MET:SD	2.80	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	202/214 (94%)	194 (96%)	8 (4%)	0	100	100
1	B	202/214 (94%)	190 (94%)	12 (6%)	0	100	100
1	C	202/214 (94%)	194 (96%)	8 (4%)	0	100	100
All	All	606/642 (94%)	578 (95%)	28 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	174/182 (96%)	173 (99%)	1 (1%)	78	84
1	B	174/182 (96%)	174 (100%)	0	100	100
1	C	175/182 (96%)	174 (99%)	1 (1%)	78	84
All	All	523/546 (96%)	521 (100%)	2 (0%)	84	89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	ILE
1	C	168	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	GLN
1	A	39	GLN
1	A	114	GLN
1	A	176	ASN
1	B	25	GLN
1	B	145	HIS
1	B	152	ASN
1	C	29	GLN
1	C	72	HIS
1	C	106	GLN
1	C	114	GLN
1	C	190	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](#)

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	206/214 (96%)	1.35	51 (24%) 2 1	39, 79, 251, 298	0
1	B	206/214 (96%)	1.16	33 (16%) 5 4	40, 79, 235, 274	0
1	C	206/214 (96%)	1.16	38 (18%) 3 3	40, 80, 266, 308	0
All	All	618/642 (96%)	1.22	122 (19%) 3 2	39, 80, 257, 308	0

All (122) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	195	LEU	7.3
1	A	168	ILE	6.4
1	B	128	ALA	5.9
1	A	133	TRP	5.5
1	C	168	ILE	5.0
1	A	159	LEU	5.0
1	A	163	THR	5.0
1	A	124	LEU	4.6
1	A	172	LEU	4.4
1	A	167	PRO	4.3
1	B	7	GLY	4.2
1	B	194	PRO	4.0
1	C	191	THR	3.9
1	A	7	GLY	3.9
1	C	193	SER	3.9
1	C	190	HIS	3.8
1	A	164	PRO	3.8
1	A	190	HIS	3.7
1	A	134	ALA	3.7
1	A	195	LEU	3.6
1	C	167	PRO	3.6
1	C	171	SER	3.6
1	C	195	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	155	LEU	3.5
1	B	6	HIS	3.5
1	A	169	LEU	3.5
1	B	168	ILE	3.5
1	C	177	ALA	3.4
1	A	9	PRO	3.3
1	A	162	GLY	3.3
1	C	192	ASN	3.3
1	B	133	TRP	3.3
1	C	128	ALA	3.2
1	B	127	SER	3.2
1	A	128	ALA	3.2
1	B	207	PRO	3.2
1	B	140	LEU	3.1
1	C	172	LEU	3.1
1	B	88	THR	3.1
1	A	193	SER	3.0
1	A	161	GLU	3.0
1	C	89	GLY	3.0
1	B	143	PRO	3.0
1	B	85	ARG	3.0
1	C	88	THR	3.0
1	C	133	TRP	3.0
1	C	205	TRP	3.0
1	A	173	ALA	2.9
1	C	174	TYR	2.9
1	A	171	SER	2.9
1	A	131	PRO	2.9
1	A	6	HIS	2.9
1	C	206	THR	2.9
1	B	3	MET	2.9
1	A	154	ALA	2.9
1	A	192	ASN	2.9
1	A	191	THR	2.8
1	A	127	SER	2.8
1	A	207	PRO	2.8
1	A	185	LEU	2.8
1	A	206	THR	2.8
1	B	191	THR	2.7
1	C	194	PRO	2.7
1	A	184	LEU	2.7
1	C	131	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	140	LEU	2.6
1	C	197	ASP	2.6
1	C	148	VAL	2.6
1	B	123	ALA	2.6
1	B	205	TRP	2.6
1	C	134	ALA	2.6
1	B	173	ALA	2.6
1	A	125	PRO	2.6
1	C	158	GLY	2.6
1	B	148	VAL	2.6
1	A	137	LEU	2.5
1	B	199	LEU	2.5
1	B	162	GLY	2.5
1	C	123	ALA	2.5
1	C	204	ALA	2.5
1	C	84	THR	2.5
1	B	172	LEU	2.5
1	A	194	PRO	2.5
1	A	181	CYS	2.4
1	C	124	LEU	2.4
1	A	204	ALA	2.4
1	C	6	HIS	2.4
1	A	170	ARG	2.4
1	B	206	THR	2.4
1	A	160	PRO	2.3
1	B	158	GLY	2.3
1	B	201	ALA	2.3
1	C	140	LEU	2.3
1	C	199	LEU	2.3
1	A	88	THR	2.3
1	A	148	VAL	2.3
1	B	167	PRO	2.3
1	A	84	THR	2.3
1	B	185	LEU	2.3
1	C	3	MET	2.3
1	A	187	ALA	2.3
1	C	200	ARG	2.3
1	C	127	SER	2.2
1	A	3	MET	2.2
1	C	187	ALA	2.2
1	A	174	TYR	2.2
1	B	144	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	144	TYR	2.2
1	B	92	PRO	2.2
1	C	188	ARG	2.1
1	A	151	LEU	2.1
1	A	198	MET	2.1
1	A	158	GLY	2.1
1	C	189	GLY	2.1
1	C	162	GLY	2.1
1	B	154	ALA	2.1
1	B	187	ALA	2.1
1	C	207	PRO	2.1
1	B	174	TYR	2.1
1	A	109	LEU	2.0
1	B	186	GLN	2.0
1	A	200	ARG	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.