



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 11:00 PM UTC

PDB ID : 8CUK / pdb_00008cuk
Title : X-ray Structure of the WD40 domain of HOPS subunit Vps11 from Yeast
Authors : Port, S.A.; Baker, R.W.; Jeffrey, P.D.; Hughson, F.M.
Deposited on : 2022-05-17
Resolution : 2.22 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

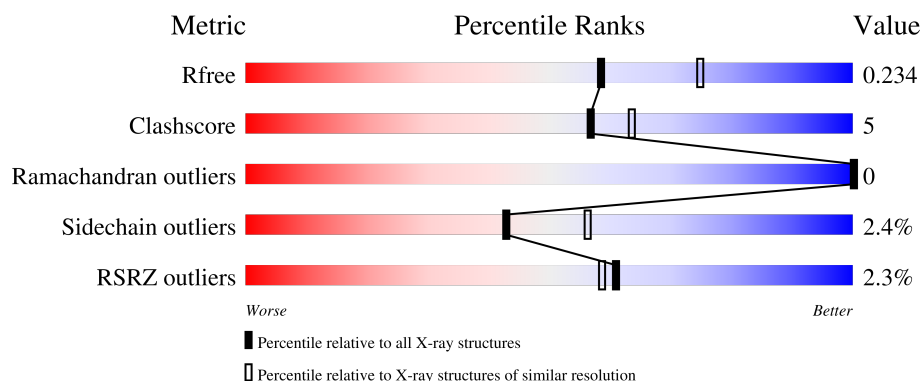
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.22 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	7682 (2.24-2.20)
Clashscore	190562	8402 (2.24-2.20)
Ramachandran outliers	187476	8303 (2.24-2.20)
Sidechain outliers	187428	8304 (2.24-2.20)
RSRZ outliers	180081	7683 (2.24-2.20)

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	379	0% 77% 10% • 13%
1	B	379	2% 76% 11% • 12%
1	C	379	2% 74% 12% • 13%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8288 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 E3 ubiquitin-protein ligase PEP5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	330	Total	C	N	O	S	0	4	0
			2627	1684	448	486	9			
1	B	334	Total	C	N	O	S	0	5	0
			2656	1704	452	491	9			
1	C	330	Total	C	N	O	S	0	2	0
			2613	1672	448	484	9			

There are 87 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-28	MET	-	initiating methionine	UNP P12868
A	-27	LYS	-	expression tag	UNP P12868
A	-26	HIS	-	expression tag	UNP P12868
A	-25	HIS	-	expression tag	UNP P12868
A	-24	HIS	-	expression tag	UNP P12868
A	-23	HIS	-	expression tag	UNP P12868
A	-22	HIS	-	expression tag	UNP P12868
A	-21	HIS	-	expression tag	UNP P12868
A	-20	HIS	-	expression tag	UNP P12868
A	-19	GLY	-	expression tag	UNP P12868
A	-18	ALA	-	expression tag	UNP P12868
A	-17	ALA	-	expression tag	UNP P12868
A	-16	GLY	-	expression tag	UNP P12868
A	-15	THR	-	expression tag	UNP P12868
A	-14	SER	-	expression tag	UNP P12868
A	-13	LEU	-	expression tag	UNP P12868
A	-12	TYR	-	expression tag	UNP P12868
A	-11	LYS	-	expression tag	UNP P12868
A	-10	LYS	-	expression tag	UNP P12868
A	-9	ALA	-	expression tag	UNP P12868
A	-8	GLY	-	expression tag	UNP P12868
A	-7	GLU	-	expression tag	UNP P12868
A	-6	ASN	-	expression tag	UNP P12868

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	LEU	-	expression tag	UNP P12868
A	-4	TYR	-	expression tag	UNP P12868
A	-3	PHE	-	expression tag	UNP P12868
A	-2	GLN	-	expression tag	UNP P12868
A	-1	GLY	-	expression tag	UNP P12868
A	0	SER	-	expression tag	UNP P12868
B	-28	MET	-	initiating methionine	UNP P12868
B	-27	LYS	-	expression tag	UNP P12868
B	-26	HIS	-	expression tag	UNP P12868
B	-25	HIS	-	expression tag	UNP P12868
B	-24	HIS	-	expression tag	UNP P12868
B	-23	HIS	-	expression tag	UNP P12868
B	-22	HIS	-	expression tag	UNP P12868
B	-21	HIS	-	expression tag	UNP P12868
B	-20	HIS	-	expression tag	UNP P12868
B	-19	GLY	-	expression tag	UNP P12868
B	-18	ALA	-	expression tag	UNP P12868
B	-17	ALA	-	expression tag	UNP P12868
B	-16	GLY	-	expression tag	UNP P12868
B	-15	THR	-	expression tag	UNP P12868
B	-14	SER	-	expression tag	UNP P12868
B	-13	LEU	-	expression tag	UNP P12868
B	-12	TYR	-	expression tag	UNP P12868
B	-11	LYS	-	expression tag	UNP P12868
B	-10	LYS	-	expression tag	UNP P12868
B	-9	ALA	-	expression tag	UNP P12868
B	-8	GLY	-	expression tag	UNP P12868
B	-7	GLU	-	expression tag	UNP P12868
B	-6	ASN	-	expression tag	UNP P12868
B	-5	LEU	-	expression tag	UNP P12868
B	-4	TYR	-	expression tag	UNP P12868
B	-3	PHE	-	expression tag	UNP P12868
B	-2	GLN	-	expression tag	UNP P12868
B	-1	GLY	-	expression tag	UNP P12868
B	0	SER	-	expression tag	UNP P12868
C	-28	MET	-	initiating methionine	UNP P12868
C	-27	LYS	-	expression tag	UNP P12868
C	-26	HIS	-	expression tag	UNP P12868
C	-25	HIS	-	expression tag	UNP P12868
C	-24	HIS	-	expression tag	UNP P12868
C	-23	HIS	-	expression tag	UNP P12868
C	-22	HIS	-	expression tag	UNP P12868

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-21	HIS	-	expression tag	UNP P12868
C	-20	HIS	-	expression tag	UNP P12868
C	-19	GLY	-	expression tag	UNP P12868
C	-18	ALA	-	expression tag	UNP P12868
C	-17	ALA	-	expression tag	UNP P12868
C	-16	GLY	-	expression tag	UNP P12868
C	-15	THR	-	expression tag	UNP P12868
C	-14	SER	-	expression tag	UNP P12868
C	-13	LEU	-	expression tag	UNP P12868
C	-12	TYR	-	expression tag	UNP P12868
C	-11	LYS	-	expression tag	UNP P12868
C	-10	LYS	-	expression tag	UNP P12868
C	-9	ALA	-	expression tag	UNP P12868
C	-8	GLY	-	expression tag	UNP P12868
C	-7	GLU	-	expression tag	UNP P12868
C	-6	ASN	-	expression tag	UNP P12868
C	-5	LEU	-	expression tag	UNP P12868
C	-4	TYR	-	expression tag	UNP P12868
C	-3	PHE	-	expression tag	UNP P12868
C	-2	GLN	-	expression tag	UNP P12868
C	-1	GLY	-	expression tag	UNP P12868
C	0	SER	-	expression tag	UNP P12868

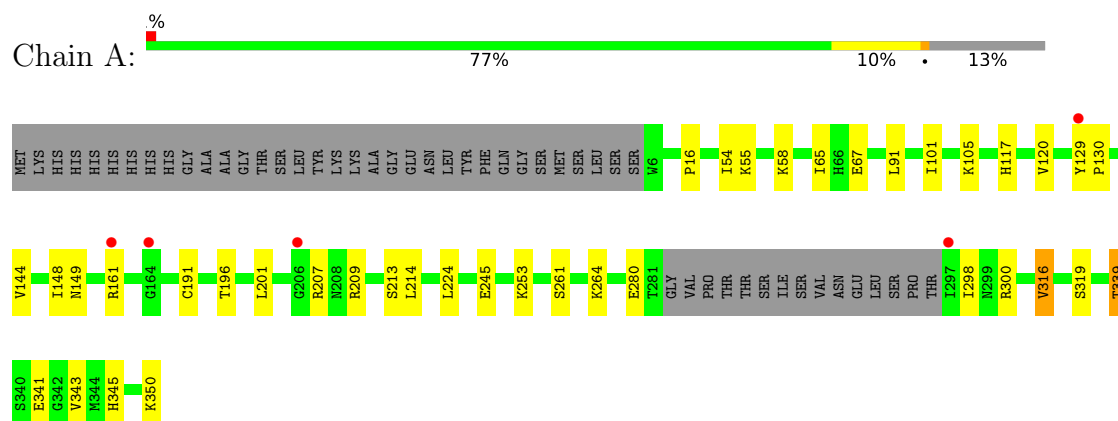
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	154	Total O 154 154	0	0
2	B	104	Total O 104 104	0	0
2	C	134	Total O 134 134	0	0

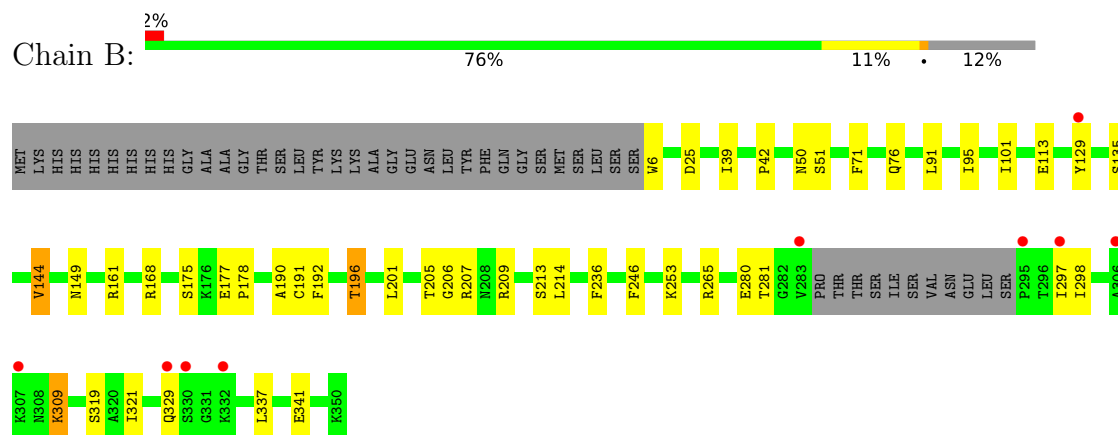
3 Residue-property plots [i](#)

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.

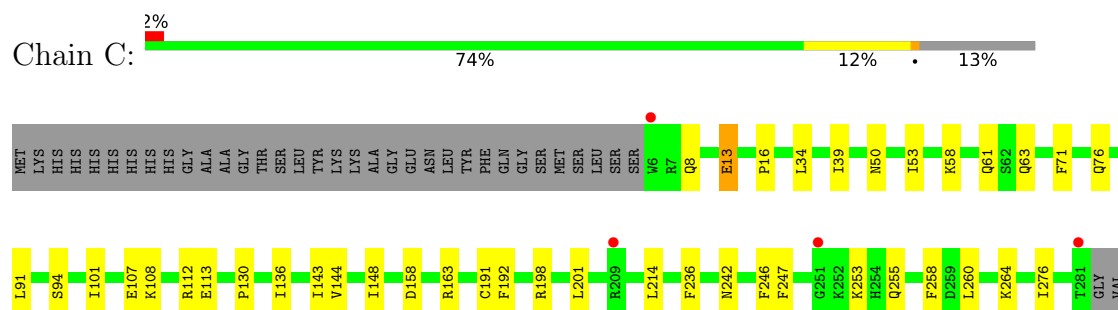
• Molecule 1: E3 ubiquitin-protein ligase PEP5

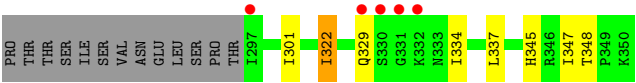


• Molecule 1: E3 ubiquitin-protein ligase PEP5



• Molecule 1: E3 ubiquitin-protein ligase PEP5





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	89.08Å 113.16Å 129.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.76 – 2.22 47.76 – 2.22	Depositor EDS
% Data completeness (in resolution range)	93.8 (47.76-2.22) 93.1 (47.76-2.22)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.20 (at 2.22Å)	Xtriage
Refinement program	PHENIX 1.17-3644	Depositor
R, R_{free}	0.174 , 0.234 0.174 , 0.234	Depositor DCC
R_{free} test set	3063 reflections (4.69%)	wwPDB-VP
Wilson B-factor (Å ²)	36.2	Xtriage
Anisotropy	0.383	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 42.3	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	0.96	EDS
Total number of atoms	8288	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.20% 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	0.33	0/2687	0.53	0/3638
1	B	0.30	0/2720	0.51	0/3683
1	C	0.33	0/2667	0.54	0/3610
All	All	0.32	0/8074	0.53	0/10931

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	2627	0	2680	22	0
1	B	2656	0	2722	29	0
1	C	2613	0	2654	30	0
2	A	154	0	0	1	0
2	B	104	0	0	0	0
2	C	134	0	0	1	0
All	All	8288	0	8056	73	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 (73) 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:168:ARG:HD2	1:B:206:GLY:HA3	1.69	0.74
1:A:245:GLU:OE2	1:A:253:LYS:NZ	2.28	0.66
1:A:207:ARG:O	1:B:76:GLN:NE2	2.29	0.65
1:C:136:ILE:HG12	1:C:143:ILE:HG12	1.78	0.65
1:C:158:ASP:HB3	1:C:163:ARG:HB2	1.80	0.64
1:B:190:ALA:HB1	1:B:201:LEU:HD11	1.82	0.62
1:B:175:SER:HB2	1:B:177:GLU:HG3	1.82	0.61
1:A:130:PRO:HG2	1:A:148:ILE:HG13	1.82	0.61
1:C:144:VAL:HG21	1:C:191[B]:CYS:SG	2.41	0.59
1:A:144:VAL:HG21	1:A:191[B]:CYS:SG	2.44	0.58
1:B:91:LEU:HG	1:B:101:ILE:HG12	1.84	0.58
1:B:209:ARG:NH1	1:C:322:ILE:HG23	2.18	0.57
1:A:339:THR:HG23	1:A:341:GLU:H	1.70	0.57
1:C:301:ILE:HG12	1:C:337:LEU:HD21	1.87	0.57
1:B:209:ARG:HH12	1:C:322:ILE:HG23	1.69	0.57
1:C:91:LEU:HG	1:C:101:ILE:HG12	1.88	0.54
1:C:198:ARG:HD2	2:C:523:HOH:O	2.07	0.54
1:A:91:LEU:HG	1:A:101:ILE:HG12	1.90	0.54
1:A:129:TYR:CD1	1:A:149:ASN:HB3	2.43	0.54
1:C:71:PHE:C	1:C:113:GLU:HG3	2.33	0.52
1:B:321:ILE:HD13	1:B:337[A]:LEU:HD11	1.92	0.52
1:B:71:PHE:C	1:B:113:GLU:HG3	2.35	0.51
1:B:6:TRP:CE2	1:B:309:LYS:HG3	2.46	0.50
1:C:107:GLU:O	1:C:108:LYS:HD3	2.12	0.49
1:A:201:LEU:HD23	1:A:214:LEU:HD12	1.94	0.49
1:B:319:SER:OG	1:B:341:GLU:HG2	2.13	0.48
1:C:130:PRO:HG2	1:C:148:ILE:HG13	1.96	0.48
1:C:50:ASN:HB2	1:C:53:ILE:HD12	1.96	0.48
1:B:207:ARG:HB2	1:C:76:GLN:HG2	1.94	0.48
1:B:201:LEU:HB3	1:B:214:LEU:HB2	1.95	0.47
1:A:55:LYS:HG2	1:A:67:GLU:HB2	1.96	0.47
1:B:42:PRO:HG2	1:B:329:GLN:CD	2.41	0.46
1:A:339:THR:HG22	1:A:343:VAL:H	1.82	0.45
1:B:25:ASP:OD1	1:B:25:ASP:N	2.50	0.45
1:B:213:SER:O	1:C:50:ASN:HA	2.18	0.44
1:B:178:PRO:HD2	1:B:196:THR:CG2	2.47	0.44
1:B:135:SER:HB3	1:B:144:VAL:HG23	1.99	0.44
1:C:201:LEU:HB3	1:C:214:LEU:HB2	2.00	0.44
1:A:161:ARG:HA	1:A:161:ARG:HD3	1.89	0.44
1:C:247:PHE:HE1	1:C:253:LYS:HD2	1.82	0.44
1:A:298:ILE:HD13	1:A:316:VAL:HB	1.99	0.44
1:A:105:LYS:HE2	1:A:117:HIS:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:264:LYS:HD2	1:C:264:LYS:HA	1.74	0.43
1:A:319:SER:OG	1:A:341:GLU:HG2	2.18	0.43
1:B:192:PHE:HB3	1:B:236:PHE:CD2	2.53	0.43
1:B:246:PHE:O	1:B:253:LYS:HA	2.18	0.43
1:A:58:LYS:HD3	1:A:65:ILE:HD13	1.99	0.42
1:A:201:LEU:HB3	1:A:214:LEU:HB2	2.02	0.42
1:B:144:VAL:HG21	1:B:191[B]:CYS:SG	2.60	0.42
1:B:207:ARG:NE	1:C:130:PRO:HB3	2.33	0.42
1:A:280:GLU:CD	1:A:300:ARG:HE	2.27	0.42
1:B:42:PRO:HG2	1:B:329:GLN:NE2	2.35	0.42
1:C:258:PHE:HD1	1:C:260:LEU:HG	1.84	0.42
1:C:192:PHE:HB3	1:C:236:PHE:CD2	2.54	0.42
1:B:281:THR:HG22	1:B:297:ILE:HG22	2.02	0.42
1:C:34:LEU:C	1:C:34:LEU:HD23	2.44	0.42
1:B:205:THR:HG21	1:C:94:SER:HA	2.00	0.42
1:C:247:PHE:CE1	1:C:253:LYS:HD2	2.55	0.42
1:C:58:LYS:HG2	1:C:61:GLN:OE1	2.20	0.41
1:C:334:ILE:HG23	1:C:348:THR:HG22	2.01	0.41
1:A:213:SER:O	1:B:50:ASN:HA	2.19	0.41
1:B:129:TYR:CD1	1:B:149:ASN:HB3	2.55	0.41
1:C:246:PHE:O	1:C:253:LYS:HA	2.20	0.41
1:A:54:ILE:O	1:A:67:GLU:HA	2.21	0.41
1:B:51:SER:HA	1:B:76:GLN:HG3	2.02	0.41
1:A:16:PRO:HB3	1:A:345:HIS:CE1	2.56	0.41
1:A:101:ILE:HB	1:A:120:VAL:HB	2.03	0.41
1:C:16:PRO:HB3	1:C:345:HIS:CE1	2.56	0.41
1:C:260:LEU:HD21	1:C:276:ILE:HD13	2.01	0.41
1:A:209:ARG:NH1	2:A:404:HOH:O	2.43	0.40
1:B:280:GLU:HG2	1:B:298:ILE:HD11	2.04	0.40
1:C:61:GLN:O	1:C:63:GLN:HG3	2.21	0.40
1:C:13:GLU:O	1:C:347:ILE:HA	2.22	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	330/379 (87%)	319 (97%)	11 (3%)	0	100	100
1	B	335/379 (88%)	324 (97%)	11 (3%)	0	100	100
1	C	328/379 (86%)	311 (95%)	17 (5%)	0	100	100
All	All	993/1137 (87%)	954 (96%)	39 (4%)	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	303/341 (89%)	296 (98%)	7 (2%)	44	58
1	B	308/341 (90%)	301 (98%)	7 (2%)	44	58
1	C	300/341 (88%)	292 (97%)	8 (3%)	39	52
All	All	911/1023 (89%)	889 (98%)	22 (2%)	43	56

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	196	THR
1	A	224	LEU
1	A	261	SER
1	A	264	LYS
1	A	316	VAL
1	A	339	THR
1	A	350	LYS
1	B	39	ILE
1	B	95	ILE
1	B	144	VAL
1	B	161	ARG
1	B	196	THR
1	B	265	ARG

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Mol	Chain	Res	Type
1	B	309	LYS
1	C	8	GLN
1	C	13	GLU
1	C	39	ILE
1	C	112	ARG
1	C	242	ASN
1	C	255	GLN
1	C	322	ILE
1	C	329	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	73	HIS
1	A	76	GLN
1	B	84	ASN
1	B	138	ASN
1	B	308	ASN
1	C	14	ASN
1	C	50	ASN
1	C	76	GLN
1	C	254	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	330/379 (87%)	-0.26	5 (1%) 72 70	19, 40, 69, 100	4 (1%)
1	B	334/379 (88%)	-0.10	9 (2%) 56 53	21, 44, 75, 122	5 (1%)
1	C	330/379 (87%)	-0.27	9 (2%) 56 53	18, 38, 70, 109	2 (0%)
All	All	994/1137 (87%)	-0.21	23 (2%) 61 59	18, 41, 71, 122	11 (1%)

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	297	ILE	4.7
1	C	297	ILE	3.9
1	C	281	THR	3.7
1	B	307	LYS	3.1
1	C	329	GLN	3.1
1	B	295	PRO	3.0
1	C	251	GLY	2.7
1	B	332	LYS	2.6
1	C	209	ARG	2.5
1	B	297	ILE	2.4
1	C	330	SER	2.4
1	A	164	GLY	2.3
1	A	161	ARG	2.3
1	B	306	ALA	2.3
1	C	332	LYS	2.3
1	C	331	GLY	2.2
1	B	283	VAL	2.2
1	B	330	SER	2.2
1	B	129	TYR	2.1
1	A	129	TYR	2.1
1	C	6	TRP	2.1
1	A	206	GLY	2.1
1	B	329	GLN	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.