



Full wwPDB X-ray Structure Validation Report ⓘ

May 27, 2026 – 12:15 PM EDT

PDB ID : 9ZCT / pdb_00009zct
Title : Crystal structure of HOPS subunits Vps33 and Vps16 in complex with the Nyv1 SNARE motif
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Deposited on : 2025-11-24
Resolution : 2.90 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

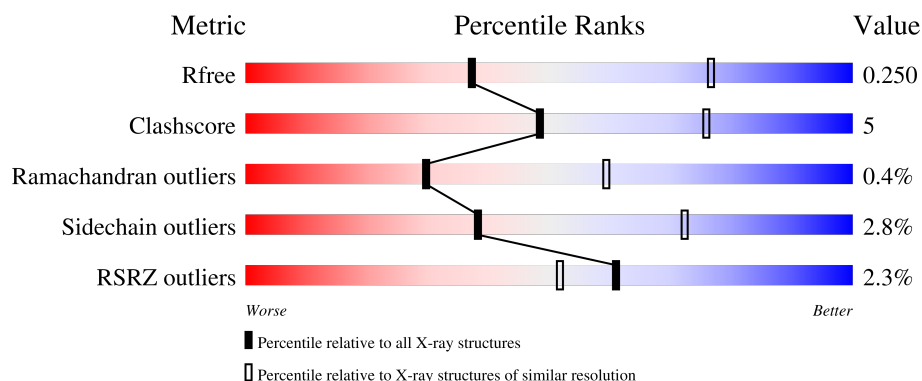
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION




The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	696	
2	B	274	
3	C	67	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7287 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 Small conjugating protein ligase-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	611	Total	C	N	O	S	0	0	0
			4825	3051	851	912	11			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-28	MET	-	initiating methionine	UNP G0SCM5
A	-27	LYS	-	expression tag	UNP G0SCM5
A	-26	HIS	-	expression tag	UNP G0SCM5
A	-25	HIS	-	expression tag	UNP G0SCM5
A	-24	HIS	-	expression tag	UNP G0SCM5
A	-23	HIS	-	expression tag	UNP G0SCM5
A	-22	HIS	-	expression tag	UNP G0SCM5
A	-21	HIS	-	expression tag	UNP G0SCM5
A	-20	HIS	-	expression tag	UNP G0SCM5
A	-19	GLY	-	expression tag	UNP G0SCM5
A	-18	ALA	-	expression tag	UNP G0SCM5
A	-17	ALA	-	expression tag	UNP G0SCM5
A	-16	GLY	-	expression tag	UNP G0SCM5
A	-15	THR	-	expression tag	UNP G0SCM5
A	-14	SER	-	expression tag	UNP G0SCM5
A	-13	LEU	-	expression tag	UNP G0SCM5
A	-12	TYR	-	expression tag	UNP G0SCM5
A	-11	LYS	-	expression tag	UNP G0SCM5
A	-10	LYS	-	expression tag	UNP G0SCM5
A	-9	ALA	-	expression tag	UNP G0SCM5
A	-8	GLY	-	expression tag	UNP G0SCM5
A	-7	GLU	-	expression tag	UNP G0SCM5
A	-6	ASN	-	expression tag	UNP G0SCM5
A	-5	LEU	-	expression tag	UNP G0SCM5
A	-4	TYR	-	expression tag	UNP G0SCM5
A	-3	PHE	-	expression tag	UNP G0SCM5
A	-2	GLN	-	expression tag	UNP G0SCM5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP G0SCM5

- Molecule 2 is a protein called Vacuolar protein sorting-associated protein 16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	267	Total	C	N	O	S	0	0	0
			2147	1356	383	399	9			

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	518	MET	-	initiating methionine	UNP G0S6M7
B	519	GLY	-	expression tag	UNP G0S6M7
B	520	SER	-	expression tag	UNP G0S6M7
B	672	ARG	-	insertion	UNP G0S6M7
B	673	MET	-	insertion	UNP G0S6M7
B	674	GLN	-	insertion	UNP G0S6M7
B	675	GLU	-	insertion	UNP G0S6M7
B	676	THR	-	insertion	UNP G0S6M7
B	677	PHE	-	insertion	UNP G0S6M7
B	678	GLU	-	insertion	UNP G0S6M7
B	679	ARG	-	insertion	UNP G0S6M7
B	680	ASP	-	insertion	UNP G0S6M7
B	681	LEU	-	insertion	UNP G0S6M7
B	682	THR	-	insertion	UNP G0S6M7
B	683	ASP	-	insertion	UNP G0S6M7
B	684	SER	-	insertion	UNP G0S6M7
B	685	PHE	-	insertion	UNP G0S6M7
B	686	VAL	-	insertion	UNP G0S6M7
B	687	GLY	-	insertion	UNP G0S6M7
B	689	SER	-	insertion	UNP G0S6M7
B	690	VAL	-	insertion	UNP G0S6M7

- Molecule 3 is a protein called Nyv1 SNARE motif.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	37	Total	C	N	O	S	0	0	0
			285	173	57	54	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	146	GLY	-	expression tag	UNP G0S5G3
C	147	SER	-	expression tag	UNP G0S5G3

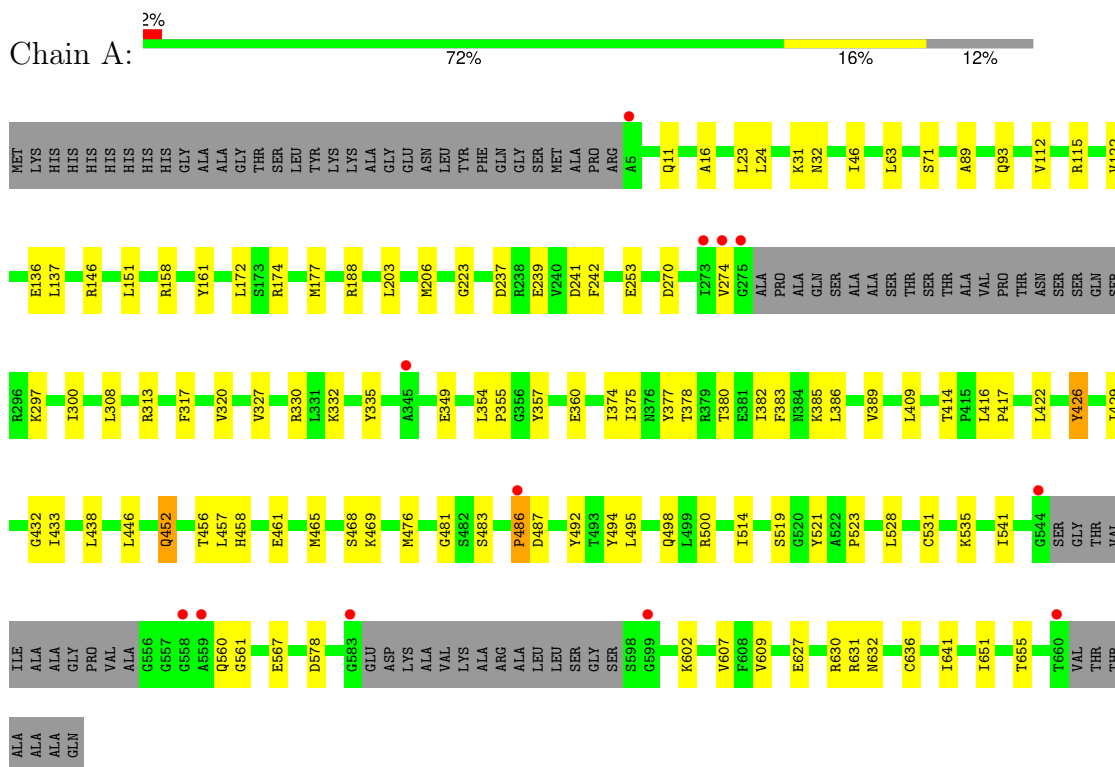
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	21	Total O 21 21	0	0
4	B	9	Total O 9 9	0	0

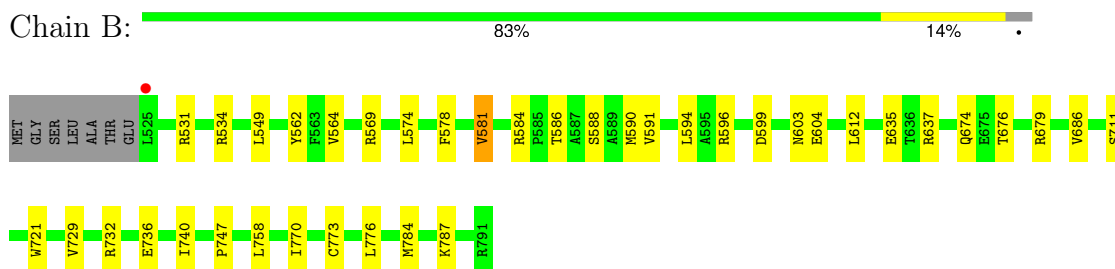
3 Residue-property plots [i](#)

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: Small conjugating protein ligase-like protein



- Molecule 2: Vacuolar protein sorting-associated protein 16



- Molecule 3: Nyv1 SNARE motif



GLY	SER	VAL	GLU	ASN	ASN	GLY	GLY	ASP	SER	ILE	ASN	SER	VAL	GLN	ARG	GLU	ILE	GLU	ASP	VAL	ARG	GLY	I169	M170	S171	L177	R180	G181	E182	S197	A198	R199	E200	F201	S205	ARG	GLY	LEU	LYS	ARG	LYS	MET
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4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	99.49Å 99.49Å 308.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.50 – 2.90 29.50 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.50-2.90) 99.7 (29.50-2.90)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 2.90Å)	Xtriage
Refinement program	PHENIX 1.17_3644	Depositor
R, R_{free}	0.189 , 0.250 0.192 , 0.250	Depositor DCC
R_{free} test set	1834 reflections (5.18%)	wwPDB-VP
Wilson B-factor (Å ²)	70.2	Xtriage
Anisotropy	0.486	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 68.0	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	0.96	EDS
Total number of atoms	7287	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.31% 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	0.35	0/4900	0.55	0/6607
2	B	0.33	0/2186	0.52	0/2948
3	C	0.30	0/285	0.49	0/378
All	All	0.34	0/7371	0.54	0/9933

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 [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	4825	0	4890	57	0
2	B	2147	0	2161	22	0
3	C	285	0	286	1	0
4	A	21	0	0	0	0
4	B	9	0	0	0	0
All	All	7287	0	7337	80	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 (80) 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:581:VAL:HG21	2:B:591:VAL:HG21	1.76	0.68
2:B:676:THR:HG22	2:B:679:ARG:NH1	2.11	0.66
1:A:32:ASN:HD21	1:A:71:SER:HB3	1.64	0.62
2:B:578:PHE:CD1	2:B:612:LEU:HD13	2.35	0.62
1:A:177:MET:HE3	1:A:206:MET:HB2	1.83	0.61
1:A:188:ARG:NH2	1:A:578:ASP:OD2	2.35	0.60
1:A:24:LEU:HD22	1:A:31:LYS:HD2	1.83	0.59
2:B:599:ASP:OD2	2:B:603:ASN:ND2	2.26	0.59
2:B:586:THR:O	2:B:590:MET:HG2	2.02	0.59
1:A:270:ASP:OD1	1:A:297:LYS:HE2	2.04	0.57
1:A:607:VAL:HG22	1:A:636:CYS:HB2	1.86	0.57
1:A:174:ARG:HA	1:A:206:MET:HE1	1.85	0.57
2:B:676:THR:HG22	2:B:679:ARG:HH12	1.69	0.56
1:A:514:ILE:HD12	1:A:523:PRO:HD2	1.89	0.55
1:A:177:MET:HG2	1:A:206:MET:HE2	1.89	0.54
2:B:773:CYS:HB2	2:B:776:LEU:HD11	1.89	0.54
1:A:177:MET:HE2	1:A:203:LEU:HD22	1.89	0.54
1:A:16:ALA:HB1	1:A:46:ILE:HD12	1.89	0.54
2:B:635:GLU:HG3	2:B:637:ARG:H	1.72	0.53
2:B:770:ILE:HG12	2:B:784:MET:HE2	1.90	0.53
2:B:562:TYR:CZ	2:B:590:MET:HE3	2.45	0.53
1:A:385:LYS:HB3	1:A:409:LEU:HD21	1.91	0.52
1:A:426:TYR:CD1	1:A:433:ILE:HG12	2.45	0.51
2:B:596:ARG:HA	2:B:604:GLU:HG2	1.91	0.51
2:B:758:LEU:HD21	2:B:787:LYS:HB3	1.93	0.51
1:A:274:VAL:HG22	1:A:300:ILE:HD11	1.93	0.50
1:A:438:LEU:HD22	1:A:468:SER:HB2	1.92	0.50
1:A:330:ARG:HH12	1:A:360:GLU:CD	2.19	0.50
3:C:198:ALA:HB1	3:C:200:GLU:HG2	1.93	0.49
1:A:112:VAL:HG22	1:A:137:LEU:HB3	1.94	0.49
2:B:531:ARG:NE	2:B:534:ARG:HD3	2.28	0.48
2:B:729:VAL:O	2:B:732:ARG:NH2	2.44	0.48
1:A:115:ARG:H	1:A:136:GLU:HG2	1.79	0.48
2:B:721:TRP:CD2	2:B:747:PRO:HD2	2.49	0.48
1:A:429:ILE:O	1:A:476:MET:HE1	2.12	0.48
1:A:335:TYR:HE1	1:A:357:TYR:HB3	1.78	0.47
1:A:535:LYS:HE3	1:A:560:GLN:HB3	1.96	0.47
1:A:432:GLY:O	1:A:469:LYS:HE2	2.14	0.47
1:A:151:LEU:HD11	1:A:172:LEU:HA	1.96	0.47
2:B:531:ARG:HG3	2:B:534:ARG:HD3	1.97	0.46
1:A:24:LEU:HA	1:A:24:LEU:HD23	1.61	0.46
1:A:237:ASP:OD1	1:A:239:GLU:HG2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:452:GLN:HG2	1:A:655:THR:HA	1.97	0.45
2:B:736:GLU:O	2:B:740:ILE:HG13	2.17	0.45
1:A:177:MET:HE2	1:A:203:LEU:CD2	2.47	0.45
1:A:500:ARG:HG2	1:A:541:ILE:HD12	1.99	0.45
1:A:521:TYR:CE2	1:A:523:PRO:HA	2.52	0.45
1:A:63:LEU:HD21	1:A:89:ALA:HB3	1.98	0.45
1:A:389:VAL:HG11	1:A:422:LEU:HD13	1.98	0.44
1:A:242:PHE:CD2	1:A:465:MET:HG2	2.53	0.44
1:A:535:LYS:NZ	1:A:561:GLY:O	2.47	0.44
1:A:161:TYR:CE1	1:A:239:GLU:HB3	2.53	0.44
1:A:627:GLU:OE1	1:A:630:ARG:HD3	2.18	0.44
1:A:237:ASP:CG	1:A:239:GLU:HG2	2.43	0.43
1:A:641:ILE:HD12	1:A:641:ILE:HA	1.86	0.43
1:A:308:LEU:HD13	1:A:327:VAL:HG21	1.99	0.43
2:B:562:TYR:CE1	2:B:590:MET:HE3	2.54	0.43
1:A:23:LEU:HD12	1:A:137:LEU:HD13	2.01	0.42
1:A:416:LEU:HB3	1:A:417:PRO:HD3	2.02	0.42
1:A:317:PHE:HA	1:A:320:VAL:HG23	2.02	0.42
1:A:456:THR:HG23	1:A:651:ILE:HA	2.01	0.42
2:B:674:GLN:OE1	2:B:686:VAL:HA	2.20	0.42
1:A:528:LEU:O	1:A:531:CYS:HB2	2.19	0.42
2:B:549:LEU:HB2	2:B:564:VAL:HG11	2.02	0.42
1:A:374:ILE:O	1:A:378:THR:HG23	2.19	0.42
1:A:377:TYR:O	1:A:380:THR:HG23	2.20	0.42
1:A:382:ILE:HD13	1:A:414:THR:OG1	2.20	0.42
1:A:378:THR:HA	1:A:383:PHE:CD1	2.55	0.42
1:A:457:LEU:HD23	1:A:457:LEU:HA	1.81	0.41
1:A:253:GLU:HB2	1:A:313:ARG:HB2	2.02	0.41
2:B:574:LEU:HG	2:B:578:PHE:CE2	2.55	0.41
2:B:635:GLU:HG3	2:B:637:ARG:N	2.34	0.41
1:A:241:ASP:HA	1:A:492:TYR:OH	2.21	0.41
1:A:486:PRO:HB2	1:A:487:ASP:H	1.67	0.41
1:A:481:GLY:O	1:A:483:SER:N	2.54	0.41
1:A:494:TYR:CZ	1:A:498:GLN:HG3	2.56	0.41
1:A:354:LEU:N	1:A:355:PRO:HD2	2.36	0.41
1:A:386:LEU:HD23	1:A:409:LEU:HD13	2.03	0.41
1:A:458:HIS:O	1:A:461:GLU:HB3	2.21	0.41
1:A:495:LEU:HA	1:A:495:LEU:HD23	1.82	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	603/696 (87%)	579 (96%)	21 (4%)	3 (0%)	24	54
2	B	265/274 (97%)	262 (99%)	3 (1%)	0	100	100
3	C	35/67 (52%)	30 (86%)	4 (11%)	1 (3%)	3	15
All	All	903/1037 (87%)	871 (96%)	28 (3%)	4 (0%)	30	59

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	223	GLY
1	A	486	PRO
1	A	146	ARG
3	C	180	ARG

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	525/585 (90%)	509 (97%)	16 (3%)	36	70
2	B	230/235 (98%)	224 (97%)	6 (3%)	40	73
3	C	29/57 (51%)	29 (100%)	0	100	100
All	All	784/877 (89%)	762 (97%)	22 (3%)	38	72

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

Mol	Chain	Res	Type
1	A	11	GLN
1	A	93	GLN
1	A	122	VAL
1	A	158	ARG
1	A	332	LYS
1	A	349	GLU
1	A	375	ILE
1	A	426	TYR
1	A	446	LEU
1	A	452	GLN
1	A	519	SER
1	A	567	GLU
1	A	602	LYS
1	A	609	VAL
1	A	631	ARG
1	A	632	ASN
2	B	569	ARG
2	B	581	VAL
2	B	584	ARG
2	B	588	SER
2	B	594	LEU
2	B	711	SER

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	32	ASN
1	A	325	ASN
1	A	361	GLN
2	B	566	HIS

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 [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	611/696 (87%)	-0.48	12 (1%) 65 56	40, 67, 144, 221	0
2	B	267/274 (97%)	-0.51	1 (0%) 88 85	47, 72, 120, 164	0
3	C	37/67 (55%)	1.14	8 (21%) 2 2	97, 144, 194, 203	0
All	All	915/1037 (88%)	-0.42	21 (2%) 61 52	40, 70, 150, 221	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	525	LEU	4.2
3	C	198	ALA	3.8
1	A	544	GLY	3.5
1	A	275	GLY	3.4
3	C	201	PHE	3.2
3	C	177	LEU	2.9
1	A	660	THR	2.8
3	C	182	GLU	2.7
1	A	599	GLY	2.7
1	A	559	ALA	2.6
1	A	345	ALA	2.6
3	C	171	SER	2.5
3	C	197	SER	2.5
1	A	583	GLY	2.4
1	A	274	VAL	2.2
3	C	205	SER	2.2
1	A	486	PRO	2.2
1	A	5	ALA	2.1
1	A	273	ILE	2.1
1	A	558	GLY	2.0
3	C	170	MET	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.