



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 4, 2026 – 11:58 PM UTC

PDB ID : 2CAZ / pdb_00002caz
Title : ESCRT-I core
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Deposited on : 2005-12-23
Resolution : 3.60 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
Xtrriage (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

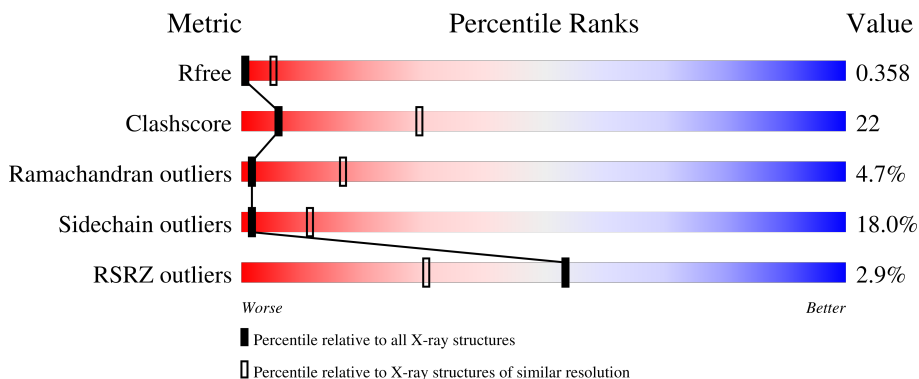
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 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.



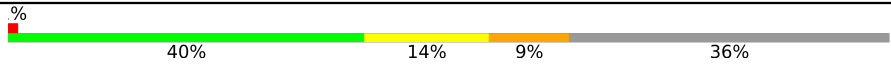
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1747 (3.70-3.50)
Clashscore	190562	1827 (3.70-3.50)
Ramachandran outliers	187476	1773 (3.70-3.50)
Sidechain outliers	187428	1772 (3.70-3.50)
RSRZ outliers	180081	1745 (3.70-3.50)

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	82	 4% 44% 23% 28%
1	D	82	 2% 46% 23% 26%
2	B	155	 25% 32% 7% 35%
2	E	155	 3% 23% 31% 10% 34%
3	C	85	 4% 45% 21% 8% 24%

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Mol	Chain	Length	Quality of chain
3	F	85	 <p>%</p> <p>40% 14% 9% 36%</p>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3602 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 SUPPRESSOR PROTEIN STP22 OF TEMPERATURE-SENSITIVE ALPHA-FACTOR RECEPTOR AND ARGININE PERMEASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	59	Total 484	C 306	N 91	O 85	S 2	0	0	1
1	D	61	Total 499	C 317	N 93	O 87	S 2	0	0	1

- Molecule 2 is a protein called VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS28.

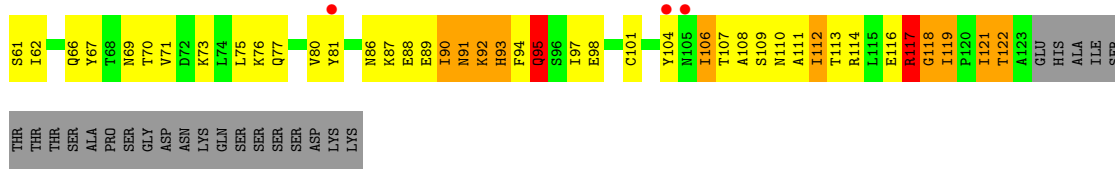
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	101	Total 813	C 515	N 131	O 166	S 1	0	0	1
2	E	102	Total 820	C 520	N 132	O 167	S 1	0	0	1

- Molecule 3 is a protein called PROTEIN SRN2.

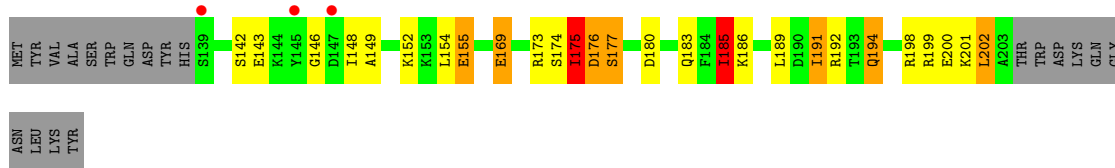
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	65	Total 536	C 331	N 93	O 112	0	0	1
3	F	54	Total 450	C 277	N 81	O 92	0	0	1

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	140	ASP	GLU	conflict	UNP Q99176
C	143	GLU	LYS	conflict	UNP Q99176



• Molecule 3: PROTEIN SRN2



• Molecule 3: PROTEIN SRN2



4 Data and refinement statistics i

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	167.91Å 167.91Å 50.24Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	145.86 – 3.60 145.42 – 3.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (145.86-3.60) 99.9 (145.42-3.60)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.45 (at 3.57Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.328 , 0.357 0.328 , 0.358	Depositor DCC
R_{free} test set	465 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	134.8	Xtrriage
Anisotropy	0.420	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 30.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.049 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	3602	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.57% 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	1.41	5/492 (1.0%)	1.31	2/666 (0.3%)
1	D	0.95	4/508 (0.8%)	0.94	1/689 (0.1%)
2	B	0.68	1/825 (0.1%)	0.91	1/1117 (0.1%)
2	E	0.70	1/832 (0.1%)	0.94	0/1128
3	C	0.74	2/541 (0.4%)	0.88	1/723 (0.1%)
3	F	0.62	1/453 (0.2%)	0.90	0/605
All	All	0.86	14/3651 (0.4%)	0.98	5/4928 (0.1%)

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
2	E	0	1

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	368	ARG	CZ-NH2	20.31	1.59	1.33
1	A	326	ASN	CG-ND2	13.90	1.62	1.33
1	D	368	ARG	CZ-NH2	12.47	1.49	1.33
3	C	142	SER	CB-OG	10.52	1.63	1.42
1	A	368	ARG	NE-CZ	8.61	1.42	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	326	ASN	OD1-CG-ND2	23.50	146.10	122.60
1	A	326	ASN	CB-CG-ND2	-9.81	101.68	116.40
2	B	97	ILE	N-CA-C	7.87	117.82	110.42
3	C	176	ASP	N-CA-C	-5.87	106.28	113.50
1	D	368	ARG	NE-CZ-NH2	-5.63	114.13	119.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	E	24	LEU	Peptide

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	484	0	491	30	0
1	D	499	0	509	28	0
2	B	813	0	809	49	0
2	E	820	0	817	60	0
3	C	536	0	529	14	0
3	F	450	0	455	10	0
All	All	3602	0	3610	162	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 22.

The worst 5 of 162 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:40:LEU:HA	2:B:43:ILE:HD12	1.42	1.02
2:E:40:LEU:HA	2:E:43:ILE:HD12	1.49	0.95
1:D:368:ARG:HG3	1:D:368:ARG:HH11	1.32	0.92
2:B:54:GLU:OE1	2:B:114:ARG:HD2	1.75	0.85
2:E:42:GLU:HG2	2:E:81:TYR:CZ	2.12	0.84

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	57/82 (70%)	50 (88%)	7 (12%)	0	100	100
1	D	59/82 (72%)	50 (85%)	9 (15%)	0	100	100
2	B	99/155 (64%)	69 (70%)	23 (23%)	7 (7%)	1	10
2	E	100/155 (64%)	65 (65%)	28 (28%)	7 (7%)	1	10
3	C	63/85 (74%)	44 (70%)	15 (24%)	4 (6%)	1	12
3	F	52/85 (61%)	37 (71%)	13 (25%)	2 (4%)	2	21
All	All	430/644 (67%)	315 (73%)	95 (22%)	20 (5%)	2	17

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	90	ILE
2	B	92	LYS
3	C	175	ILE
2	E	92	LYS
2	E	95	GLN

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	53/74 (72%)	47 (89%)	6 (11%)	5	26
1	D	55/74 (74%)	49 (89%)	6 (11%)	6	27
2	B	95/145 (66%)	77 (81%)	18 (19%)	1	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	96/145 (66%)	73 (76%)	23 (24%)	1	5
3	C	61/79 (77%)	51 (84%)	10 (16%)	2	14
3	F	52/79 (66%)	41 (79%)	11 (21%)	1	7
All	All	412/596 (69%)	338 (82%)	74 (18%)	2	11

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	112	ILE
3	F	191	ILE
2	E	117	ARG
3	F	169	GLU
3	C	148	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	27	ASN
2	E	77	GLN
2	E	95	GLN
2	E	91	ASN
2	E	93	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	59/82 (71%)	0.51	3 (5%) 33 19	72, 72, 72, 72	0
1	D	61/82 (74%)	0.48	2 (3%) 49 28	72, 72, 72, 72	0
2	B	101/155 (65%)	0.39	0 100 100	72, 72, 72, 72	0
2	E	102/155 (65%)	0.51	4 (3%) 43 24	72, 72, 72, 72	0
3	C	65/85 (76%)	0.17	3 (4%) 37 21	72, 72, 72, 72	0
3	F	54/85 (63%)	0.15	1 (1%) 66 39	72, 72, 72, 72	0
All	All	442/644 (68%)	0.38	13 (2%) 53 30	72, 72, 72, 72	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	145	TYR	4.0
1	D	325	LEU	3.2
2	E	22	VAL	3.0
3	C	139	SER	2.9
1	A	374	ARG	2.6

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.