



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 07:07 AM GMT

PDB ID : 2ZME
Title : Integrated structural and functional model of the human ESCRT-II complex
Authors : Im, Y.J.; Hurley, J.H.
Deposited on : 2008-04-17
Resolution : 2.90 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

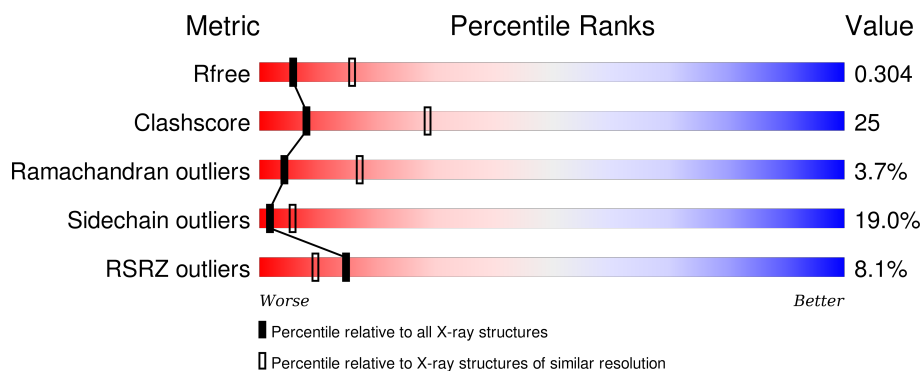
1 Overall quality at a glance ⓘ

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}	91344	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	258	<div> <div>8%</div> <div>47% 31% 6% 16%</div> </div>
2	B	238	<div> <div>8%</div> <div>45% 32% 12% 10%</div> </div>
3	C	102	<div> <div>45% 37% 15%</div> </div>
3	D	102	<div> <div>28%</div> <div>40% 41% 12% 5%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5127 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 Vacuolar-sorting protein SNF8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	217	Total	C	N	O	S	0	0	0
			1718	1103	290	318	7			

- Molecule 2 is a protein called Vacuolar protein-sorting-associated protein 36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	215	Total	C	N	O	S	0	0	0
			1678	1058	281	324	15			

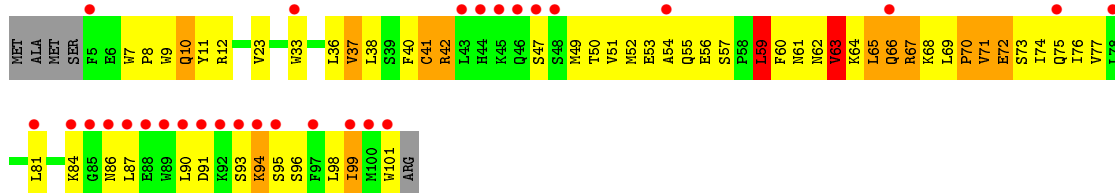
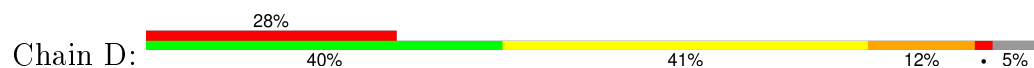
- Molecule 3 is a protein called Vacuolar protein-sorting-associated protein 25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	99	Total	C	N	O	S	0	0	0
			838	546	144	143	5			
3	D	97	Total	C	N	O	S	0	0	0
			821	537	139	140	5			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	31	Total	O	0	0
			31	31		
4	B	21	Total	O	0	0
			21	21		
4	C	12	Total	O	0	0
			12	12		
4	D	8	Total	O	0	0
			8	8		

- Molecule 3: Vacuolar protein-sorting-associated protein 25



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 1 2	Depositor
Cell constants a, b, c, α , β , γ	81.48Å 81.48Å 226.24Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.74 – 2.90 40.74 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.5 (40.74-2.90) 99.6 (40.74-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.93 (at 2.90Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.214 , 0.313 0.212 , 0.304	Depositor DCC
R_{free} test set	990 reflections (5.39%)	DCC
Wilson B-factor (Å ²)	94.6	Xtriage
Anisotropy	0.003	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 90.7	EDS
Estimated twinning fraction	0.052 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 19358 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5127	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.03% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.88	1/1752 (0.1%)	0.90	1/2365 (0.0%)
2	B	0.73	2/1696 (0.1%)	0.82	2/2273 (0.1%)
3	C	0.85	0/862	0.82	1/1165 (0.1%)
3	D	0.60	0/845	0.72	1/1143 (0.1%)
All	All	0.78	3/5155 (0.1%)	0.83	5/6946 (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
1	A	0	1
3	C	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	271	CYS	CB-SG	-9.30	1.66	1.82
1	A	123	GLU	CG-CD	8.32	1.64	1.51
2	B	268	GLU	CG-CD	5.09	1.59	1.51

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	59	LEU	CA-CB-CG	6.30	129.80	115.30
1	A	118	LEU	CA-CB-CG	5.75	128.52	115.30
3	C	98	LEU	CA-CB-CG	5.37	127.64	115.30
2	B	271	CYS	CA-CB-SG	-5.26	104.54	114.00
2	B	372	VAL	CB-CA-C	-5.22	101.48	111.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	241	THR	Peptide
3	C	90	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	1718	0	1730	63	0
2	B	1678	0	1735	118	0
3	C	838	0	846	48	0
3	D	821	0	828	47	0
4	A	31	0	0	1	0
4	B	21	0	0	5	0
4	C	12	0	0	4	0
4	D	8	0	0	2	0
All	All	5127	0	5139	252	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 25.

The worst 5 of 252 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:265:SER:HB3	2:B:268:GLU:HG3	1.23	1.12
3:D:71:VAL:HA	4:D:103:HOH:O	1.49	1.09
4:A:261:HOH:O	3:C:67:ARG:HD2	1.52	1.08
1:A:194:THR:HG22	1:A:197:GLU:H	1.26	1.00
2:B:274:ASN:HD21	2:B:282:LEU:H	1.11	0.96

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	215/258 (83%)	184 (86%)	22 (10%)	9 (4%)	3	13
2	B	213/238 (90%)	175 (82%)	32 (15%)	6 (3%)	6	24
3	C	97/102 (95%)	90 (93%)	6 (6%)	1 (1%)	19	54
3	D	95/102 (93%)	77 (81%)	11 (12%)	7 (7%)	1	3
All	All	620/700 (89%)	526 (85%)	71 (12%)	23 (4%)	4	17

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	177	ASN
1	A	243	LEU
1	A	245	SER
2	B	227	ALA
2	B	385	GLN

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	182/211 (86%)	151 (83%)	31 (17%)	2	7
2	B	188/207 (91%)	153 (81%)	35 (19%)	2	6
3	C	95/97 (98%)	72 (76%)	23 (24%)	1	2
3	D	93/97 (96%)	76 (82%)	17 (18%)	2	6
All	All	558/612 (91%)	452 (81%)	106 (19%)	2	6

5 of 106 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	255	VAL
2	B	316	GLN
3	D	56	GLU
2	B	266	LEU
2	B	275	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	318	HIS
3	C	22	ASN
3	D	66	GLN
3	C	10	GLN
3	C	27	GLN

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 carbohydrates 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 ⓘ

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	217/258 (84%)	0.03	2 (0%) 85 84	57, 71, 107, 116	0
2	B	215/238 (90%)	0.49	19 (8%) 12 8	69, 94, 116, 120	0
3	C	99/102 (97%)	0.02	1 (1%) 84 82	57, 80, 103, 118	0
3	D	97/102 (95%)	1.33	29 (29%) 1 0	87, 114, 143, 146	0
All	All	628/700 (89%)	0.39	51 (8%) 15 9	57, 90, 124, 146	0

The worst 5 of 51 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	207	GLY	8.5
3	D	99	ILE	6.7
3	D	89	TRP	6.5
2	B	208	ASP	6.2
3	D	93	SER	5.4

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 carbohydrates 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.