



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 04:05 AM UTC

PDB ID : 8EAZ / pdb_00008eaz
Title : HOIL-1/E2-Ub/Ub transthiolation complex
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Deposited on : 2022-08-30
Resolution : 3.08 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
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

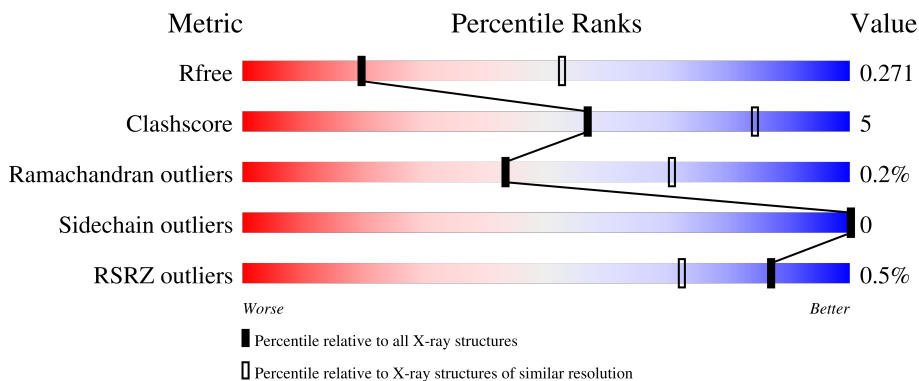
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.08 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	2010 (3.10-3.06)
Clashscore	190562	2102 (3.10-3.06)
Ramachandran outliers	187476	1982 (3.10-3.06)
Sidechain outliers	187428	1981 (3.10-3.06)
RSRZ outliers	180081	2010 (3.10-3.06)

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	280	
1	B	280	
2	C	157	
2	D	157	
3	E	76	

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Mol	Chain	Length	Quality of chain
3	F	76	 91% 9%
3	G	76	 86% 13%
3	H	76	 91% 9%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8813 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 RanBP-type and C3HC4-type zinc finger-containing protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	254	1990	1228	355	378	29	0	0	0
1	B	245	1912	1181	340	362	29	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	231	GLY	-	expression tag	UNP Q9BYM8
A	460	ALA	CYS	engineered mutation	UNP Q9BYM8
B	231	GLY	-	expression tag	UNP Q9BYM8
B	460	ALA	CYS	engineered mutation	UNP Q9BYM8

- Molecule 2 is a protein called Ubiquitin-conjugating enzyme E2 L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	152	1244	798	216	226	4	0	0	0
2	D	152	1244	798	216	226	4	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	GLY	-	expression tag	UNP P68036
C	-1	PRO	-	expression tag	UNP P68036
C	0	GLY	-	expression tag	UNP P68036
C	86	LYS	CYS	engineered mutation	UNP P68036
D	-2	GLY	-	expression tag	UNP P68036
D	-1	PRO	-	expression tag	UNP P68036
D	0	GLY	-	expression tag	UNP P68036
D	86	LYS	CYS	engineered mutation	UNP P68036

- Molecule 3 is a protein called Ubiquitin.


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	76	Total	C	N	O	S	0	0	0
			601	378	105	117	1			
3	F	76	Total	C	N	O	S	0	0	0
			601	378	105	117	1			
3	G	75	Total	C	N	O	S	0	0	0
			597	376	104	116	1			
3	H	76	Total	C	N	O	S	0	0	0
			602	378	105	118	1			

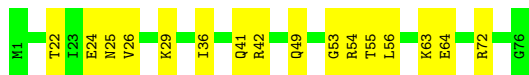
- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	7	Total	Zn	0	0
			7	7		
4	B	7	Total	Zn	0	0
			7	7		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	O	0	0
			2	2		
5	B	2	Total	O	0	0
			2	2		
5	E	1	Total	O	0	0
			1	1		
5	F	1	Total	O	0	0
			1	1		
5	G	1	Total	O	0	0
			1	1		
5	H	1	Total	O	0	0
			1	1		

Chain E:  79% 21%




• Molecule 3: Ubiquitin

Chain F:  91% 9%




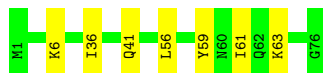
• Molecule 3: Ubiquitin

Chain G:  86% 13%



• Molecule 3: Ubiquitin

Chain H:  91% 9%



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	83.95Å 95.48Å 115.01Å 90.00° 110.58° 90.00°	Depositor
Resolution (Å)	47.74 – 3.08 47.74 – 3.08	Depositor EDS
% Data completeness (in resolution range)	99.1 (47.74-3.08) 99.6 (47.74-3.08)	Depositor EDS
R_{merge}	0.23	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.26 (at 3.07Å)	Xtrriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.232 , 0.266 (Not available) , 0.271	Depositor DCC
R_{free} test set	1493 reflections (4.72%)	wwPDB-VP
Wilson B-factor (Å ²)	81.0	Xtrriage
Anisotropy	0.548	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 79.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.037 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8813	wwPDB-VP
Average B, all atoms (Å ²)	110.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.71% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section:
ZN

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	0.08	0/2032	0.24	0/2752
1	B	0.08	0/1952	0.25	0/2644
2	C	0.09	0/1275	0.24	0/1722
2	D	0.09	0/1275	0.24	0/1722
3	E	0.09	0/607	0.27	0/816
3	F	0.09	0/607	0.28	0/816
3	G	0.07	0/603	0.27	0/811
3	H	0.07	0/608	0.24	0/816
All	All	0.08	0/8959	0.25	0/12099

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	1990	0	1886	18	0
1	B	1912	0	1820	17	0
2	C	1244	0	1260	16	0
2	D	1244	0	1260	15	0
3	E	601	0	629	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	601	0	629	5	0
3	G	597	0	626	7	0
3	H	602	0	629	6	0
4	A	7	0	0	0	0
4	B	7	0	0	0	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
5	G	1	0	0	0	0
5	H	1	0	0	0	0
All	All	8813	0	8739	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.

The worst 5 of 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)
1:A:271:ARG:O	1:A:298:ARG:NH2	2.25	0.69
1:B:271:ARG:O	1:B:298:ARG:NH2	2.28	0.66
1:A:462:TRP:HB3	1:A:509:CYS:HA	1.78	0.65
1:B:328:ASN:ND2	2:D:103:GLN:OE1	2.28	0.65
1:B:298:ARG:HD2	1:B:337:LEU:HD12	1.79	0.64

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	252/280 (90%)	237 (94%)	14 (6%)	1 (0%)	30 58

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	243/280 (87%)	227 (93%)	15 (6%)	1 (0%)	30	58
2	C	150/157 (96%)	143 (95%)	7 (5%)	0	100	100
2	D	150/157 (96%)	142 (95%)	8 (5%)	0	100	100
3	E	74/76 (97%)	68 (92%)	6 (8%)	0	100	100
3	F	74/76 (97%)	69 (93%)	5 (7%)	0	100	100
3	G	73/76 (96%)	70 (96%)	3 (4%)	0	100	100
3	H	74/76 (97%)	70 (95%)	4 (5%)	0	100	100
All	All	1090/1178 (92%)	1026 (94%)	62 (6%)	2 (0%)	43	71

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	458	ASP
1	B	458	ASP

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	224/245 (91%)	224 (100%)	0	100	100
1	B	216/245 (88%)	216 (100%)	0	100	100
2	C	136/139 (98%)	136 (100%)	0	100	100
2	D	136/139 (98%)	136 (100%)	0	100	100
3	E	68/68 (100%)	68 (100%)	0	100	100
3	F	68/68 (100%)	68 (100%)	0	100	100
3	G	68/68 (100%)	68 (100%)	0	100	100
3	H	68/68 (100%)	68 (100%)	0	100	100
All	All	984/1040 (95%)	984 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	B	455	GLN
2	C	26	GLN
3	F	41	GLN
2	D	119	HIS
3	E	41	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 14 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	254/280 (90%)	0.06	1 (0%) 88 75	62, 102, 166, 183	0
1	B	245/280 (87%)	0.13	4 (1%) 70 47	67, 101, 163, 194	0
2	C	152/157 (96%)	0.23	1 (0%) 84 66	78, 115, 167, 192	0
2	D	152/157 (96%)	0.22	0 100 100	89, 121, 161, 182	0
3	E	76/76 (100%)	-0.01	0 100 100	71, 96, 122, 132	0
3	F	76/76 (100%)	-0.01	0 100 100	69, 94, 117, 122	0
3	G	75/76 (98%)	0.15	0 100 100	76, 106, 136, 151	0
3	H	76/76 (100%)	0.18	0 100 100	85, 110, 141, 165	0
All	All	1106/1178 (93%)	0.13	6 (0%) 87 72	62, 107, 161, 194	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	273	LEU	3.1
1	A	458	ASP	2.7
1	B	268	LEU	2.6
1	B	280	ALA	2.2
1	B	383	GLU	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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	ZN	B	1004	1/1	0.97	0.05	111,111,111,111	0
4	ZN	B	1007	1/1	0.97	0.05	72,72,72,72	0
4	ZN	A	1003	1/1	0.99	0.04	93,93,93,93	0
4	ZN	A	1004	1/1	0.99	0.04	106,106,106,106	0
4	ZN	A	1005	1/1	0.99	0.04	71,71,71,71	0
4	ZN	A	1006	1/1	0.99	0.04	76,76,76,76	0
4	ZN	A	1007	1/1	0.99	0.04	64,64,64,64	0
4	ZN	B	1001	1/1	0.99	0.04	138,138,138,138	0
4	ZN	B	1002	1/1	0.99	0.03	113,113,113,113	0
4	ZN	B	1003	1/1	0.99	0.04	79,79,79,79	0
4	ZN	A	1001	1/1	0.99	0.02	125,125,125,125	0
4	ZN	B	1005	1/1	0.99	0.02	65,65,65,65	0
4	ZN	B	1006	1/1	0.99	0.03	62,62,62,62	0
4	ZN	A	1002	1/1	0.99	0.06	118,118,118,118	0

6.5 Other polymers [i](#)

There are no such residues in this entry.