wwPDB X-ray Structure Validation Summary Report (i)

Oct 24, 2023 – 07:39 PM EDT

PDB ID	:	3A8J
Title	:	Crystal Structure of ET-EHred complex
Authors	:	Okamura-Ikeda, K.; Hosaka, H.
Deposited on	:	2009-10-06
Resolution	:	1.98 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 (i) 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 (i)) were used in the production of this report:

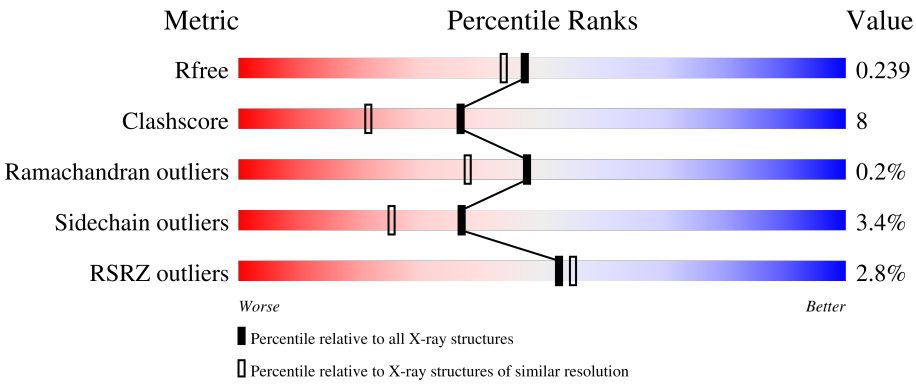
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.98 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}	130704	11647 (2.00-1.96)
Clashscore	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)
RSRZ outliers	127900	11410 (2.00-1.96)

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 <=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	364	%, 86%, 13%
1	B	364	84%, 15%
1	C	364	3%, 85%, 14%
1	D	364	5%, 82%, 16%
2	E	129	6%, 88%, 8%

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Mol	Chain	Length	Quality of chain
2	F	129	5% 75% 20%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 14613 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 Aminomethyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	363	2823	1782	492	534	15	0	2	0
1	B	363	2825	1784	492	533	16	0	2	0
1	C	363	2818	1779	492	532	15	0	1	0
1	D	363	2839	1794	497	533	15	0	2	0

- Molecule 2 is a protein called Glycine cleavage system H protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	E	127	964	606	146	208	4	0	0	0
2	F	128	982	616	148	213	5	0	1	0

- Molecule 3 is water.

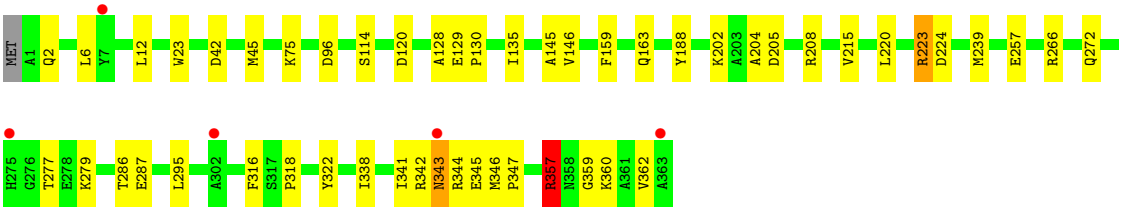
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	332	332	332	0	0
3	B	326	326	326	0	0
3	C	280	280	280	0	0
3	D	273	273	273	0	0
3	E	77	77	77	0	0
3	F	74	74	74	0	0

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.

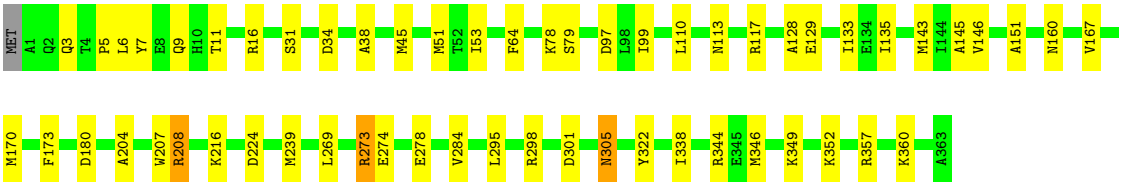
• Molecule 1: Aminomethyltransferase

Chain A:



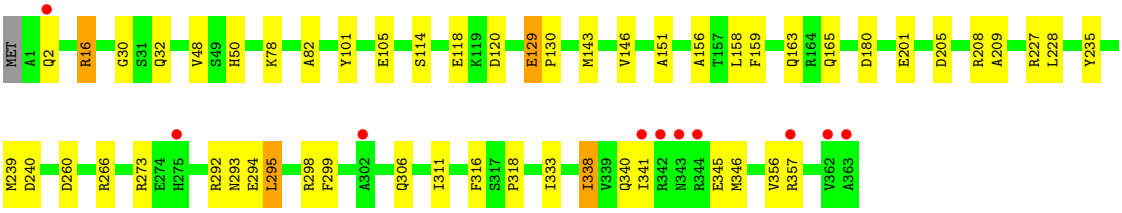
• Molecule 1: Aminomethyltransferase

Chain B:



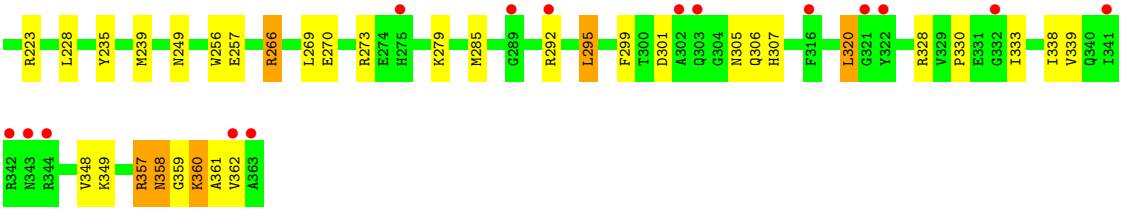
• Molecule 1: Aminomethyltransferase

Chain C:



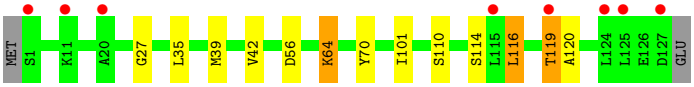
• Molecule 1: Aminomethyltransferase

Chain D:



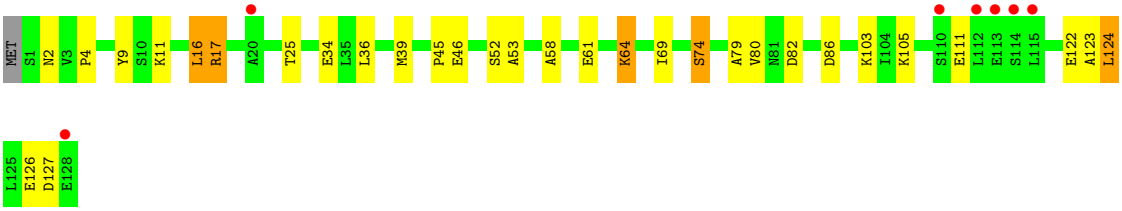
• Molecule 2: Glycine cleavage system H protein

Chain E:



• Molecule 2: Glycine cleavage system H protein

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	54.02Å 88.53Å 97.24Å 91.51° 102.16° 89.66°	Depositor
Resolution (Å)	44.42 – 1.98 44.42 – 1.98	Depositor EDS
% Data completeness (in resolution range)	97.2 (44.42-1.98) 97.1 (44.42-1.98)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.07 (at 1.98Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.172 , 0.238 0.172 , 0.239	Depositor DCC
R_{free} test set	5960 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	22.6	Xtriage
Anisotropy	0.158	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 54.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.066 for -h,k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	14613	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.46% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: LA2

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	1.11	1/2887 (0.0%)	0.95	5/3910 (0.1%)
1	B	1.04	1/2889 (0.0%)	0.95	6/3912 (0.2%)
1	C	1.02	4/2879 (0.1%)	0.92	5/3899 (0.1%)
1	D	0.99	3/2900 (0.1%)	0.92	8/3929 (0.2%)
2	E	0.89	0/960	0.81	1/1309 (0.1%)
2	F	0.84	0/978	0.85	3/1331 (0.2%)
All	All	1.02	9/13493 (0.1%)	0.92	28/18290 (0.2%)

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	180	ASP	CB-CG	6.79	1.66	1.51
1	D	235	TYR	CD2-CE2	6.19	1.48	1.39
1	D	180	ASP	CB-CG	5.83	1.64	1.51
1	C	129	GLU	CB-CG	5.74	1.63	1.52
1	B	31	SER	CB-OG	5.53	1.49	1.42

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	208	ARG	NE-CZ-NH1	9.50	125.05	120.30
1	C	180	ASP	CB-CG-OD1	8.63	126.07	118.30
1	B	208	ARG	NE-CZ-NH1	8.40	124.50	120.30
1	D	266	ARG	NE-CZ-NH2	-8.00	116.30	120.30
2	F	16	LEU	CA-CB-CG	7.84	133.33	115.30

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	2823	0	2780	43	0
1	B	2825	0	2784	37	0
1	C	2818	0	2776	38	0
1	D	2839	0	2786	56	0
2	E	964	0	917	14	0
2	F	982	0	931	28	0
3	A	332	0	0	9	0
3	B	326	0	0	7	0
3	C	280	0	0	5	1
3	D	273	0	0	6	1
3	E	77	0	0	2	0
3	F	74	0	0	3	0
All	All	14613	0	12974	207	1

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 8.

The worst 5 of 207 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:D:23[B]:TRP:CE3	1:D:50[B]:HIS:CD2	1.96	1.53
1:D:23[B]:TRP:CZ3	1:D:50[B]:HIS:NE2	1.80	1.46
1:D:23[B]:TRP:CD2	1:D:50[B]:HIS:CD2	2.17	1.30
2:F:36:LEU:HD21	2:F:39[B]:MET:SD	1.72	1.27
1:D:23[B]:TRP:CZ3	1:D:50[B]:HIS:CE1	2.28	1.20

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:678:HOH:O	3:D:674:HOH:O[1_656]	2.05	0.15

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	363/364 (100%)	353 (97%)	9 (2%)	1 (0%)	41	29
1	B	363/364 (100%)	354 (98%)	8 (2%)	1 (0%)	41	29
1	C	362/364 (100%)	348 (96%)	14 (4%)	0	100	100
1	D	363/364 (100%)	347 (96%)	14 (4%)	2 (1%)	25	14
2	E	124/129 (96%)	122 (98%)	2 (2%)	0	100	100
2	F	126/129 (98%)	121 (96%)	5 (4%)	0	100	100
All	All	1701/1714 (99%)	1645 (97%)	52 (3%)	4 (0%)	47	38

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	358	ASN
1	B	278	GLU
1	A	42	ASP
1	D	361	ALA

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	293/292 (100%)	287 (98%)	6 (2%)	55	48
1	B	293/292 (100%)	284 (97%)	9 (3%)	40	28
1	C	292/292 (100%)	284 (97%)	8 (3%)	44	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	D	293/292 (100%)	280 (96%)	13 (4%)	28 16
2	E	101/103 (98%)	98 (97%)	3 (3%)	41 29
2	F	103/103 (100%)	95 (92%)	8 (8%)	12 4
All	All	1375/1374 (100%)	1328 (97%)	47 (3%)	37 25

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	269	LEU
1	D	362	VAL
1	D	295	LEU
1	D	339	VAL
2	E	116	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	9	GLN
1	D	303	GLN
2	E	2	ASN
1	D	306	GLN
1	B	113	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	LA2	E	64	2	17,19,20	0.61	0	12,21,23	2.97	2 (16%)
2	LA2	F	64	2	17,19,20	0.63	0	12,21,23	2.69	4 (33%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	LA2	E	64	2	-	9/18/20/22	-
2	LA2	F	64	2	-	9/18/20/22	-

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	64	LA2	C7-C8-S8	-8.23	105.17	113.74
2	F	64	LA2	C7-C8-S8	-6.84	106.61	113.74
2	E	64	LA2	CE-NZ-C1	5.59	133.21	122.84
2	F	64	LA2	CE-NZ-C1	3.74	129.78	122.84
2	F	64	LA2	CD-CE-NZ	-3.49	102.23	112.21

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	64	LA2	C5-C6-C7-C8
2	E	64	LA2	C6-C7-C8-S8
2	F	64	LA2	C4-C5-C6-C7
2	F	64	LA2	C5-C6-C7-C8
2	F	64	LA2	C6-C7-C8-S8

There are no ring outliers.

2 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	64	LA2	6	0
2	F	64	LA2	4	0

5.5 Carbohydrates (i)

There are no monosaccharides 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	363/364 (99%)	-0.18	5 (1%) 75 77	13, 19, 41, 59	0
1	B	363/364 (99%)	-0.22	0 100 100	13, 20, 40, 56	0
1	C	363/364 (99%)	-0.11	10 (2%) 53 55	14, 23, 46, 66	0
1	D	363/364 (99%)	0.02	18 (4%) 28 31	15, 26, 46, 71	0
2	E	126/129 (97%)	0.19	8 (6%) 20 22	20, 33, 58, 69	0
2	F	127/129 (98%)	0.34	7 (5%) 25 27	23, 36, 51, 66	0
All	All	1705/1714 (99%)	-0.06	48 (2%) 53 55	13, 24, 48, 71	0

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	363	ALA	7.8
1	A	363	ALA	6.7
2	E	1	SER	5.7
1	C	363	ALA	5.2
1	D	316	PHE	4.3

6.2 Non-standard residues in protein, DNA, RNA chains (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(Å^2)	Q<0.9
2	LA2	F	64	20/21	0.93	0.12	23,47,55,61	0
2	LA2	E	64	20/21	0.96	0.10	24,30,45,51	0

6.3 Carbohydrates (i)

There are no monosaccharides 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.