Full wwPDB X-ray Structure Validation Report (i)

Oct 15, 2023 – 01:42 PM EDT

PDB ID	:	7S94
Title	:	Structure of the core postfusion porcine endogenous retrovirus fusion protein
Authors	:	Dean, T.T.; Lee, J.E.
Deposited on	:	2021-09-20
Resolution	:	2.00 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 (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 (1)) were used in the production of this report:

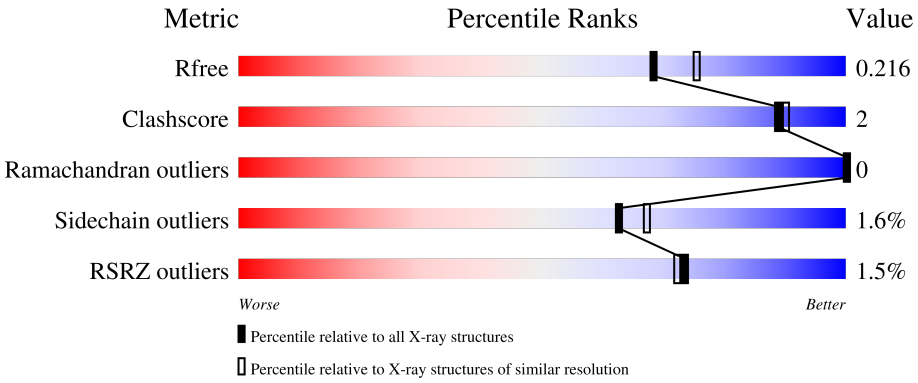
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 2.00 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.



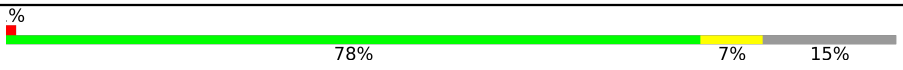
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	98	90% · 6%
1	B	98	84% 7% 9%
1	C	98	97%
1	D	98	3% 92% 8%
1	E	98	3% 74% · 22%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	98	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 8338 atoms, of which 3982 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 Endogenous retrovirus group S71 member 1 Env polyprotein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	92	Total	C	H	N	O	S	0	0	0
			1403	434	699	130	137	3			
1	B	89	Total	C	H	N	O	S	0	0	0
			1382	426	693	123	137	3			
1	C	97	Total	C	H	N	O	S	0	1	0
			1513	465	758	137	150	3			
1	D	90	Total	C	H	N	O	S	0	3	0
			1377	428	681	126	139	3			
1	E	76	Total	C	H	N	O	S	0	0	0
			1103	348	539	98	115	3			
1	F	83	Total	C	H	N	O	S	0	0	0
			1214	383	592	108	128	3			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	490	GLY	-	expression tag	UNP B3VQ66
A	491	SER	-	expression tag	UNP B3VQ66
A	492	GLY	-	expression tag	UNP B3VQ66
A	557	SER	CYS	engineered mutation	UNP B3VQ66
B	490	GLY	-	expression tag	UNP B3VQ66
B	491	SER	-	expression tag	UNP B3VQ66
B	492	GLY	-	expression tag	UNP B3VQ66
B	557	SER	CYS	engineered mutation	UNP B3VQ66
C	490	GLY	-	expression tag	UNP B3VQ66
C	491	SER	-	expression tag	UNP B3VQ66
C	492	GLY	-	expression tag	UNP B3VQ66
C	557	SER	CYS	engineered mutation	UNP B3VQ66
D	490	GLY	-	expression tag	UNP B3VQ66
D	491	SER	-	expression tag	UNP B3VQ66
D	492	GLY	-	expression tag	UNP B3VQ66
D	557	SER	CYS	engineered mutation	UNP B3VQ66
E	490	GLY	-	expression tag	UNP B3VQ66

Continued on next page...

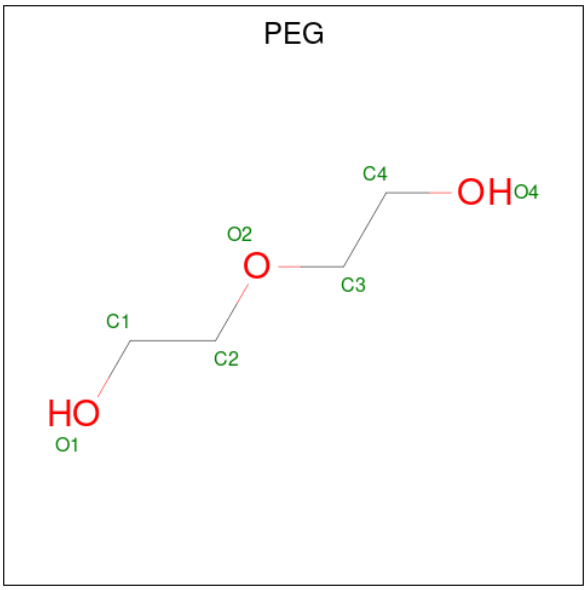
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	491	SER	-	expression tag	UNP B3VQ66
E	492	GLY	-	expression tag	UNP B3VQ66
E	557	SER	CYS	engineered mutation	UNP B3VQ66
F	490	GLY	-	expression tag	UNP B3VQ66
F	491	SER	-	expression tag	UNP B3VQ66
F	492	GLY	-	expression tag	UNP B3VQ66
F	557	SER	CYS	engineered mutation	UNP B3VQ66

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Cl 1 1	0	0
2	D	1	Total Cl 1 1	0	0

- Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C H O 17 4 10 3	0	0
3	E	1	Total C H O 17 4 10 3	0	0

- Molecule 4 is water.

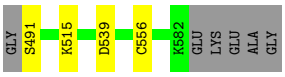
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	60	Total O 60 60	0	0
4	B	41	Total O 41 41	0	0
4	C	83	Total O 83 83	0	0
4	D	53	Total O 53 53	0	0
4	E	33	Total O 33 33	0	0
4	F	40	Total O 40 40	0	0

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.

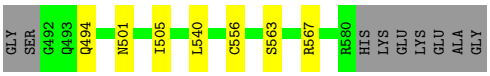
• Molecule 1: Endogenous retrovirus group S71 member 1 Env polyprotein

Chain A:



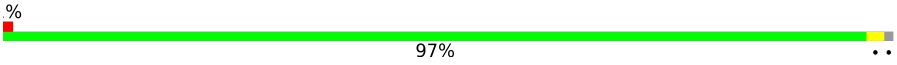
• Molecule 1: Endogenous retrovirus group S71 member 1 Env polyprotein

Chain B:



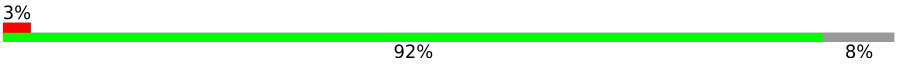
• Molecule 1: Endogenous retrovirus group S71 member 1 Env polyprotein

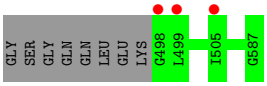
Chain C:



• Molecule 1: Endogenous retrovirus group S71 member 1 Env polyprotein

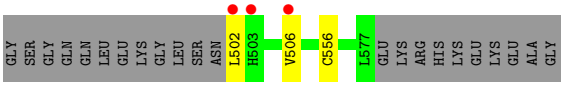
Chain D:





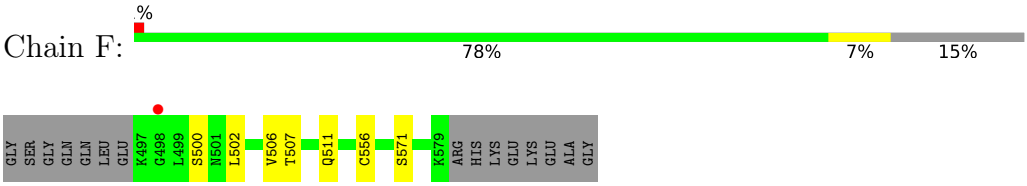
• Molecule 1: Endogenous retrovirus group S71 member 1 Env polyprotein

Chain E:



• Molecule 1: Endogenous retrovirus group S71 member 1 Env polyprotein

Chain F:


%
78%
7%
15%
GLY
SER
GLY
GLN
GLN
LEU
GLU
K497
G498
L499
S500
N501
L502
V506
T507
Q511
C556
S571
K579
ARG
HIS
LYS
GLU
LYS
GLU
ALA
GLY

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	96.86Å 34.22Å 100.44Å 90.00° 99.95° 90.00°	Depositor
Resolution (Å)	47.70 – 2.00 47.70 – 2.00	Depositor EDS
% Data completeness (in resolution range)	91.3 (47.70-2.00) 90.6 (47.70-2.00)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.06 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.174 , 0.217 0.174 , 0.216	Depositor DCC
R_{free} test set	2047 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	19.8	Xtriage
Anisotropy	0.051	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.43 , 57.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.027 for l,-k,h	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	8338	wwPDB-VP
Average B, all atoms (Å^2)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.10% 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

5.1 Standard geometry

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

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	0.58	0/709	0.71	0/951
1	B	0.61	0/693	0.71	0/928
1	C	0.55	0/763	0.71	0/1019
1	D	0.49	0/709	0.67	0/951
1	E	0.49	0/567	0.70	0/764
1	F	0.53	0/626	0.68	0/843
All	All	0.54	0/4067	0.70	0/5456

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

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	704	699	698	3	0
1	B	689	693	692	7	0
1	C	755	758	760	2	0
1	D	696	681	667	0	0
1	E	564	539	537	1	0
1	F	622	592	592	2	0
2	A	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1	0	0	0	0
3	A	7	10	10	0	0
3	E	7	10	10	0	0
4	A	60	0	0	3	0
4	B	41	0	0	2	0
4	C	83	0	0	2	0
4	D	53	0	0	0	0
4	E	33	0	0	0	0
4	F	40	0	0	0	0
All	All	4356	3982	3966	15	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 2.

All (15) 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:539:ASP:OD2	4:A:702:HOH:O	2.11	0.68
1:B:494:GLN:NE2	4:B:601:HOH:O	2.22	0.61
1:C:515:LYS:HE2	4:C:647:HOH:O	2.01	0.59
1:A:491:SER:OG	4:A:701:HOH:O	2.05	0.57
1:E:502:LEU:O	1:E:506:VAL:HG23	2.10	0.52
1:B:501:ASN:O	1:B:505:ILE:HD13	2.11	0.51
1:B:501:ASN:O	1:B:505:ILE:CD1	2.60	0.49
1:B:501:ASN:HB2	4:B:619:HOH:O	2.13	0.48
1:B:563:SER:OG	1:B:567:ARG:NH1	2.48	0.46
1:B:540:LEU:HD23	1:B:540:LEU:O	2.16	0.45
1:C:515:LYS:CE	4:C:647:HOH:O	2.60	0.45
1:A:515:LYS:HE2	4:A:757:HOH:O	2.17	0.44
1:F:502:LEU:O	1:F:506:VAL:HG13	2.19	0.43
1:F:507:THR:O	1:F:511:GLN:HG3	2.20	0.42
1:B:540:LEU:HD23	1:B:540:LEU:C	2.41	0.41

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	90/98 (92%)	90 (100%)	0	0	100	100
1	B	87/98 (89%)	87 (100%)	0	0	100	100
1	C	96/98 (98%)	96 (100%)	0	0	100	100
1	D	91/98 (93%)	91 (100%)	0	0	100	100
1	E	74/98 (76%)	74 (100%)	0	0	100	100
1	F	81/98 (83%)	81 (100%)	0	0	100	100
All	All	519/588 (88%)	519 (100%)	0	0	100	100

There are no Ramachandran outliers to report.

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	77/86 (90%)	76 (99%)	1 (1%)	69	74
1	B	77/86 (90%)	76 (99%)	1 (1%)	69	74
1	C	84/86 (98%)	83 (99%)	1 (1%)	71	76
1	D	76/86 (88%)	76 (100%)	0	100	100
1	E	60/86 (70%)	59 (98%)	1 (2%)	60	65
1	F	67/86 (78%)	64 (96%)	3 (4%)	27	24
All	All	441/516 (86%)	434 (98%)	7 (2%)	62	67

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	556	CYS
1	B	556	CYS
1	C	556	CYS
1	E	556	CYS
1	F	500	SER
1	F	556	CYS
1	F	571	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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	$\#\|Z\| > 2$
3	PEG	A	602	-	6,6,6	0.48	0	5,5,5	0.42	0
3	PEG	E	601	-	6,6,6	0.50	0	5,5,5	0.31	0

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
3	PEG	A	602	-	-	3/4/4/4	-
3	PEG	E	601	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	601	PEG	O1-C1-C2-O2
3	A	602	PEG	O2-C3-C4-O4
3	E	601	PEG	C4-C3-O2-C2
3	A	602	PEG	C1-C2-O2-C3
3	A	602	PEG	O1-C1-C2-O2

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 (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, 95^{th} 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	92/98 (93%)	-0.37	0	100	100	11, 20, 34, 63	0
1	B	89/98 (90%)	-0.32	0	100	100	12, 21, 39, 63	0
1	C	97/98 (98%)	-0.35	1 (1%)	82	81	11, 21, 40, 53	0
1	D	90/98 (91%)	-0.21	3 (3%)	46	45	12, 23, 57, 72	0
1	E	76/98 (77%)	-0.13	3 (3%)	39	38	12, 24, 60, 69	0
1	F	83/98 (84%)	-0.14	1 (1%)	79	78	12, 25, 59, 70	0
All	All	527/588 (89%)	-0.26	8 (1%)	73	72	11, 23, 53, 72	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	499	LEU	4.4
1	E	502	LEU	4.0
1	E	503	HIS	3.6
1	D	505	ILE	3.3
1	E	506	VAL	2.7
1	F	498	GLY	2.5
1	D	498	GLY	2.2
1	C	587	GLY	2.2

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

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, 95^{th} 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
3	PEG	A	602	7/7	0.82	0.28	44,53,60,60	0
3	PEG	E	601	7/7	0.84	0.33	39,53,62,62	0
2	CL	D	601	1/1	0.99	0.12	11,11,11,11	0
2	CL	A	601	1/1	1.00	0.09	11,11,11,11	0

6.5 Other polymers

There are no such residues in this entry.