



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 03:20 PM UTC

PDB ID : 8EZK / pdb_00008ezk
Title : Pfs25 in complex with transmission-reducing antibody AS01-04
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Deposited on : 2022-11-01
Resolution : 2.30 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 ⓘ 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

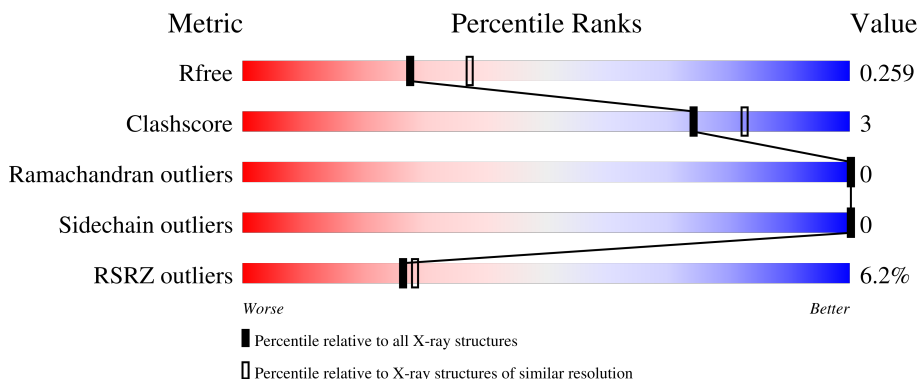
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	182	9% 87% 8% 5%
1	B	182	10% 90% 5% 5%
2	H	263	3% 83% 6% 10%
2	I	263	4% 82% 8% 10%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12173 atoms, of which 5997 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 25 kDa ookinete surface antigen.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	172	Total	C	H	N	O	S	0	0	0
			2559	786	1268	218	263	24			
1	B	173	Total	C	H	N	O	S	0	0	0
			2566	788	1271	219	264	24			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	THR	-	expression tag	UNP P13829
A	0	GLY	-	expression tag	UNP P13829
A	90	GLN	ASN	conflict	UNP P13829
A	143	GLN	ASN	conflict	UNP P13829
A	165	GLN	ASN	conflict	UNP P13829
A	172	GLY	-	expression tag	UNP P13829
A	173	THR	-	expression tag	UNP P13829
A	174	LYS	-	expression tag	UNP P13829
A	175	HIS	-	expression tag	UNP P13829
A	176	HIS	-	expression tag	UNP P13829
A	177	HIS	-	expression tag	UNP P13829
A	178	HIS	-	expression tag	UNP P13829
A	179	HIS	-	expression tag	UNP P13829
A	180	HIS	-	expression tag	UNP P13829
B	-1	THR	-	expression tag	UNP P13829
B	0	GLY	-	expression tag	UNP P13829
B	90	GLN	ASN	conflict	UNP P13829
B	143	GLN	ASN	conflict	UNP P13829
B	165	GLN	ASN	conflict	UNP P13829
B	172	GLY	-	expression tag	UNP P13829
B	173	THR	-	expression tag	UNP P13829
B	174	LYS	-	expression tag	UNP P13829
B	175	HIS	-	expression tag	UNP P13829
B	176	HIS	-	expression tag	UNP P13829
B	177	HIS	-	expression tag	UNP P13829

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Chain	Residue	Modelled	Actual	Comment	Reference
B	178	HIS	-	expression tag	UNP P13829
B	179	HIS	-	expression tag	UNP P13829
B	180	HIS	-	expression tag	UNP P13829

- Molecule 2 is a protein called Transmission-reducing antibody AS01-4, single-chain Fv.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	H	236	Total	C	H	N	O	S	0	0	0
			3509	1119	1727	310	348	5			
2	I	237	Total	C	H	N	O	S	0	0	0
			3520	1122	1731	311	351	5			

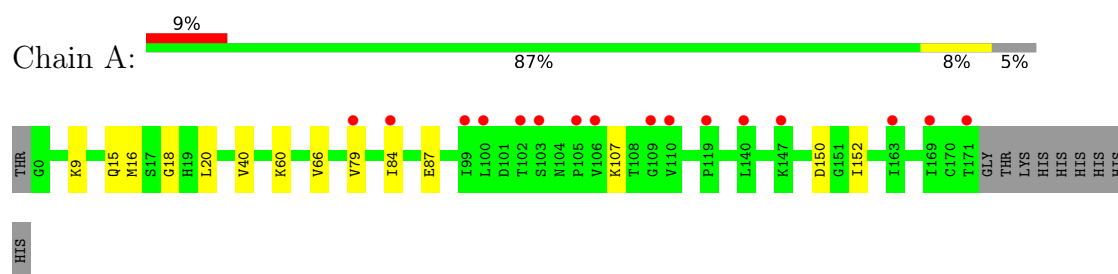
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	7	Total	O	0	0
			7	7		
3	H	4	Total	O	0	0
			4	4		
3	I	8	Total	O	0	0
			8	8		

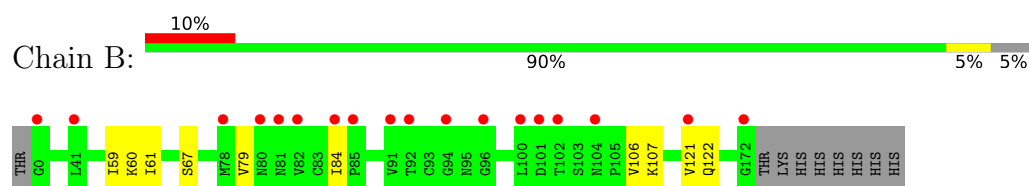
3 Residue-property plots [i](#)

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.

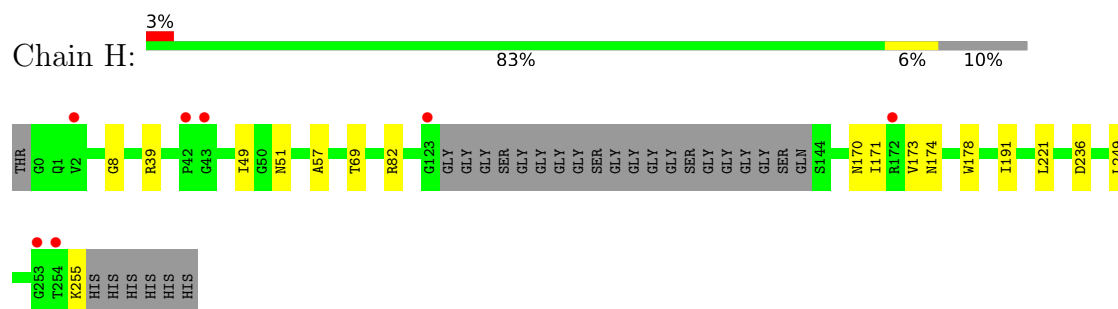
- Molecule 1: 25 kDa ookinete surface antigen



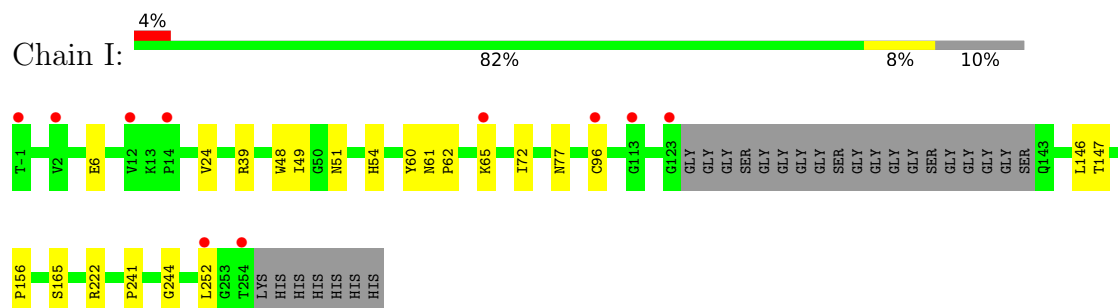
- Molecule 1: 25 kDa ookinete surface antigen



- Molecule 2: Transmission-reducing antibody AS01-4, single-chain Fv



- Molecule 2: Transmission-reducing antibody AS01-4, single-chain Fv



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	68.25Å 91.72Å 122.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.06 – 2.30 38.06 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (38.06-2.30) 99.8 (38.06-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.54 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.229 , 0.260 0.229 , 0.259	Depositor DCC
R_{free} test set	2000 reflections (5.75%)	wwPDB-VP
Wilson B-factor (Å ²)	50.6	Xtriage
Anisotropy	0.648	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 38.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12173	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.03% 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, 0.333 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	0.19	0/1302	0.42	0/1748
1	B	0.21	0/1306	0.48	0/1753
2	H	0.20	0/1827	0.48	0/2490
2	I	0.20	0/1834	0.48	0/2501
All	All	0.20	0/6269	0.47	0/8492

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	1291	1268	1270	9	2
1	B	1295	1271	1273	7	0
2	H	1782	1727	1729	12	0
2	I	1789	1731	1731	14	2
3	B	7	0	0	0	0
3	H	4	0	0	0	0
3	I	8	0	0	0	0
All	All	6176	5997	6003	38	2

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 3.

All (38) 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:I:54:HIS:HA	2:I:72:ILE:HD13	1.89	0.53
2:I:61:ASN:O	2:I:65:LYS:HG3	2.09	0.52
1:A:87:GLU:CD	1:A:107:LYS:HE3	2.36	0.50
2:I:62:PRO:HA	2:I:65:LYS:HG3	1.93	0.50
2:H:39:ARG:HB3	2:H:49:ILE:HD11	1.93	0.50
2:I:39:ARG:HB3	2:I:49:ILE:HD11	1.96	0.48
2:H:221:LEU:HD11	2:H:249:LEU:HD21	1.96	0.47
1:A:15:GLN:HB2	1:A:20:LEU:HD23	1.98	0.46
1:B:106:VAL:HG23	1:B:107:LYS:HG2	1.97	0.46
1:A:79:VAL:HG21	1:A:84:ILE:HD11	1.98	0.45
2:I:6:GLU:HG3	2:I:96:CYS:SG	2.55	0.45
1:B:106:VAL:HG12	2:H:8:GLY:HA2	1.97	0.45
2:I:51:ASN:C	2:I:51:ASN:OD1	2.60	0.45
1:A:16:MET:O	1:A:18:GLY:N	2.49	0.45
2:H:170:ASN:OD1	2:H:171:ILE:N	2.48	0.45
2:H:178:TRP:HB2	2:H:191:ILE:HB	2.00	0.44
2:H:69:THR:HG21	2:H:82:ARG:HH22	1.83	0.43
1:A:40:VAL:HG12	2:H:236:ASP:HB3	2.00	0.43
2:I:62:PRO:HA	2:I:65:LYS:HZ3	1.82	0.43
2:I:24:VAL:HG22	2:I:77:ASN:HB3	2.01	0.43
2:I:146:LEU:HB2	2:I:244:GLY:HA2	2.00	0.43
1:B:59:ILE:HG22	1:B:60:LYS:N	2.32	0.43
1:B:61:ILE:HB	1:B:67:SER:OG	2.17	0.43
2:H:255:LYS:HD2	2:H:255:LYS:H	1.84	0.43
2:H:173:VAL:HG23	2:H:174:ASN:ND2	2.33	0.43
2:I:60:TYR:HB2	2:I:65:LYS:HG2	2.01	0.42
1:B:121:VAL:HG13	1:B:122:GLN:OE1	2.20	0.42
2:H:51:ASN:OD1	2:H:51:ASN:C	2.63	0.42
2:I:62:PRO:CA	2:I:65:LYS:HZ3	2.32	0.41
1:B:79:VAL:HG21	1:B:84:ILE:HD11	2.02	0.41
1:B:106:VAL:HG12	2:H:8:GLY:CA	2.50	0.41
1:A:16:MET:HG2	1:A:152:ILE:HG22	2.02	0.41
2:I:48:TRP:CG	2:I:241:PRO:HG2	2.55	0.41
2:I:147:THR:OG1	2:I:165:SER:HB3	2.21	0.41
2:I:156:PRO:HD3	2:I:252:LEU:O	2.21	0.40
1:A:60:LYS:HE3	1:A:66:VAL:HG11	2.02	0.40
1:A:9:LYS:HB3	2:H:57:ALA:HB2	2.04	0.40
1:A:87:GLU:CD	1:A:87:GLU:N	2.78	0.40

All (2) 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)
1:A:150:ASP:O	2:I:222:ARG:NH1[1_455]	2.16	0.04
1:A:150:ASP:O	2:I:222:ARG:HH12[1_455]	1.59	0.01

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	170/182 (93%)	163 (96%)	7 (4%)	0	100	100
1	B	171/182 (94%)	165 (96%)	6 (4%)	0	100	100
2	H	232/263 (88%)	222 (96%)	10 (4%)	0	100	100
2	I	233/263 (89%)	224 (96%)	9 (4%)	0	100	100
All	All	806/890 (91%)	774 (96%)	32 (4%)	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	157/166 (95%)	157 (100%)	0	100	100
1	B	157/166 (95%)	157 (100%)	0	100	100
2	H	194/206 (94%)	194 (100%)	0	100	100
2	I	195/206 (95%)	195 (100%)	0	100	100
All	All	703/744 (94%)	703 (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. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	90	GLN
1	B	104	ASN
2	H	54	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

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, 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	172/182 (94%)	0.84	16 (9%) 14 16	53, 92, 146, 180	0
1	B	173/182 (95%)	0.80	18 (10%) 11 13	50, 80, 119, 177	0
2	H	236/263 (89%)	0.38	7 (2%) 52 54	48, 63, 98, 182	0
2	I	237/263 (90%)	0.32	10 (4%) 40 42	46, 64, 104, 134	0
All	All	818/890 (91%)	0.55	51 (6%) 26 28	46, 69, 120, 182	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	100	LEU	4.1
1	B	85	PRO	3.8
1	A	110	VAL	3.4
1	B	41	LEU	3.4
2	I	12	VAL	3.2
2	I	254	THR	3.0
2	H	43	GLY	2.9
1	B	81	ASN	2.9
1	A	99	ILE	2.9
2	H	42	PRO	2.8
1	A	163	ILE	2.7
1	B	172	GLY	2.7
2	I	2	VAL	2.7
1	B	0	GLY	2.7
1	B	80	ASN	2.7
1	B	82	VAL	2.7
1	A	119	PRO	2.6
1	A	84	ILE	2.6
1	B	104	ASN	2.6
2	H	253	GLY	2.5
1	A	102	THR	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	106	VAL	2.4
1	A	169	ILE	2.4
1	A	109	GLY	2.4
2	I	113	GLY	2.4
1	B	92	THR	2.4
2	I	96	CYS	2.4
2	H	2	VAL	2.4
2	I	-1	THR	2.4
1	A	79	VAL	2.4
1	B	121	VAL	2.4
1	A	140	LEU	2.3
1	A	105	PRO	2.3
1	B	94	GLY	2.3
1	A	147	LYS	2.3
2	I	14	PRO	2.2
1	B	84	ILE	2.2
1	A	103	SER	2.2
1	B	100	LEU	2.2
1	B	91	VAL	2.2
1	B	96	GLY	2.2
1	B	101	ASP	2.1
2	I	65	LYS	2.1
2	I	123	GLY	2.1
2	H	172	ARG	2.1
2	H	123	GLY	2.1
1	A	171	THR	2.1
2	H	254	THR	2.1
1	B	102	THR	2.1
1	B	78	MET	2.0
2	I	252	LEU	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.