



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:35 AM UTC

PDB ID : 5N47 / pdb_00005n47
Title : Structure of Anticalin N7E in complex with the three-domain fragment Fn7B8 of human oncofetal fibronectin
Authors : Schiefner, A.; Skerra, A.
Deposited on : 2017-02-10
Resolution : 3.00 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 ⓘ 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

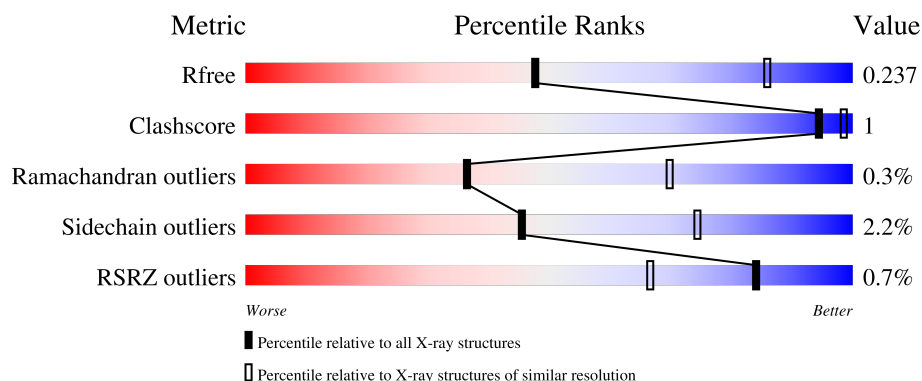
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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 $\leq 5\%$. 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	188	89% 7% .
1	C	188	% 84% 10% 6%
1	E	188	87% . 9%
2	B	284	61% . 36%
2	D	284	94% 5% .

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Mol	Chain	Length	Quality of chain
2	F	284	2% 94%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9943 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 Neutrophil gelatinase-associated lipocalin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	180	Total	C	N	O	S	0	0	0
			1463	943	250	266	4			
1	C	176	Total	C	N	O	S	0	0	0
			1436	925	245	262	4			
1	E	172	Total	C	N	O	S	0	0	0
			1409	911	241	253	4			

There are 81 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	HIS	GLN	engineered mutation	UNP P80188
A	36	GLU	LEU	engineered mutation	UNP P80188
A	40	SER	ALA	engineered mutation	UNP P80188
A	41	LEU	ILE	engineered mutation	UNP P80188
A	49	ARG	GLN	engineered mutation	UNP P80188
A	70	ARG	LEU	engineered mutation	UNP P80188
A	73	SER	LYS	engineered mutation	UNP P80188
A	77	HIS	ASP	engineered mutation	UNP P80188
A	79	LEU	TRP	engineered mutation	UNP P80188
A	87	SER	CYS	engineered mutation	UNP P80188
A	96	LEU	ASN	engineered mutation	UNP P80188
A	100	LYS	TYR	engineered mutation	UNP P80188
A	103	HIS	LEU	engineered mutation	UNP P80188
A	106	PHE	TYR	engineered mutation	UNP P80188
A	125	THR	LYS	engineered mutation	UNP P80188
A	127	ALA	SER	engineered mutation	UNP P80188
A	134	PHE	LYS	engineered mutation	UNP P80188
A	179	SER	-	expression tag	UNP P80188
A	180	ALA	-	expression tag	UNP P80188
A	181	TRP	-	expression tag	UNP P80188
A	182	SER	-	expression tag	UNP P80188
A	183	HIS	-	expression tag	UNP P80188
A	184	PRO	-	expression tag	UNP P80188

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Chain	Residue	Modelled	Actual	Comment	Reference
A	185	GLN	-	expression tag	UNP P80188
A	186	PHE	-	expression tag	UNP P80188
A	187	GLU	-	expression tag	UNP P80188
A	188	LYS	-	expression tag	UNP P80188
C	28	HIS	GLN	engineered mutation	UNP P80188
C	36	GLU	LEU	engineered mutation	UNP P80188
C	40	SER	ALA	engineered mutation	UNP P80188
C	41	LEU	ILE	engineered mutation	UNP P80188
C	49	ARG	GLN	engineered mutation	UNP P80188
C	70	ARG	LEU	engineered mutation	UNP P80188
C	73	SER	LYS	engineered mutation	UNP P80188
C	77	HIS	ASP	engineered mutation	UNP P80188
C	79	LEU	TRP	engineered mutation	UNP P80188
C	87	SER	CYS	engineered mutation	UNP P80188
C	96	LEU	ASN	engineered mutation	UNP P80188
C	100	LYS	TYR	engineered mutation	UNP P80188
C	103	HIS	LEU	engineered mutation	UNP P80188
C	106	PHE	TYR	engineered mutation	UNP P80188
C	125	THR	LYS	engineered mutation	UNP P80188
C	127	ALA	SER	engineered mutation	UNP P80188
C	134	PHE	LYS	engineered mutation	UNP P80188
C	179	SER	-	expression tag	UNP P80188
C	180	ALA	-	expression tag	UNP P80188
C	181	TRP	-	expression tag	UNP P80188
C	182	SER	-	expression tag	UNP P80188
C	183	HIS	-	expression tag	UNP P80188
C	184	PRO	-	expression tag	UNP P80188
C	185	GLN	-	expression tag	UNP P80188
C	186	PHE	-	expression tag	UNP P80188
C	187	GLU	-	expression tag	UNP P80188
C	188	LYS	-	expression tag	UNP P80188
E	28	HIS	GLN	engineered mutation	UNP P80188
E	36	GLU	LEU	engineered mutation	UNP P80188
E	40	SER	ALA	engineered mutation	UNP P80188
E	41	LEU	ILE	engineered mutation	UNP P80188
E	49	ARG	GLN	engineered mutation	UNP P80188
E	70	ARG	LEU	engineered mutation	UNP P80188
E	73	SER	LYS	engineered mutation	UNP P80188
E	77	HIS	ASP	engineered mutation	UNP P80188
E	79	LEU	TRP	engineered mutation	UNP P80188
E	87	SER	CYS	engineered mutation	UNP P80188
E	96	LEU	ASN	engineered mutation	UNP P80188

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Chain	Residue	Modelled	Actual	Comment	Reference
E	100	LYS	TYR	engineered mutation	UNP P80188
E	103	HIS	LEU	engineered mutation	UNP P80188
E	106	PHE	TYR	engineered mutation	UNP P80188
E	125	THR	LYS	engineered mutation	UNP P80188
E	127	ALA	SER	engineered mutation	UNP P80188
E	134	PHE	LYS	engineered mutation	UNP P80188
E	179	SER	-	expression tag	UNP P80188
E	180	ALA	-	expression tag	UNP P80188
E	181	TRP	-	expression tag	UNP P80188
E	182	SER	-	expression tag	UNP P80188
E	183	HIS	-	expression tag	UNP P80188
E	184	PRO	-	expression tag	UNP P80188
E	185	GLN	-	expression tag	UNP P80188
E	186	PHE	-	expression tag	UNP P80188
E	187	GLU	-	expression tag	UNP P80188
E	188	LYS	-	expression tag	UNP P80188

- Molecule 2 is a protein called Fibronectin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	183	Total	C	N	O	S	0	0	0
			1392	883	222	286	1			
2	D	280	Total	C	N	O	S	0	0	0
			2134	1341	345	446	2			
2	F	277	Total	C	N	O	S	0	0	0
			2109	1326	338	443	2			

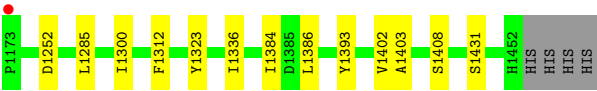
There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1449	SER	-	expression tag	UNP P02751
B	1450	ALA	-	expression tag	UNP P02751
B	1451	HIS	-	expression tag	UNP P02751
B	1452	HIS	-	expression tag	UNP P02751
B	1453	HIS	-	expression tag	UNP P02751
B	1454	HIS	-	expression tag	UNP P02751
B	1455	HIS	-	expression tag	UNP P02751
B	1456	HIS	-	expression tag	UNP P02751
D	1449	SER	-	expression tag	UNP P02751
D	1450	ALA	-	expression tag	UNP P02751
D	1451	HIS	-	expression tag	UNP P02751
D	1452	HIS	-	expression tag	UNP P02751

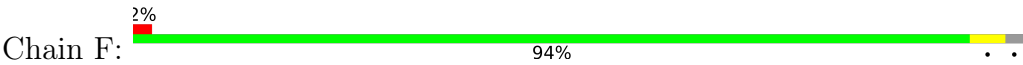
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Chain	Residue	Modelled	Actual	Comment	Reference
D	1453	HIS	-	expression tag	UNP P02751
D	1454	HIS	-	expression tag	UNP P02751
D	1455	HIS	-	expression tag	UNP P02751
D	1456	HIS	-	expression tag	UNP P02751
F	1449	SER	-	expression tag	UNP P02751
F	1450	ALA	-	expression tag	UNP P02751
F	1451	HIS	-	expression tag	UNP P02751
F	1452	HIS	-	expression tag	UNP P02751
F	1453	HIS	-	expression tag	UNP P02751
F	1454	HIS	-	expression tag	UNP P02751
F	1455	HIS	-	expression tag	UNP P02751
F	1456	HIS	-	expression tag	UNP P02751



● Molecule 2: Fibronectin



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	135.15Å 135.15Å 203.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.00 – 3.00 35.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (35.00-3.00) 99.9 (35.00-3.00)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.91 (at 3.00Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.208 , 0.241 0.206 , 0.237	Depositor DCC
R_{free} test set	1926 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	70.0	Xtriage
Anisotropy	0.264	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 65.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9943	wwPDB-VP
Average B, all atoms (Å ²)	99.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.47% 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	0.72	0/1503	0.85	2/2034 (0.1%)
1	C	0.71	0/1474	0.82	1/1994 (0.1%)
1	E	0.62	0/1447	0.78	2/1957 (0.1%)
2	B	0.65	0/1424	0.84	0/1960
2	D	0.66	0/2185	0.82	1/3009 (0.0%)
2	F	0.65	0/2158	0.71	0/2972
All	All	0.67	0/10191	0.80	6/13926 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1312	PHE	N-CA-C	6.12	117.54	108.60
1	E	168	PHE	CA-C-N	5.66	125.68	119.90
1	E	168	PHE	C-N-CA	5.66	125.68	119.90
1	A	168	PHE	CA-C-N	5.07	125.07	119.90
1	A	168	PHE	C-N-CA	5.07	125.07	119.90
1	C	8	ILE	N-CA-C	-5.03	104.02	108.95

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	1463	0	1449	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1436	0	1425	10	0
1	E	1409	0	1404	3	0
2	B	1392	0	1368	3	0
2	D	2134	0	2068	4	0
2	F	2109	0	2049	2	0
All	All	9943	0	9763	26	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 1.

All (26) 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:C:5:SER:O	1:C:130:ARG:NH2	2.15	0.79
1:C:34:VAL:HG11	1:C:144:LEU:HD13	1.72	0.72
1:A:33:VAL:HG21	1:A:52:TYR:CZ	2.29	0.66
1:C:94:LEU:HD13	1:C:106:PHE:CD1	2.39	0.58
1:C:33:VAL:HG21	1:C:52:TYR:CZ	2.39	0.58
1:E:33:VAL:HG21	1:E:52:TYR:CZ	2.40	0.57
1:A:135:ILE:HD11	1:A:159:LEU:HD12	1.91	0.52
1:E:33:VAL:HG21	1:E:52:TYR:CE2	2.45	0.51
2:F:1330:PRO:HA	2:F:1356:THR:OG1	2.11	0.50
2:D:1285:LEU:HD21	2:D:1336:ILE:HG21	1.95	0.49
2:B:1392:ARG:HA	2:B:1403:ALA:O	2.12	0.48
2:D:1384:ILE:HG22	2:D:1386:LEU:HG	1.95	0.48
1:C:34:VAL:HG12	1:C:144:LEU:HD22	1.95	0.48
1:C:34:VAL:CG1	1:C:144:LEU:HD13	2.39	0.48
2:D:1300:ILE:HD13	2:D:1323:TYR:CG	2.49	0.47
1:A:179:SER:CB	1:C:103:HIS:HA	2.45	0.46
1:A:75:LYS:HA	1:C:9:PRO:HD3	1.98	0.46
1:C:16:VAL:HG11	1:C:122:PHE:CD2	2.52	0.45
2:B:1384:ILE:HG22	2:B:1386:LEU:HG	2.00	0.43
1:C:83:PHE:CD1	1:C:94:LEU:HD11	2.54	0.42
2:F:1396:VAL:HG22	2:F:1426:VAL:HG13	2.01	0.42
2:B:1426:VAL:HG12	2:B:1444:ARG:HG2	2.02	0.41
1:A:25:ASN:O	1:A:28:HIS:ND1	2.49	0.41
1:A:33:VAL:HG21	1:A:52:TYR:CE2	2.56	0.40
2:D:1393:TYR:CE1	2:D:1403:ALA:HB3	2.56	0.40
1:E:118:HIS:CE1	1:E:148:LEU:HD11	2.57	0.40

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	178/188 (95%)	169 (95%)	8 (4%)	1 (1%)	21	56
1	C	174/188 (93%)	166 (95%)	7 (4%)	1 (1%)	21	56
1	E	170/188 (90%)	163 (96%)	7 (4%)	0	100	100
2	B	181/284 (64%)	177 (98%)	4 (2%)	0	100	100
2	D	278/284 (98%)	262 (94%)	15 (5%)	1 (0%)	30	65
2	F	275/284 (97%)	259 (94%)	15 (6%)	1 (0%)	30	65
All	All	1256/1416 (89%)	1196 (95%)	56 (4%)	4 (0%)	36	70

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	1252	ASP
2	F	1252	ASP
1	C	99	SER
1	A	61	ASP

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	164/172 (95%)	161 (98%)	3 (2%)	51	77
1	C	162/172 (94%)	159 (98%)	3 (2%)	50	76
1	E	158/172 (92%)	153 (97%)	5 (3%)	34	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	163/256 (64%)	158 (97%)	5 (3%)	35	68
2	D	252/256 (98%)	249 (99%)	3 (1%)	63	82
2	F	250/256 (98%)	244 (98%)	6 (2%)	43	73
All	All	1149/1284 (90%)	1124 (98%)	25 (2%)	45	74

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	THR
1	A	128	GLN
1	A	150	GLU
2	B	1274	SER
2	B	1294	THR
2	B	1296	ILE
2	B	1384	ILE
2	B	1431	SER
1	C	112	SER
1	C	148	LEU
1	C	159	LEU
2	D	1402	VAL
2	D	1408	SER
2	D	1431	SER
1	E	28	HIS
1	E	34	VAL
1	E	54	THR
1	E	146	SER
1	E	148	LEU
2	F	1363	ASP
2	F	1372	ASP
2	F	1384	ILE
2	F	1402	VAL
2	F	1405	LEU
2	F	1434	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	ASN
2	B	1368	ASN
1	C	26	GLN

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Mol	Chain	Res	Type
2	D	1185	ASN
2	D	1244	ASN
2	D	1354	GLN
2	D	1445	GLN
1	E	118	HIS
2	F	1185	ASN
2	F	1244	ASN
2	F	1388	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](#)

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 [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	180/188 (95%)	-0.55	0 100 100	39, 56, 106, 129	0
1	C	176/188 (93%)	-0.42	1 (0%) 85 69	42, 62, 112, 166	0
1	E	172/188 (91%)	-0.16	0 100 100	58, 96, 157, 222	0
2	B	183/284 (64%)	-0.59	0 100 100	41, 67, 101, 142	0
2	D	280/284 (98%)	-0.17	1 (0%) 88 76	42, 82, 168, 216	0
2	F	277/284 (97%)	0.44	7 (2%) 58 35	98, 175, 213, 229	0
All	All	1268/1416 (89%)	-0.19	9 (0%) 84 66	39, 82, 199, 229	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	1203	ILE	2.8
2	D	1173	PRO	2.7
2	F	1173	PRO	2.6
2	F	1246	SER	2.6
2	F	1227	ALA	2.3
1	C	99	SER	2.2
2	F	1449	SER	2.2
2	F	1228	ASP	2.1
2	F	1254	LYS	2.1

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.