



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 10:02 PM GMT

PDB ID : 1RRL
Title : Soybean Lipoxygenase (LOX-3) at 93K at 2.0 Å resolution
Authors : Borbulevych, O.Y.; Jankun, J.; Skrzypczak-Jankun, E.
Deposited on : 2003-12-08
Resolution : 2.09 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

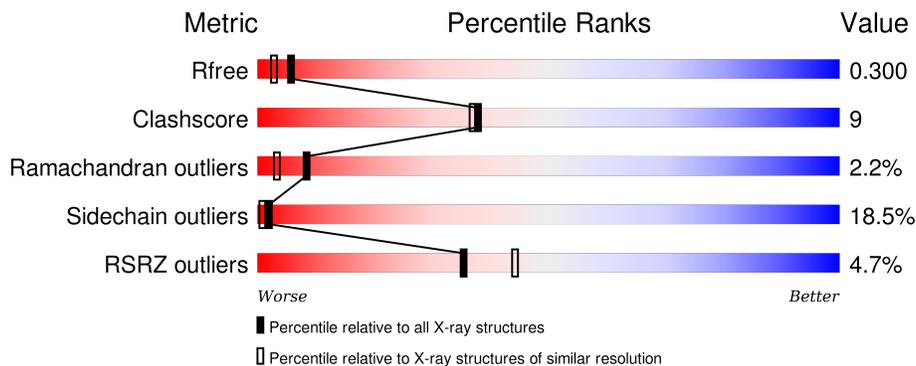
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.09 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}	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	857	 5% (poor fit), 65% (0-1 outliers), 26% (2 outliers), 7% (3+ outliers), .. (not modelled)
1	B	857	 4% (poor fit), 66% (0-1 outliers), 25% (2 outliers), 8% (3+ outliers), . (not modelled)

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 14643 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 Seed lipoxygenase-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	850	6789	4335	1167	1269	18	0	0	0
1	B	850	6789	4335	1167	1269	18	0	0	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	25	ASP	HIS	SEE REMARK 99	UNP P09186
A	57	SER	PRO	SEE REMARK 999	UNP P09186
A	112	PRO	LEU	SEE REMARK 999	UNP P09186
A	201	ILE	VAL	SEE REMARK 999	UNP P09186
A	382	ASP	GLU	SEE REMARK 999	UNP P09186
A	428	ASP	GLY	SEE REMARK 999	UNP P09186
A	630	THR	ALA	SEE REMARK 999	UNP P09186
B	25	ASP	HIS	SEE REMARK 999	UNP P09186
B	57	SER	PRO	SEE REMARK 999	UNP P09186
B	112	PRO	LEU	SEE REMARK 999	UNP P09186
B	201	ILE	VAL	SEE REMARK 999	UNP P09186
B	382	ASP	GLU	SEE REMARK 999	UNP P09186
B	428	ASP	GLY	SEE REMARK 999	UNP P09186
B	630	THR	ALA	SEE REMARK 999	UNP P09186

- Molecule 2 is FE (II) ION (three-letter code: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Fe	0	0
			1	1		
2	A	1	Total	Fe	0	0
			1	1		

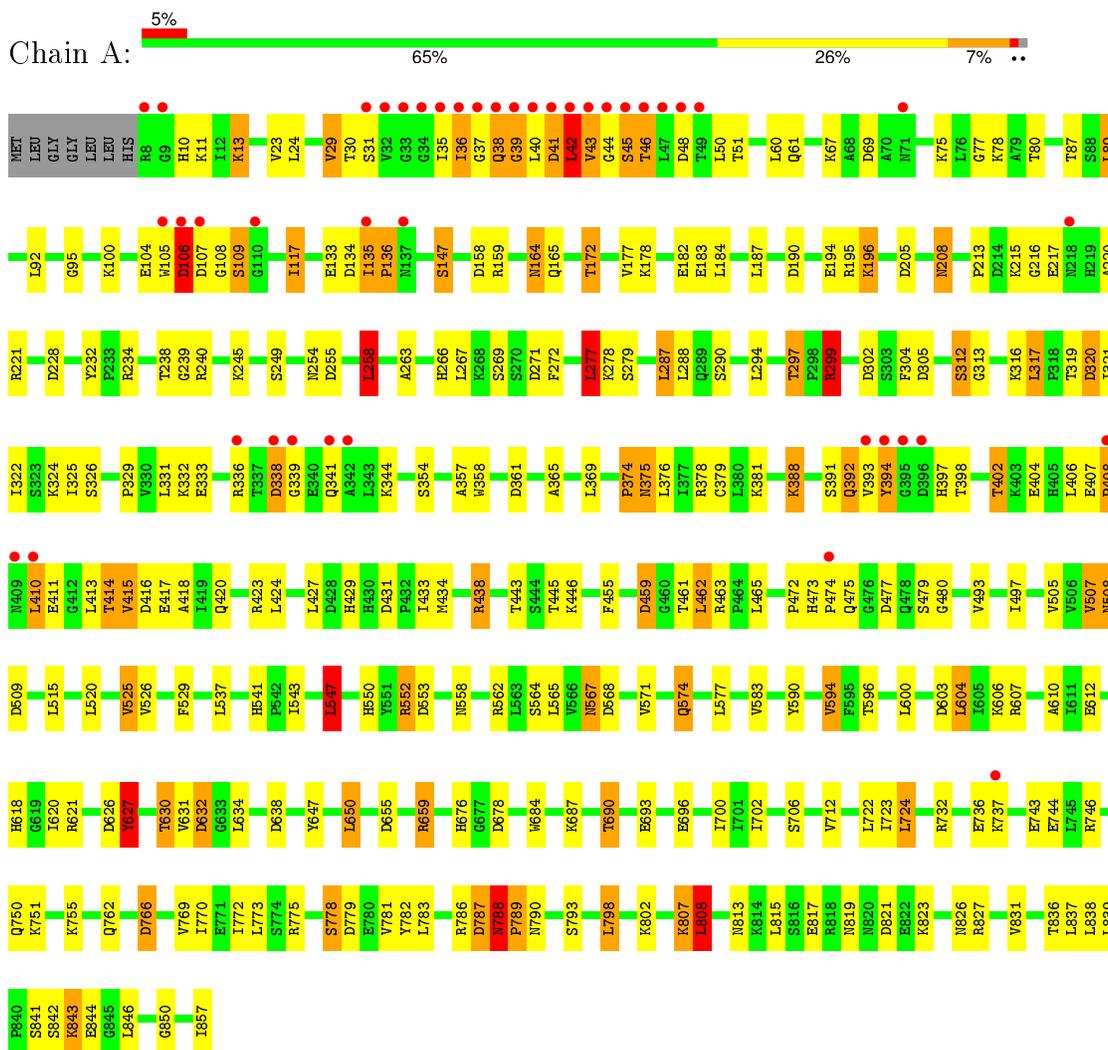
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	500	Total 500	O 500	0	0
3	B	563	Total 563	O 563	0	0

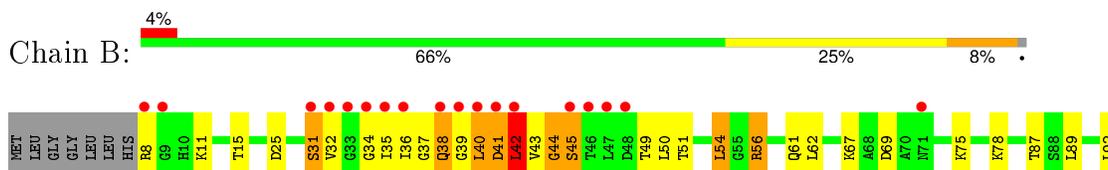
3 Residue-property plots [i](#)

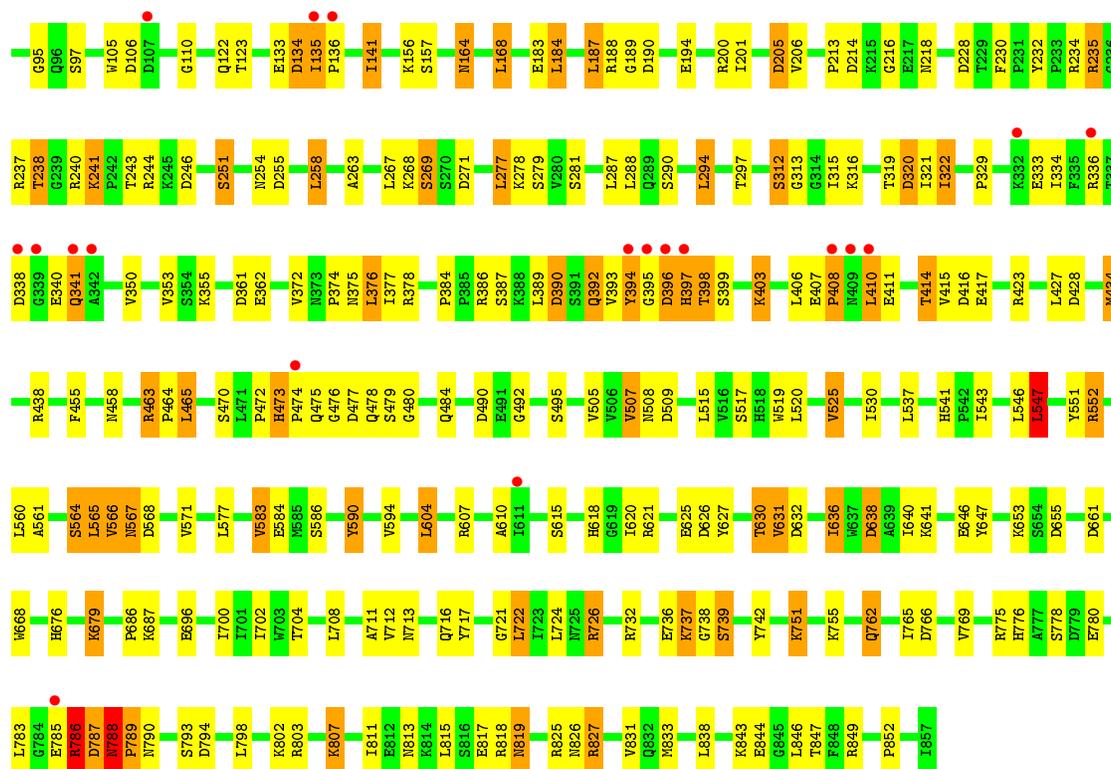
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Seed lipoxygenase-3



- Molecule 1: Seed lipoxygenase-3





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	106.40 Å 133.50 Å 60.70 Å 90.00° 97.30° 90.00°	Depositor
Resolution (Å)	10.00 – 2.09 10.00 – 2.09	Depositor EDS
% Data completeness (in resolution range)	65.4 (10.00-2.09) 65.4 (10.00-2.09)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.44 (at 2.09 Å)	Xtrriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.207 , 0.305 0.209 , 0.300	Depositor DCC
R_{free} test set	3245 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	26.3	Xtrriage
Anisotropy	0.156	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 61.4	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Outliers	0 of 64208 reflections	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14643	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 50.66 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 6.2683e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: FE2

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	0.83	2/6961 (0.0%)	1.14	41/9453 (0.4%)
1	B	0.88	5/6961 (0.1%)	1.17	39/9453 (0.4%)
All	All	0.85	7/13922 (0.1%)	1.16	80/18906 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
1	B	0	3
All	All	0	8

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	594	VAL	CB-CG1	6.95	1.67	1.52
1	B	394	TYR	CE2-CZ	-6.47	1.30	1.38
1	B	434	MET	CG-SD	-6.30	1.64	1.81
1	A	647	TYR	CD1-CE1	-6.27	1.29	1.39
1	B	394	TYR	CD2-CE2	-5.53	1.31	1.39

The worst 5 of 80 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	205	ASP	CB-CG-OD2	11.02	128.21	118.30
1	B	726	ARG	NE-CZ-NH2	9.89	125.25	120.30
1	B	25	ASP	CB-CG-OD2	8.72	126.15	118.30
1	A	787	ASP	CB-CG-OD2	8.40	125.86	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	726	ARG	NE-CZ-NH1	-8.29	116.15	120.30

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	133	GLU	Peptide
1	A	208	ASN	Peptide
1	A	30	THR	Peptide
1	A	40	LEU	Peptide
1	A	43	VAL	Peptide

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	6789	0	6714	128	0
1	B	6789	0	6714	124	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	500	0	0	18	0
3	B	563	0	0	18	0
All	All	14643	0	13428	249	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 9.

The worst 5 of 249 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:B:708:LEU:HA	3:B:1171:HOH:O	1.63	0.97
1:B:789:PRO:HA	3:B:1136:HOH:O	1.73	0.86
1:A:194:GLU:HA	1:A:239:GLY:HA3	1.58	0.85
1:B:790:ASN:HA	3:B:1071:HOH:O	1.75	0.85
1:A:507:VAL:HG13	1:A:577:LEU:HD13	1.63	0.78

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	848/857 (99%)	767 (90%)	61 (7%)	20 (2%)	7 3
1	B	848/857 (99%)	772 (91%)	59 (7%)	17 (2%)	9 4
All	All	1696/1714 (99%)	1539 (91%)	120 (7%)	37 (2%)	8 3

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	45	SER
1	A	136	PRO
1	A	408	PRO
1	A	410	LEU
1	A	789	PRO

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	744/749 (99%)	604 (81%)	140 (19%)	2 1
1	B	744/749 (99%)	608 (82%)	136 (18%)	2 1
All	All	1488/1498 (99%)	1212 (82%)	276 (18%)	2 1

5 of 276 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	788	ASN
1	B	56	ARG
1	B	739	SER
1	A	808	LEU
1	B	8	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	10	HIS
1	B	375	ASN
1	B	788	ASN
1	B	254	ASN
1	A	458	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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 [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	850/857 (99%)	-0.02	43 (5%) 32 40	2, 17, 34, 49	0
1	B	850/857 (99%)	-0.13	37 (4%) 38 47	2, 16, 35, 46	0
All	All	1700/1714 (99%)	-0.08	80 (4%) 35 44	2, 16, 35, 49	0

The worst 5 of 80 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	36	ILE	7.0
1	A	410	LEU	6.9
1	A	35	ILE	6.2
1	A	33	GLY	6.0
1	A	8	ARG	6.0

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	FE2	A	858	1/1	1.00	0.08	-1.13	28,28,28,28	0
2	FE2	B	858	1/1	1.00	0.04	-2.67	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.