Full wwPDB X-ray Structure Validation Report (i)

Dec 6, 2023 – 09:19 pm GMT

PDB ID	:	2VEN
Title	:	Structure-based enzyme engineering efforts with an inactive monomeric TIM variant: the importance of a single point mutation for generating an active site with suitable binding properties
Authors	:	Alahuhta, M.; Salin, M.; Casteleijn, M.G.; Kemmer, C.; El-Sayed, I.; Augustyns, K.; Neubauer, P.; Wierenga, R.K.
Deposited on	:	2007-10-25
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 (i)) were used in the production of this report:

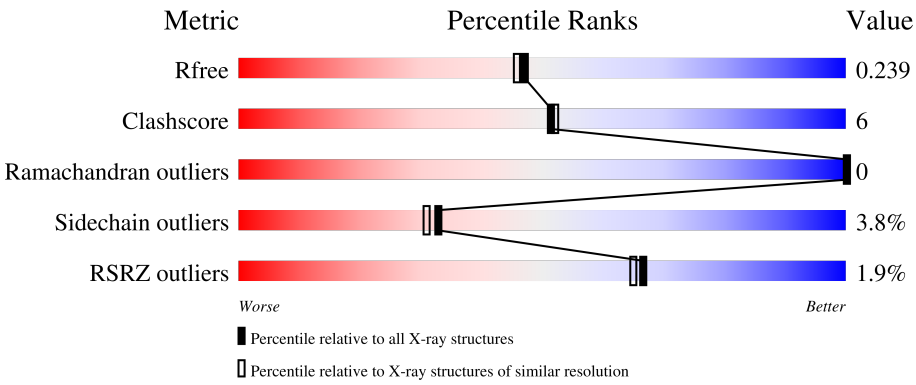
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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	238	3% 84% 9% • •
1	B	238	% 91% 8% •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3982 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 GLYCOSOMAL TRIOSEPHOSPHATE ISOMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	228	1768	1130	312	322	4	0	3	0
1	B	238	1853	1175	323	350	5	0	12	0

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	15	SER	CYS	conflict	UNP P04789
A	?	-	ASN	deletion	UNP P04789
A	18	PRO	GLN	conflict	UNP P04789
A	19	ASP	GLN	conflict	UNP P04789
A	68	GLY	ILE	conflict	UNP P04789
A	69	ASN	ALA	conflict	UNP P04789
A	70	ALA	LYS	conflict	UNP P04789
A	71	ASP	SER	conflict	UNP P04789
A	?	-	GLY	deletion	UNP P04789
A	?	-	ALA	deletion	UNP P04789
A	?	-	PHE	deletion	UNP P04789
A	?	-	THR	deletion	UNP P04789
A	?	-	GLY	deletion	UNP P04789
A	?	-	GLU	deletion	UNP P04789
A	?	-	VAL	deletion	UNP P04789
A	72	ALA	SER	conflict	UNP P04789
A	81	ALA	PRO	conflict	UNP P04789
A	82	SER	ILE	conflict	UNP P04789
A	100	TRP	ALA	conflict	UNP P04789
A	233	ALA	VAL	engineered mutation	UNP P04789
A	?	-	GLY	deletion	UNP P04789
A	?	-	ALA	deletion	UNP P04789
A	?	-	SER	deletion	UNP P04789
B	15	SER	CYS	conflict	UNP P04789
B	?	-	ASN	deletion	UNP P04789

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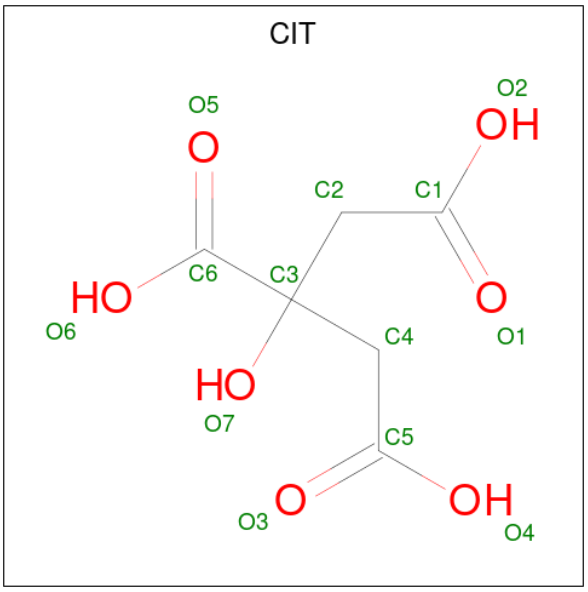
Chain	Residue	Modelled	Actual	Comment	Reference
B	18	PRO	GLN	conflict	UNP P04789
B	19	ASP	GLN	conflict	UNP P04789
B	68	GLY	ILE	conflict	UNP P04789
B	69	ASN	ALA	conflict	UNP P04789
B	70	ALA	LYS	conflict	UNP P04789
B	71	ASP	SER	conflict	UNP P04789
B	?	-	GLY	deletion	UNP P04789
B	?	-	ALA	deletion	UNP P04789
B	?	-	PHE	deletion	UNP P04789
B	?	-	THR	deletion	UNP P04789
B	?	-	GLY	deletion	UNP P04789
B	?	-	GLU	deletion	UNP P04789
B	?	-	VAL	deletion	UNP P04789
B	72	ALA	SER	conflict	UNP P04789
B	81	ALA	PRO	conflict	UNP P04789
B	82	SER	ILE	conflict	UNP P04789
B	100	TRP	ALA	conflict	UNP P04789
B	233	ALA	VAL	engineered mutation	UNP P04789
B	?	-	GLY	deletion	UNP P04789
B	?	-	ALA	deletion	UNP P04789
B	?	-	SER	deletion	UNP P04789

- Molecule 2 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	B	1	13	6	7	0	0

- Molecule 3 is water.

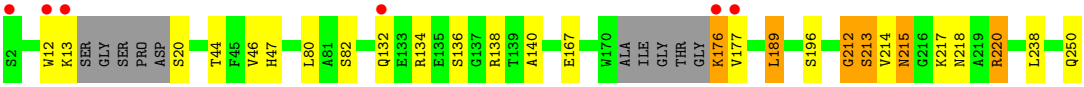
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	143	144	144	0	1
			Total	O		
3	B	198	204	204	0	6

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.

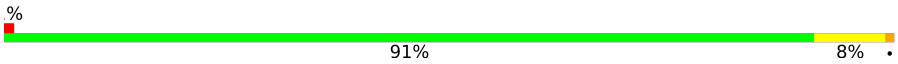
- Molecule 1: GLYCOSOMAL TRIOSEPHOSPHATE ISOMERASE

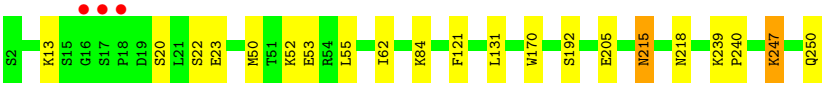
Chain A:



- Molecule 1: GLYCOSOMAL TRIOSEPHOSPHATE ISOMERASE

Chain B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	46.10Å 88.30Å 56.50Å 90.00° 97.00° 90.00°	Depositor
Resolution (Å)	19.88 – 2.00 19.88 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.88-2.00) 99.0 (19.88-2.00)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.95 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.3.0028	Depositor
R, R_{free}	0.186 , 0.237 0.186 , 0.239	Depositor DCC
R_{free} test set	1502 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	17.8	Xtriage
Anisotropy	0.452	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 40.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	3982	wwPDB-VP
Average B, all atoms (Å^2)	9.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.17% 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: CIT

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	0.66	0/1809	0.72	2/2452 (0.1%)
1	B	0.72	0/1928	0.66	0/2615
All	All	0.69	0/3737	0.69	2/5067 (0.0%)

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	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	213	SER	N-CA-C	5.33	125.40	111.00
1	A	134	ARG	NE-CZ-NH2	-5.12	117.74	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	212	GLY	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	1768	0	1790	21	0
1	B	1853	0	1856	20	0
2	B	13	0	5	0	0
3	A	144	0	0	1	0
3	B	204	0	0	4	0
All	All	3982	0	3651	41	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 6.

All (41) 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:220:ARG:HH11	1:A:220:ARG:HG3	1.31	0.95
1:B:205[B]:GLU:OE2	3:B:2179:HOH:O	1.96	0.83
1:A:132:GLN:HG3	3:A:2093:HOH:O	1.79	0.83
1:A:215:ASN:C	1:A:215:ASN:HD22	1.86	0.80
1:A:220:ARG:HG3	1:A:220:ARG:NH1	2.00	0.76
1:A:212:GLY:O	1:A:214:VAL:HG23	1.92	0.68
1:A:177:VAL:HG23	1:A:213:SER:HB3	1.77	0.67
1:A:12[B]:TRP:HE3	1:A:238:LEU:HB3	1.60	0.66
1:B:205[A]:GLU:OE1	3:B:2182[A]:HOH:O	2.14	0.66
1:A:12[A]:TRP:CE3	1:A:13:LYS:HA	2.35	0.61
1:B:52:LYS:HA	1:B:62:ILE:CD1	2.30	0.61
1:B:84:LYS:HG2	1:B:121:PHE:CE1	2.36	0.60
1:A:177:VAL:HG23	1:A:213:SER:CB	2.31	0.59
1:B:250:GLN:NE2	3:B:2202:HOH:O	2.38	0.57
1:A:215:ASN:C	1:A:215:ASN:ND2	2.58	0.56
1:B:22[B]:SER:HB3	1:B:50[B]:MET:CE	2.35	0.56
1:A:220:ARG:NH1	1:A:250:GLN:O	2.38	0.55
1:B:247:LYS:HB2	1:B:247:LYS:NZ	2.22	0.55
1:A:136:SER:OG	1:A:138[B]:ARG:HD3	2.08	0.53
1:B:20:SER:HB3	1:B:23:GLU:HG3	1.93	0.51
1:A:12[B]:TRP:CE3	1:A:238:LEU:HD23	2.46	0.50
1:B:52:LYS:HA	1:B:62:ILE:HD13	1.93	0.50
1:B:215:ASN:ND2	1:B:218:ASN:H	2.09	0.50
1:B:22[B]:SER:HB3	1:B:50[B]:MET:HE1	1.94	0.50
1:B:215:ASN:HD22	1:B:215:ASN:C	2.16	0.49
1:B:239:LYS:HB2	1:B:240:PRO:CD	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:VAL:HG13	1:A:47:HIS:CD2	2.50	0.47
1:B:52:LYS:HA	1:B:62:ILE:HD11	1.96	0.47
1:A:12[B]:TRP:CE3	1:A:238:LEU:HB3	2.46	0.46
1:A:215:ASN:ND2	1:A:218:ASN:H	2.14	0.46
1:A:217:LYS:HE3	1:A:217:LYS:HB2	1.74	0.45
1:A:177:VAL:CG2	1:A:213:SER:HB3	2.46	0.44
1:B:13:LYS:HE3	1:B:13:LYS:HB3	1.79	0.44
1:B:55:LEU:HD23	1:B:62:ILE:HG13	2.00	0.44
1:B:22[B]:SER:HB3	1:B:50[B]:MET:HE2	1.98	0.44
1:B:13:LYS:HD2	3:B:2012:HOH:O	2.17	0.43
1:A:215:ASN:HD21	1:A:218:ASN:H	1.67	0.43
1:A:176:LYS:NZ	1:A:176:LYS:HA	2.35	0.42
1:B:20:SER:CB	1:B:23:GLU:HG3	2.50	0.41
1:A:140:ALA:HA	1:A:189:LEU:HD21	2.02	0.41
1:B:131:LEU:HB2	1:B:170:TRP:HB3	2.01	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	224/238 (94%)	219 (98%)	5 (2%)	0	100	100
1	B	247/238 (104%)	244 (99%)	3 (1%)	0	100	100
All	All	471/476 (99%)	463 (98%)	8 (2%)	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	183/187 (98%)	173 (94%)	10 (6%)	21	17
1	B	198/187 (106%)	193 (98%)	5 (2%)	47	49
All	All	381/374 (102%)	366 (96%)	15 (4%)	33	30

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	SER
1	A	44	THR
1	A	80	LEU
1	A	82	SER
1	A	167[A]	GLU
1	A	176	LYS
1	A	189	LEU
1	A	196	SER
1	A	215	ASN
1	A	220	ARG
1	B	53	GLU
1	B	192[A]	SER
1	B	192[B]	SER
1	B	215	ASN
1	B	247	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	GLN
1	A	89	ASN
1	A	181	GLN
1	A	215	ASN
1	B	65	GLN
1	B	89	ASN
1	B	215	ASN
1	B	250	GLN

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)

1 ligand is 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	CIT	B	1251	-	12,12,12	1.00	0	17,17,17	1.66	1 (5%)

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	CIT	B	1251	-	-	0/16/16/16	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1251	CIT	O6-C6-C3	4.58	121.00	113.05

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	228/238 (95%)	-0.15	6 (2%)	56	54	2, 7, 20, 25	0
1	B	238/238 (100%)	-0.32	3 (1%)	77	76	3, 8, 17, 26	0
All	All	466/476 (97%)	-0.23	9 (1%)	66	65	2, 8, 19, 26	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	16	GLY	4.0
1	A	2	SER	3.8
1	B	18	PRO	3.6
1	A	12[A]	TRP	3.4
1	A	177	VAL	2.3
1	A	176	LYS	2.2
1	B	17[A]	SER	2.1
1	A	13	LYS	2.0
1	A	132	GLN	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 monosaccharides 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. 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	CIT	B	1251	13/13	0.95	0.15	9,11,13,14	0

6.5 Other polymers (i)

There are no such residues in this entry.