



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 08:12 PM GMT

PDB ID : 4XT2
Title : Crystal structure of the high affinity heterodimer of HIF2 alpha and ARNT C-terminal PAS domains in complex with a tetrazole-containing antagonist
Authors : Scheuermann, T.H.; Gardner, K.H.
Deposited on : 2015-01-22
Resolution : 1.70 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
<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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
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) : rb-20026982

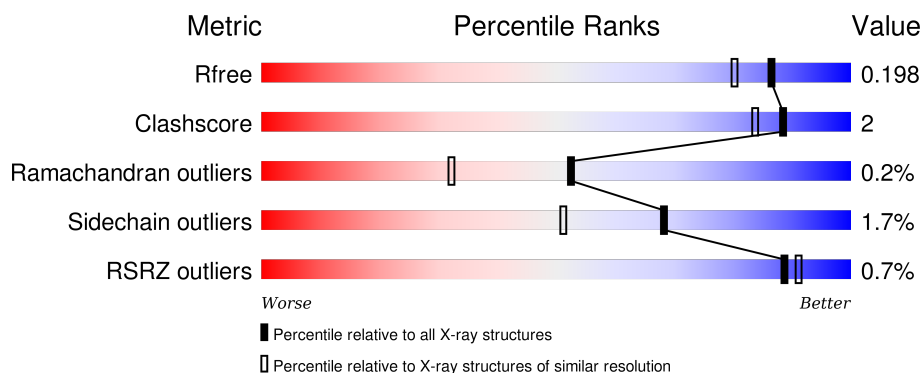
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	3190 (1.70-1.70)
Clashscore	102246	3585 (1.70-1.70)
Ramachandran outliers	100387	3527 (1.70-1.70)
Sidechain outliers	100360	3527 (1.70-1.70)
RSRZ outliers	91569	3200 (1.70-1.70)

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	B	121	<div> <div>84%</div> <div>7% • 8%</div> </div>
1	D	121	<div> <div>82%</div> <div>6% • 12%</div> </div>
2	A	117	<div> <div>%</div> <div>96%</div> <div>• •</div> </div>
2	C	117	<div> <div>2%</div> <div>89%</div> <div>8% • •</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7822 atoms, of which 3697 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 Aryl hydrocarbon receptor nuclear translocator.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	111	Total	C	H	N	O	S	37	18	0
			1889	607	935	166	174	7			
1	D	107	Total	C	H	N	O	S	11	18	0
			1873	600	932	168	168	5			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	350	GLY	-	expression tag	UNP P27540
B	351	GLU	-	expression tag	UNP P27540
B	352	PHE	-	expression tag	UNP P27540
B	353	LYS	-	expression tag	UNP P27540
B	354	GLY	-	expression tag	UNP P27540
B	355	LEU	-	expression tag	UNP P27540
B	362	ARG	GLU	engineered mutation	UNP P27540
D	350	GLY	-	expression tag	UNP P27540
D	351	GLU	-	expression tag	UNP P27540
D	352	PHE	-	expression tag	UNP P27540
D	353	LYS	-	expression tag	UNP P27540
D	354	GLY	-	expression tag	UNP P27540
D	355	LEU	-	expression tag	UNP P27540
D	362	ARG	GLU	engineered mutation	UNP P27540

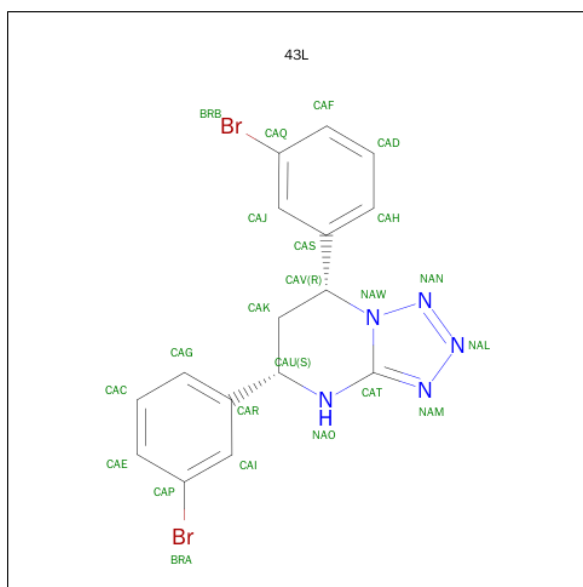
- Molecule 2 is a protein called Endothelial PAS domain-containing protein 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	A	116	Total	C	H	N	O	S	75	16	0
			1851	594	910	157	181	9			
2	C	114	Total	C	H	N	O	S	78	12	0
			1827	590	894	156	177	10			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	234	GLY	-	expression tag	UNP Q99814
C	235	GLU	-	expression tag	UNP Q99814
C	236	PHE	-	expression tag	UNP Q99814
C	237	LYS	-	expression tag	UNP Q99814
C	238	GLY	-	expression tag	UNP Q99814
C	247	GLU	ARG	engineered mutation	UNP Q99814
A	234	GLY	-	expression tag	UNP Q99814
A	235	GLU	-	expression tag	UNP Q99814
A	236	PHE	-	expression tag	UNP Q99814
A	237	LYS	-	expression tag	UNP Q99814
A	238	GLY	-	expression tag	UNP Q99814
A	247	GLU	ARG	engineered mutation	UNP Q99814

- Molecule 3 is (5S,7R)-5,7-bis(3-bromophenyl)-4,5,6,7-tetrahydrotetrazolo[1,5-a]pyrimidine (three-letter code: 43L) (formula: C₁₆H₁₃Br₂N₅).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	Br	C	H	N	0	0
			36	2	16	13	5		
3	C	1	Total	Br	C	H	N	0	0
			36	2	16	13	5		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	84	Total	O	0	0
			84	84		

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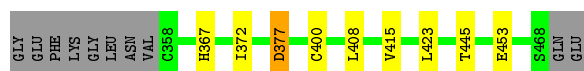
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	94	Total 94	O 94	0	0
4	A	60	Total 60	O 60	0	0
4	C	72	Total 72	O 72	0	0

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: Aryl hydrocarbon receptor nuclear translocator

Chain B: 



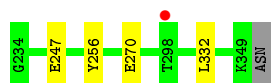
- Molecule 1: Aryl hydrocarbon receptor nuclear translocator

Chain D: 




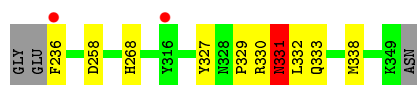
- Molecule 2: Endothelial PAS domain-containing protein 1

Chain A: 



- Molecule 2: Endothelial PAS domain-containing protein 1

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	74.25Å 84.39Å 82.78Å 90.00° 104.39° 90.00°	Depositor
Resolution (Å)	41.69 – 1.70 41.69 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.6 (41.69-1.70) 99.5 (41.69-1.70)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.91 (at 1.70Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.159 , 0.192 0.171 , 0.198	Depositor DCC
R_{free} test set	2743 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	16.8	Xtriage
Anisotropy	0.326	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 59.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 54343 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7822	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 29.86 % 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 1.4431e-03. 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 43L

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	B	0.57	0/988	0.71	1/1336 (0.1%)
1	D	0.56	0/979	0.73	2/1322 (0.2%)
2	A	0.44	0/965	0.59	0/1300
2	C	0.46	0/954	0.63	0/1285
All	All	0.51	0/3886	0.67	3/5243 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	377	ASP	CB-CG-OD1	7.51	125.06	118.30
1	D	377	ASP	CB-CG-OD2	-6.15	112.76	118.30
1	B	377	ASP	CB-CG-OD1	5.52	123.27	118.30

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	B	954	935	848	6	0
1	D	941	932	843	7	0
2	A	941	910	808	4	1
2	C	933	894	824	5	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	23	13	13	0	0
3	C	23	13	13	0	0
4	A	60	0	0	0	0
4	B	84	0	0	0	1
4	C	72	0	0	0	1
4	D	94	0	0	2	0
All	All	4125	3697	3349	18	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 2.

All (18) 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:D:361:THR:OG1	1:D:463[B]:ASN:ND2	2.10	0.85
1:B:400[B]:CYS:SG	1:B:408:LEU:HD22	2.28	0.73
1:D:463[B]:ASN:ND2	4:D:502:HOH:O	2.24	0.68
1:B:400[B]:CYS:SG	1:B:408:LEU:CD2	2.81	0.67
1:D:460[B]:THR:HG23	2:C:338[B]:MET:SD	2.44	0.58
2:A:332:LEU:HD13	2:C:332:LEU:HA	1.86	0.56
2:A:247:GLU:HB3	2:A:256:TYR:HB3	1.91	0.53
2:A:332:LEU:HD12	2:C:327:TYR:HB3	1.93	0.50
1:D:362:ARG:HB3	1:D:462[B]:THR:HG22	1.95	0.46
1:D:362:ARG:CB	1:D:462[B]:THR:HG22	2.46	0.46
2:A:332:LEU:HD11	2:C:329:PRO:HA	1.98	0.45
1:B:415[B]:VAL:HG22	1:B:423:LEU:HB3	1.99	0.44
1:B:415[B]:VAL:HG12	1:B:445:THR:HG23	2.00	0.44
1:D:462[B]:THR:CG2	4:D:519:HOH:O	2.66	0.43
2:C:330:ARG:O	2:C:331:ASN:HB3	2.19	0.43
1:B:400[B]:CYS:SG	1:B:408:LEU:HD23	2.60	0.40
1:B:367:HIS:HA	1:B:372:ILE:O	2.22	0.40
1:D:366:ARG:HB3	1:D:375:PHE:HB3	2.03	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)
2:A:270:GLU:OE2	2:C:268:HIS:HE2[1_455]	1.46	0.14
4:B:543:HOH:O	4:C:551:HOH:O[3_445]	2.14	0.06

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	B	115/121 (95%)	114 (99%)	1 (1%)	0	100	100
1	D	112/121 (93%)	111 (99%)	1 (1%)	0	100	100
2	A	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
2	C	113/117 (97%)	112 (99%)	0	1 (1%)	21	5
All	All	455/476 (96%)	451 (99%)	3 (1%)	1 (0%)	52	32

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	331	ASN

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	B	112/114 (98%)	110 (98%)	2 (2%)	66	49
1	D	109/114 (96%)	107 (98%)	2 (2%)	66	49
2	A	105/105 (100%)	105 (100%)	0	100	100
2	C	104/105 (99%)	100 (96%)	4 (4%)	40	17
All	All	430/438 (98%)	422 (98%)	8 (2%)	68	46

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	377	ASP
1	B	453	GLU
1	D	463[A]	ASN
1	D	463[B]	ASN
2	C	236	PHE
2	C	258	ASP
2	C	331	ASN
2	C	333	GLN

Some 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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

2 ligands are 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	$\# Z > 2$
3	43L	A	401	-	25,26,26	1.93	4 (16%)	28,37,37	1.91	6 (21%)
3	43L	C	401	-	25,26,26	2.12	5 (20%)	28,37,37	1.86	5 (17%)

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	43L	A	401	-	-	0/8/20/20	0/3/4/4
3	43L	C	401	-	-	0/8/20/20	0/3/4/4

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	401	43L	CAK-CAV	-6.12	1.46	1.53
3	C	401	43L	CAK-CAU	-6.11	1.46	1.53
3	A	401	43L	CAK-CAU	-4.41	1.48	1.53
3	C	401	43L	CAR-CAU	-3.52	1.47	1.52
3	C	401	43L	CAK-CAV	-3.52	1.49	1.53
3	C	401	43L	CAE-CAP	-2.28	1.33	1.38
3	A	401	43L	CAR-CAU	-2.20	1.48	1.52
3	A	401	43L	NAN-NAW	2.42	1.39	1.34
3	C	401	43L	CAU-NAO	4.60	1.50	1.46

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	401	43L	CAI-CAR-CAU	-2.19	117.27	120.05
3	C	401	43L	CAE-CAP-CAI	2.06	124.52	121.43
3	A	401	43L	CAS-CAJ-CAQ	2.11	121.42	119.57
3	A	401	43L	CAK-CAU-CAR	2.47	117.68	112.64
3	C	401	43L	CAK-CAU-CAR	2.56	117.85	112.64
3	C	401	43L	CAR-CAU-NAO	3.09	114.50	110.71
3	A	401	43L	CAR-CAU-NAO	3.80	115.39	110.71
3	C	401	43L	NAM-NAL-NAN	3.86	114.78	110.07
3	A	401	43L	NAM-NAL-NAN	3.96	114.91	110.07
3	C	401	43L	NAO-CAT-NAM	6.30	132.30	122.31
3	A	401	43L	NAO-CAT-NAM	6.32	132.34	122.31

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 ⓘ

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	B	111/121 (91%)	-0.29	0 100 100	9, 18, 32, 39	5 (4%)
1	D	107/121 (88%)	-0.13	0 100 100	10, 16, 30, 45	2 (1%)
2	A	116/117 (99%)	-0.11	1 (0%) 85 88	13, 26, 38, 56	10 (8%)
2	C	114/117 (97%)	-0.26	2 (1%) 71 76	11, 20, 43, 62	9 (7%)
All	All	448/476 (94%)	-0.20	3 (0%) 89 91	9, 20, 38, 62	26 (5%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	316	TYR	3.9
2	C	236	PHE	3.9
2	A	298	THR	2.0

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 carbohydrates 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. 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
3	43L	C	401	23/23	0.98	0.08	0.45	6,10,17,23	36
3	43L	A	401	23/23	0.98	0.07	-0.72	8,13,20,25	36

6.5 Other polymers [i](#)

There are no such residues in this entry.