



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 17, 2026 – 11:20 PM UTC

PDB ID : 6DK7 / pdb_00006dk7
Title : RetS histidine kinase region with cobalt
Authors : Mancl, J.M.; Schubot, F.D.
Deposited on : 2018-05-29
Resolution : 2.60 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

<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
Xtrriage (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

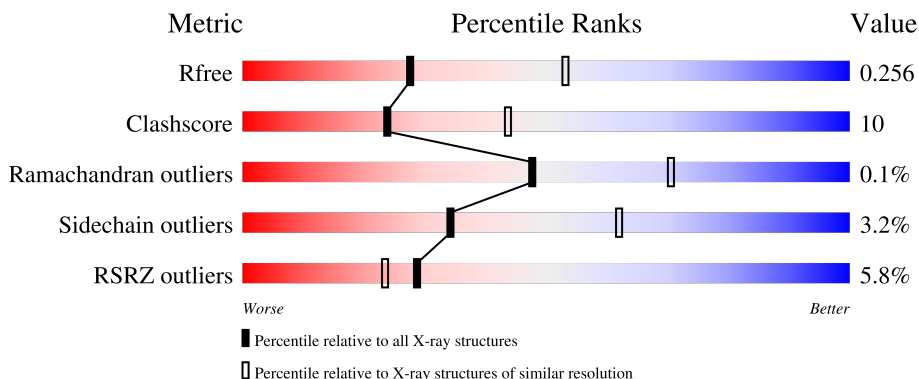
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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.



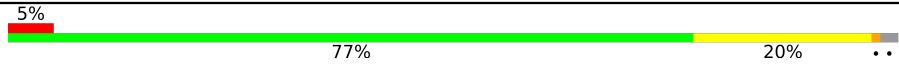

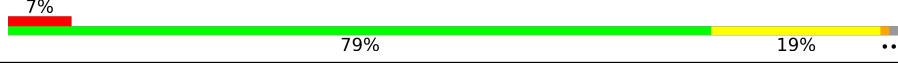
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	227	 7% 68% 30%
1	B	227	 5% 79% 18%
1	C	227	 8% 78% 19%
1	D	227	 6% 78% 19%
1	E	227	 6% 79% 19%

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Mol	Chain	Length	Quality of chain
1	F	227	 5% 77% 20% ..
1	G	227	 3% 80% 17% ..
1	H	227	 7% 79% 19% ..

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 14138 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 RetS (Regulator of Exopolysaccharide and Type III Secretion).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	223	Total 1724	C 1087	N 296	O 337	S 4	0	0	0
1	C	225	Total 1735	C 1093	N 298	O 340	S 4	0	0	0
1	D	225	Total 1735	C 1093	N 298	O 340	S 4	0	0	0
1	B	224	Total 1731	C 1091	N 297	O 339	S 4	0	0	0
1	E	225	Total 1736	C 1093	N 298	O 341	S 4	0	0	0
1	F	223	Total 1726	C 1087	N 297	O 338	S 4	0	0	0
1	G	225	Total 1739	C 1095	N 299	O 341	S 4	0	0	0
1	H	225	Total 1738	C 1095	N 299	O 340	S 4	0	0	0

- Molecule 2 is COBALT (II) ION (CCD ID: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total 2	Co 2	0	0
2	C	4	Total 4	Co 4	0	0
2	D	3	Total 3	Co 3	0	0
2	B	4	Total 4	Co 4	0	0
2	E	4	Total 4	Co 4	0	0
2	F	2	Total 2	Co 2	0	0


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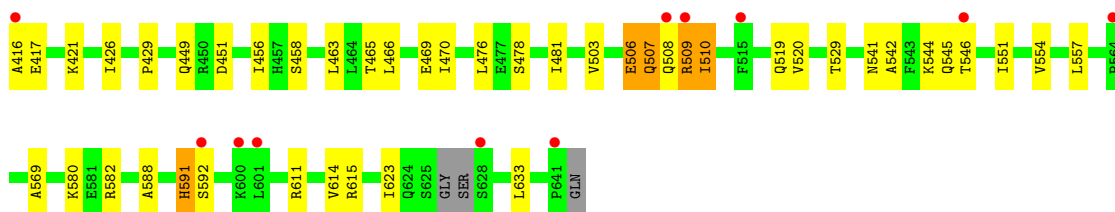
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	2	Total 2	Co 2	0	0
2	H	3	Total 3	Co 3	0	0


- Molecule 3 is water.

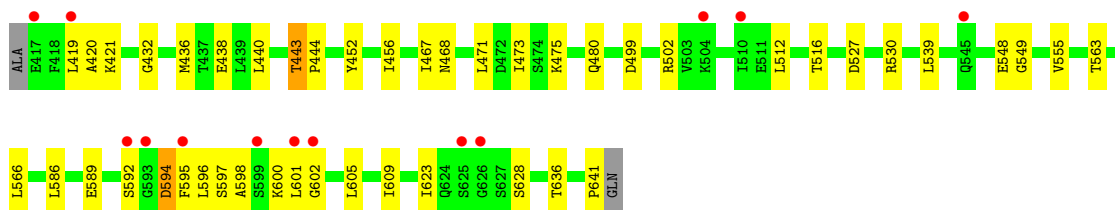
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	29	Total 29	O 29	0	0
3	C	23	Total 23	O 23	0	0
3	D	41	Total 41	O 41	0	0
3	B	33	Total 33	O 33	0	0
3	E	32	Total 32	O 32	0	0
3	F	38	Total 38	O 38	0	0
3	G	22	Total 22	O 22	0	0
3	H	32	Total 32	O 32	0	0

Chain B:  5% 79% 18% ..




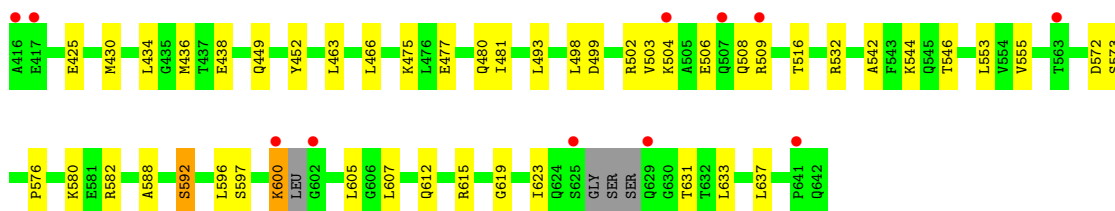
• Molecule 1: RetS (Regulator of Exopolysaccharide and Type III Secretion)

Chain E:  6% 79% 19% ..




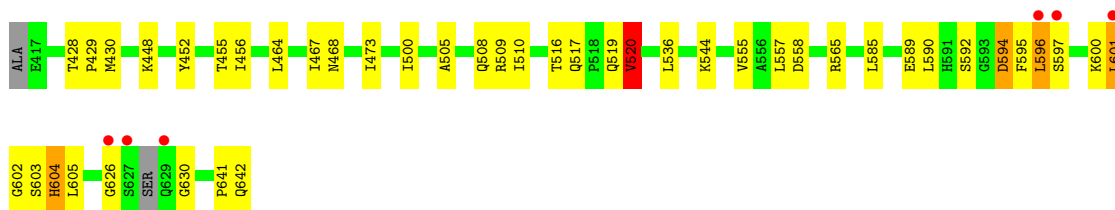
• Molecule 1: RetS (Regulator of Exopolysaccharide and Type III Secretion)

Chain F:  5% 77% 20% ..




• Molecule 1: RetS (Regulator of Exopolysaccharide and Type III Secretion)

Chain G:  3% 80% 17% ..



• Molecule 1: RetS (Regulator of Exopolysaccharide and Type III Secretion)

Chain H:  7% 79% 19% ..





4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	158.71Å 158.71Å 243.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	56.78 – 2.60 56.78 – 2.60	Depositor EDS
% Data completeness (in resolution range)	96.3 (56.78-2.60) 96.3 (56.78-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 2.61Å)	Xtrriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.211 , 0.261 0.211 , 0.256	Depositor DCC
R_{free} test set	4021 reflections (2.73%)	wwPDB-VP
Wilson B-factor (Å ²)	51.2	Xtrriage
Anisotropy	0.226	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14138	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.57% 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

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

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	0.58	0/1745	0.62	0/2360
1	B	0.37	0/1752	0.53	2/2370 (0.1%)
1	C	0.36	0/1756	0.52	2/2375 (0.1%)
1	D	0.60	3/1756 (0.2%)	0.68	5/2375 (0.2%)
1	E	0.26	0/1758	0.49	1/2379 (0.0%)
1	F	0.44	0/1746	0.57	2/2360 (0.1%)
1	G	0.58	2/1760 (0.1%)	0.68	7/2380 (0.3%)
1	H	0.46	1/1759 (0.1%)	0.63	4/2379 (0.2%)
All	All	0.47	6/14032 (0.0%)	0.59	23/18978 (0.1%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	591	HIS	CA-CB	6.89	1.62	1.53
1	D	563	THR	C-N	5.36	1.40	1.33
1	D	517	GLN	C-N	5.30	1.40	1.34
1	D	518	PRO	N-CD	5.17	1.54	1.47
1	G	520	VAL	C-N	5.09	1.40	1.33

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	563	THR	CA-C-N	-8.25	111.28	119.78
1	H	563	THR	C-N-CA	-8.25	111.28	119.78
1	C	549	GLY	N-CA-C	6.67	122.28	110.95
1	H	591	HIS	CA-CB-CG	6.65	120.45	113.80
1	D	560	GLN	N-CA-C	-6.39	101.66	110.35

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	1724	0	1758	48	0
1	B	1731	0	1765	28	0
1	C	1735	0	1768	32	0
1	D	1735	0	1768	35	0
1	E	1736	0	1769	45	0
1	F	1726	0	1756	43	0
1	G	1739	0	1771	52	0
1	H	1738	0	1771	37	0
2	A	2	0	0	0	0
2	B	4	0	0	0	0
2	C	4	0	0	0	0
2	D	3	0	0	0	0
2	E	4	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	3	0	0	0	0
3	A	29	0	0	6	0
3	B	33	0	0	5	0
3	C	23	0	0	2	0
3	D	41	0	0	3	0
3	E	32	0	0	2	0
3	F	38	0	0	2	0
3	G	22	0	0	1	0
3	H	32	0	0	5	0
All	All	14138	0	14126	284	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 10.

The worst 5 of 284 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:627:SER:HB2	1:D:629:GLN:N	1.15	1.45
1:G:448:LYS:HE3	1:G:452:TYR:CZ	1.62	1.32
1:C:627:SER:HA	1:C:629:GLN:N	1.46	1.29

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:591:HIS:NE2	3:H:801:HOH:O	1.69	1.23
1:C:627:SER:CA	1:C:629:GLN:N	2.05	1.20

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	219/227 (96%)	213 (97%)	6 (3%)	0	100	100
1	B	220/227 (97%)	215 (98%)	5 (2%)	0	100	100
1	C	221/227 (97%)	221 (100%)	0	0	100	100
1	D	221/227 (97%)	218 (99%)	2 (1%)	1 (0%)	24	46
1	E	223/227 (98%)	219 (98%)	4 (2%)	0	100	100
1	F	217/227 (96%)	214 (99%)	3 (1%)	0	100	100
1	G	221/227 (97%)	219 (99%)	2 (1%)	0	100	100
1	H	221/227 (97%)	219 (99%)	2 (1%)	0	100	100
All	All	1763/1816 (97%)	1738 (99%)	24 (1%)	1 (0%)	48	70

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	602	GLY

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	192/195 (98%)	186 (97%)	6 (3%)	35	63
1	B	193/195 (99%)	186 (96%)	7 (4%)	31	58
1	C	193/195 (99%)	185 (96%)	8 (4%)	27	54
1	D	193/195 (99%)	182 (94%)	11 (6%)	18	40
1	E	194/195 (100%)	189 (97%)	5 (3%)	40	68
1	F	192/195 (98%)	190 (99%)	2 (1%)	68	86
1	G	194/195 (100%)	187 (96%)	7 (4%)	31	58
1	H	193/195 (99%)	190 (98%)	3 (2%)	55	79
All	All	1544/1560 (99%)	1495 (97%)	49 (3%)	34	62

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	508	GLN
1	E	594	ASP
1	B	509	ARG
1	E	443	THR
1	F	592	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	517	GLN
1	H	519	GLN
1	G	604	HIS
1	E	560	GLN
1	G	508	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 24 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	223/227 (98%)	0.29	17 (7%) 20 16	35, 58, 95, 111	0
1	B	224/227 (98%)	0.27	11 (4%) 35 29	37, 58, 93, 112	0
1	C	225/227 (99%)	0.25	18 (8%) 18 14	32, 56, 103, 126	0
1	D	225/227 (99%)	0.20	13 (5%) 29 23	34, 53, 90, 117	0
1	E	225/227 (99%)	0.20	13 (5%) 29 23	34, 56, 102, 123	0
1	F	223/227 (98%)	0.22	11 (4%) 35 29	36, 57, 93, 109	0
1	G	225/227 (99%)	0.24	6 (2%) 56 50	35, 55, 100, 119	0
1	H	225/227 (99%)	0.34	16 (7%) 22 17	33, 61, 100, 117	0
All	All	1795/1816 (98%)	0.25	105 (5%) 29 23	32, 57, 99, 126	0

The worst 5 of 105 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	626	GLY	6.1
1	C	416	ALA	5.4
1	F	602	GLY	4.9
1	A	549	GLY	4.7
1	H	601	LEU	4.7

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](#)

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	CO	C	704	1/1	0.85	0.11	117,117,117,117	0
2	CO	A	701	1/1	0.86	0.14	132,132,132,132	0
2	CO	F	702	1/1	0.86	0.13	132,132,132,132	0
2	CO	H	702	1/1	0.88	0.10	123,123,123,123	0
2	CO	E	704	1/1	0.91	0.10	109,109,109,109	0
2	CO	D	703	1/1	0.91	0.14	124,124,124,124	0
2	CO	B	704	1/1	0.91	0.09	119,119,119,119	0
2	CO	H	703	1/1	0.92	0.09	57,57,57,57	0
2	CO	G	702	1/1	0.93	0.07	126,126,126,126	0
2	CO	H	701	1/1	0.94	0.06	106,106,106,106	0
2	CO	F	701	1/1	0.95	0.08	97,97,97,97	0
2	CO	B	701	1/1	0.95	0.07	56,56,56,56	0
2	CO	B	703	1/1	0.95	0.06	92,92,92,92	0
2	CO	A	702	1/1	0.96	0.14	89,89,89,89	0
2	CO	E	701	1/1	0.96	0.10	56,56,56,56	0
2	CO	C	702	1/1	0.96	0.11	56,56,56,56	0
2	CO	G	701	1/1	0.97	0.06	72,72,72,72	0
2	CO	E	702	1/1	0.98	0.10	59,59,59,59	0
2	CO	E	703	1/1	0.98	0.04	70,70,70,70	0
2	CO	C	701	1/1	0.98	0.07	64,64,64,64	0
2	CO	D	702	1/1	0.98	0.04	76,76,76,76	0
2	CO	B	702	1/1	0.98	0.11	56,56,56,56	0
2	CO	C	703	1/1	0.99	0.04	63,63,63,63	0
2	CO	D	701	1/1	1.00	0.02	34,34,34,34	0

6.5 Other polymers [i](#)

There are no such residues in this entry.