



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 1, 2026 – 09:28 PM UTC

PDB ID : 1UIJ / pdb_00001uij
Title : Crystal Structure Of Soybean beta-Conglycinin Beta Homotrimer (I122M/K124W)
Authors : Maruyama, N.; Maruyama, Y.; Tsuruki, T.; Okuda, E.; Yoshikawa, M.; Utsumi, S.
Deposited on : 2003-07-16
Resolution : 2.50 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
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

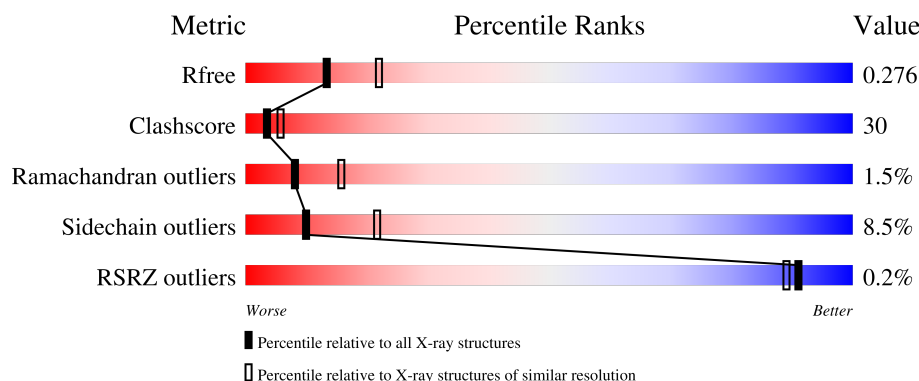
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	416	
1	B	416	
1	C	416	
1	D	416	
1	E	416	

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Mol	Chain	Length	Quality of chain
1	F	416	 A horizontal bar chart showing the quality of chain F. The bar is divided into four segments: green (36%), yellow (42%), orange (6%), and grey (17%).

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 18133 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 beta subunit of beta conglycinin.

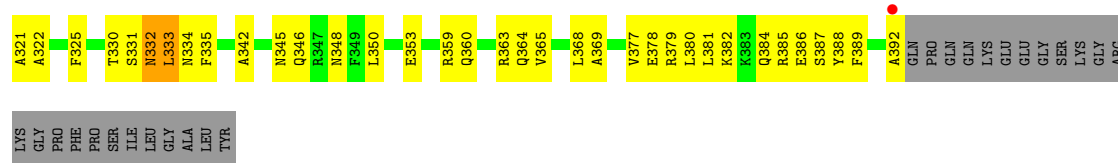
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	377	Total	C	N	O	S	0	0	0
			3087	1947	550	589	1			
1	B	370	Total	C	N	O	S	0	0	0
			3022	1911	538	572	1			
1	C	346	Total	C	N	O	S	0	0	0
			2824	1797	494	532	1			
1	D	377	Total	C	N	O	S	0	0	0
			3087	1947	550	589	1			
1	E	370	Total	C	N	O	S	0	0	0
			3022	1911	538	572	1			
1	F	346	Total	C	N	O	S	0	0	0
			2824	1797	494	532	1			

There are 12 discrepancies between the modelled and reference sequences:

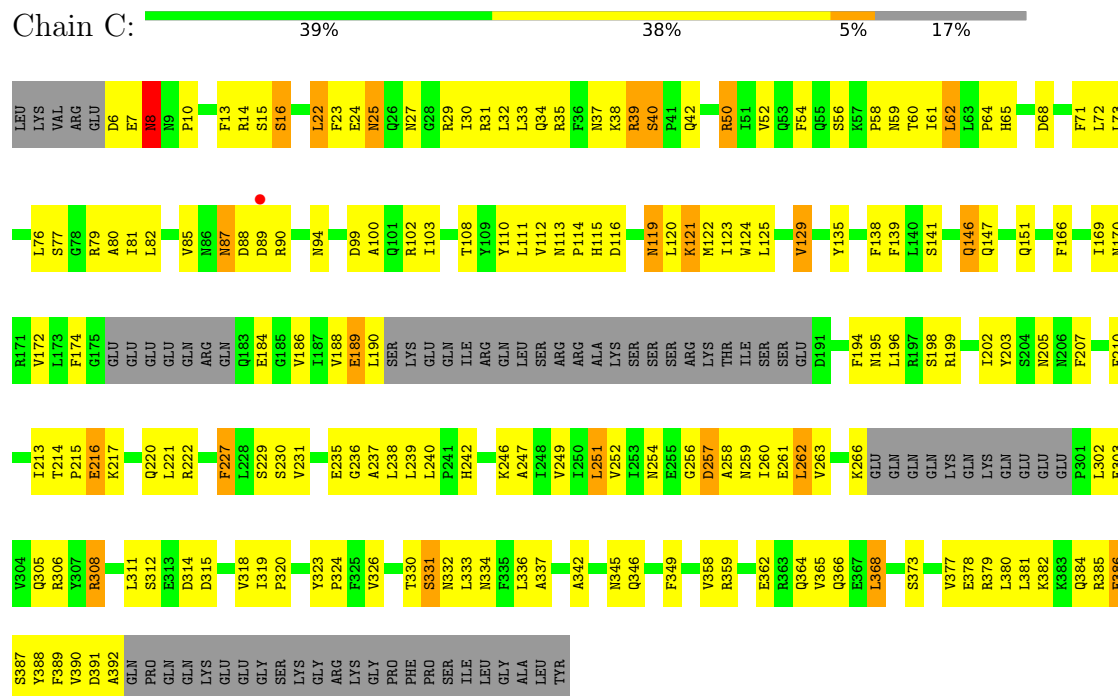
Chain	Residue	Modelled	Actual	Comment	Reference
A	122	MET	ILE	engineered mutation	UNP P25974
A	124	TRP	LYS	engineered mutation	UNP P25974
B	122	MET	ILE	engineered mutation	UNP P25974
B	124	TRP	LYS	engineered mutation	UNP P25974
C	122	MET	ILE	engineered mutation	UNP P25974
C	124	TRP	LYS	engineered mutation	UNP P25974
D	122	MET	ILE	engineered mutation	UNP P25974
D	124	TRP	LYS	engineered mutation	UNP P25974
E	122	MET	ILE	engineered mutation	UNP P25974
E	124	TRP	LYS	engineered mutation	UNP P25974
F	122	MET	ILE	engineered mutation	UNP P25974
F	124	TRP	LYS	engineered mutation	UNP P25974

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	62	Total 62	O 62	0	0
2	B	53	Total 53	O 53	0	0
2	C	19	Total 19	O 19	0	0
2	D	65	Total 65	O 65	0	0
2	E	47	Total 47	O 47	0	0
2	F	21	Total 21	O 21	0	0

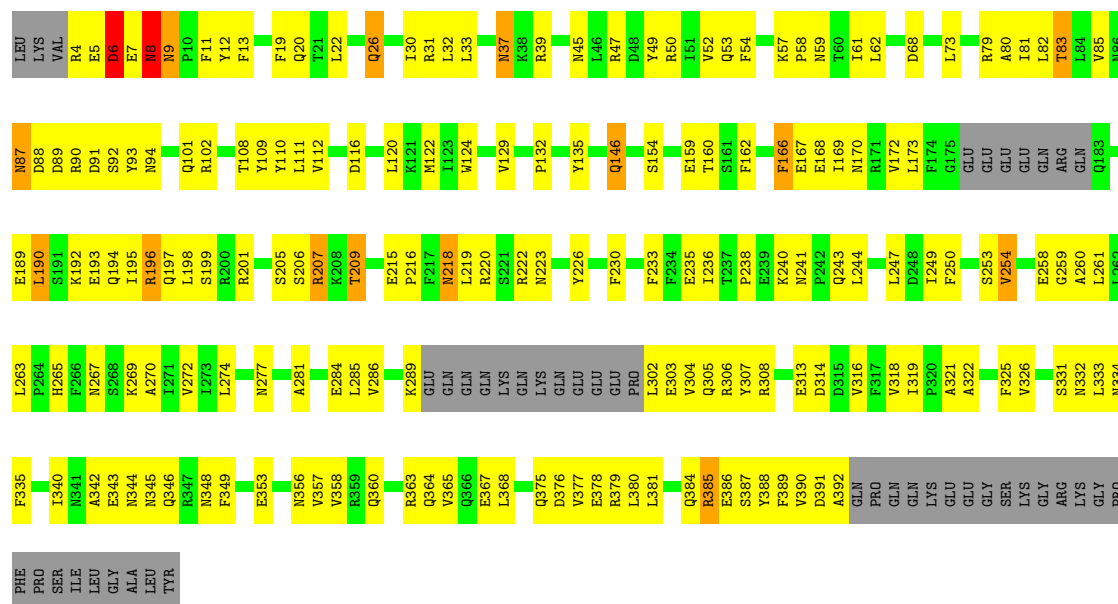


- Molecule 1: beta subunit of beta conglycinin



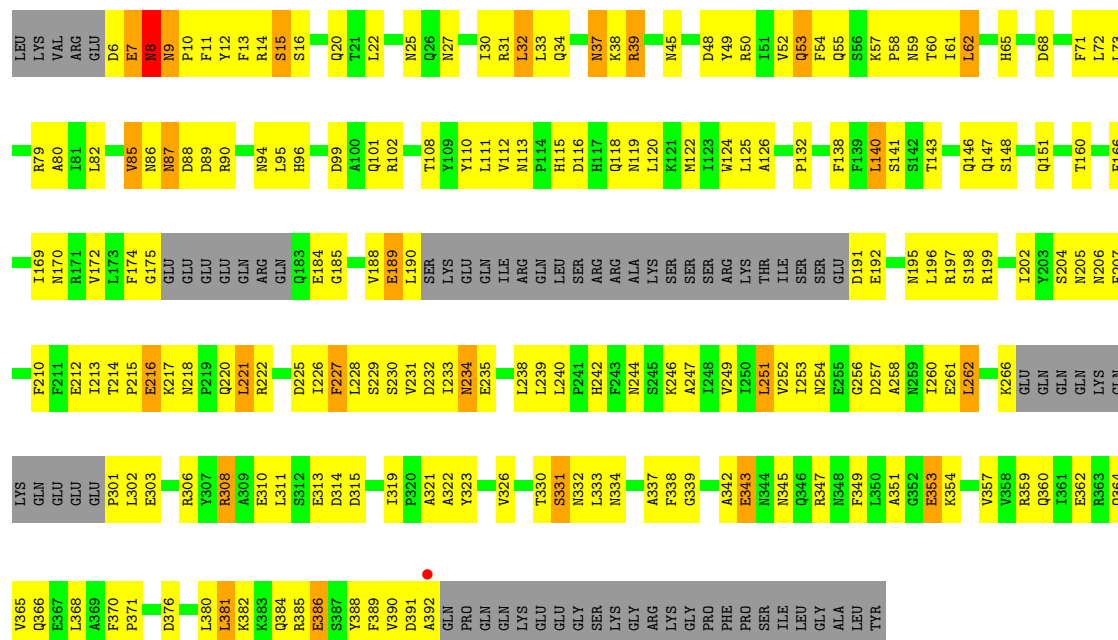
• Molecule 1: beta subunit of beta conglycinin

Chain E:  45% 40% 11%



• Molecule 1: beta subunit of beta conglycinin

Chain F:  36% 42% 6% 17%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	130.26Å 62.58Å 159.01Å 90.00° 90.44° 90.00°	Depositor
Resolution (Å)	8.00 – 2.50 8.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-2.50) 90.9 (8.00-2.50)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 2.50Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.221 , 0.273 0.225 , 0.276	Depositor DCC
R_{free} test set	4277 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	39.4	Xtriage
Anisotropy	0.638	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.47 , 79.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.018 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	18133	wwPDB-VP
Average B, all atoms (Å ²)	43.0	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 43.83 % 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 1.6659e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.46	0/3150	0.97	11/4260 (0.3%)
1	B	0.46	1/3084 (0.0%)	0.97	9/4171 (0.2%)
1	C	0.38	0/2886	0.91	5/3910 (0.1%)
1	D	0.46	0/3150	0.98	8/4260 (0.2%)
1	E	0.45	0/3084	0.96	7/4171 (0.2%)
1	F	0.39	0/2886	0.90	8/3910 (0.2%)
All	All	0.44	1/18240 (0.0%)	0.95	48/24682 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	122	MET	SD-CE	-5.59	1.65	1.79

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	342	ALA	N-CA-C	8.79	123.30	112.23
1	D	26	GLN	N-CA-C	-8.41	103.02	113.28
1	D	172	VAL	N-CA-C	8.23	118.80	110.82
1	D	342	ALA	N-CA-C	7.61	120.64	111.82
1	A	38	LYS	N-CA-C	-7.29	103.33	111.28

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	3087	0	3004	163	0
1	B	3022	0	2950	160	0
1	C	2824	0	2739	206	0
1	D	3087	0	3004	170	0
1	E	3022	0	2950	183	0
1	F	2824	0	2739	216	0
2	A	62	0	0	3	0
2	B	53	0	0	3	0
2	C	19	0	0	0	0
2	D	65	0	0	4	0
2	E	47	0	0	5	0
2	F	21	0	0	3	0
All	All	18133	0	17386	1043	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 30.

The worst 5 of 1043 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:F:111:LEU:HD21	1:F:122:MET:HE1	1.28	1.10
1:B:59:ASN:HD22	1:B:195:ILE:HD12	1.03	1.07
1:E:90:ARG:HH11	1:F:362:GLU:HG2	1.19	1.05
1:E:59:ASN:HD22	1:E:195:ILE:HD12	1.20	1.05
1:B:111:LEU:HD21	1:B:122:MET:HE1	1.06	1.03

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	373/416 (90%)	348 (93%)	21 (6%)	4 (1%)	11 22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	364/416 (88%)	343 (94%)	14 (4%)	7 (2%)	6	11
1	C	338/416 (81%)	306 (90%)	25 (7%)	7 (2%)	5	9
1	D	373/416 (90%)	342 (92%)	27 (7%)	4 (1%)	11	22
1	E	364/416 (88%)	340 (93%)	20 (6%)	4 (1%)	11	22
1	F	338/416 (81%)	295 (87%)	37 (11%)	6 (2%)	6	12
All	All	2150/2496 (86%)	1974 (92%)	144 (7%)	32 (2%)	8	16

5 of 32 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	6	ASP
1	C	7	GLU
1	D	6	ASP
1	E	6	ASP
1	E	201	ARG

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	341/375 (91%)	310 (91%)	31 (9%)	9	19
1	B	334/375 (89%)	303 (91%)	31 (9%)	8	18
1	C	311/375 (83%)	288 (93%)	23 (7%)	13	27
1	D	341/375 (91%)	309 (91%)	32 (9%)	8	18
1	E	334/375 (89%)	309 (92%)	25 (8%)	12	26
1	F	311/375 (83%)	286 (92%)	25 (8%)	11	24
All	All	1972/2250 (88%)	1805 (92%)	167 (8%)	10	22

5 of 167 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	380	LEU

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Mol	Chain	Res	Type
1	F	9	ASN
1	E	9	ASN
1	E	207	ARG
1	F	62	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 185 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	277	ASN
1	E	194	GLN
1	D	341	ASN
1	E	34	GLN
1	E	328	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	377/416 (90%)	-0.66	0 100 100	18, 34, 67, 82	0
1	B	370/416 (88%)	-0.57	2 (0%) 87 85	14, 36, 62, 76	0
1	C	346/416 (83%)	-0.21	1 (0%) 90 87	25, 54, 74, 85	0
1	D	377/416 (90%)	-0.65	0 100 100	17, 32, 67, 80	0
1	E	370/416 (88%)	-0.55	0 100 100	15, 39, 69, 78	0
1	F	346/416 (83%)	-0.26	1 (0%) 90 87	28, 53, 75, 84	0
All	All	2186/2496 (87%)	-0.49	4 (0%) 91 89	14, 40, 70, 85	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	8	ASN	2.5
1	B	392	ALA	2.2
1	F	392	ALA	2.1
1	C	89	ASP	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.