Full wwPDB X-ray Structure Validation Report ⓘ

Jun 25, 2024 – 03:01 AM EDT

PDB ID	:	6FAX
Title	:	Complex of Human CD40 Ectodomain with Lob 7.4 Fab
Authors	:	Orr, C.M.; Tews, I.; Pearson, A.R.
Deposited on	:	2017-12-18
Resolution	:	2.99 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 ⓘ 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:

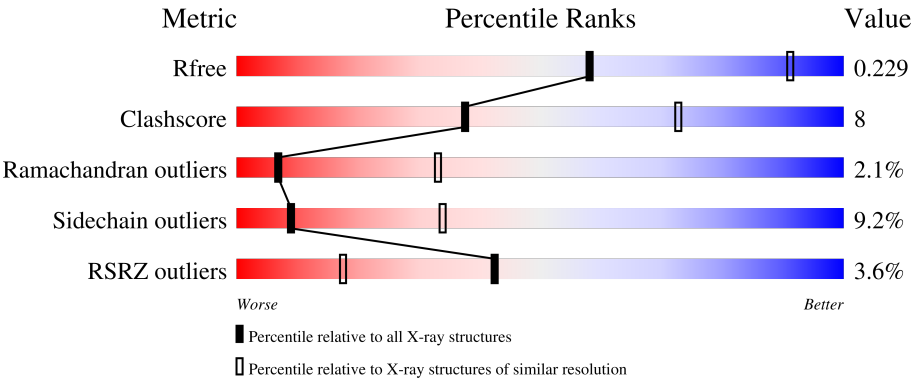
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.99 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	L	214	76% 21% ..
2	H	240	70% 19% 10%
3	R	173	11% 39% 14% 5% 42%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4084 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 Lob 7.4 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	211	Total	C	N	O	S	0	0	0
			1629	1018	269	337	5			

- Molecule 2 is a protein called Lob 7.4 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	216	Total	C	N	O	S	0	0	0
			1648	1044	272	325	7			

- Molecule 3 is a protein called Tumor necrosis factor receptor superfamily member 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	R	100	Total	C	N	O	S	0	1	0
			786	472	134	165	15			

- Molecule 4 is water.

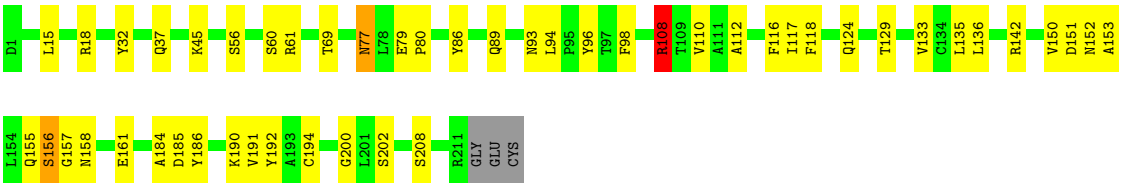
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	L	10	Total	O	0	0
			10	10		
4	H	8	Total	O	0	0
			8	8		
4	R	3	Total	O	0	0
			3	3		

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.

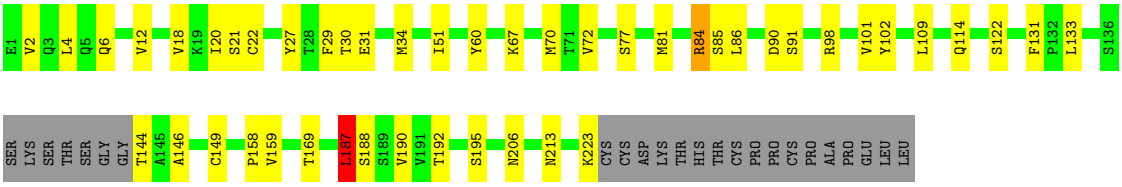
• Molecule 1: Lob 7.4 light chain

Chain L:



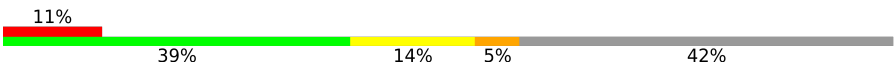
• Molecule 2: Lob 7.4 heavy chain

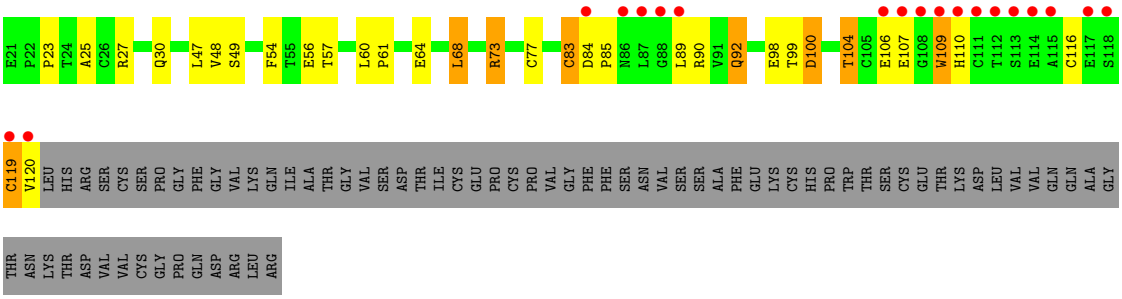
Chain H:



• Molecule 3: Tumor necrosis factor receptor superfamily member 5

Chain R:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	158.75Å 158.75Å 93.62Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	137.48 – 2.99 51.96 – 2.99	Depositor EDS
% Data completeness (in resolution range)	99.7 (137.48-2.99) 99.7 (51.96-2.99)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.12 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.185 , 0.231 0.190 , 0.229	Depositor DCC
R_{free} test set	1319 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å^2)	86.7	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 52.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.014 for -h,-k,l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4084	wwPDB-VP
Average B, all atoms (Å^2)	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.64% 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

5.1 Standard geometry

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	L	0.84	0/1663	1.03	3/2261 (0.1%)
2	H	0.86	0/1688	0.99	2/2296 (0.1%)
3	R	1.03	0/802	1.18	3/1088 (0.3%)
All	All	0.89	0/4153	1.04	8/5645 (0.1%)

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
3	R	0	2

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	R	109	TRP	CA-CB-CG	7.04	127.07	113.70
2	H	187	LEU	CA-CB-CG	6.60	130.49	115.30
1	L	110	VAL	CB-CA-C	-6.51	99.04	111.40
3	R	119	CYS	CA-CB-SG	6.20	125.15	114.00
2	H	81	MET	CG-SD-CE	-6.06	90.50	100.20
1	L	108	ARG	NE-CZ-NH1	6.04	123.32	120.30
1	L	96	TYR	CB-CG-CD1	5.86	124.52	121.00
3	R	73	ARG	NE-CZ-NH1	5.45	123.03	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	R	106	GLU	Peptide
3	R	83	CYS	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	L	1629	0	1573	25	0
2	H	1648	0	1620	27	0
3	R	786	0	699	16	0
4	H	8	0	0	0	0
4	L	10	0	0	1	0
4	R	3	0	0	0	0
All	All	4084	0	3892	61	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 8.

All (61) 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)
3:R:27:ARG:HB2	3:R:30:GLN:HE21	1.63	0.63
2:H:12:VAL:HG21	2:H:86:LEU:HD13	1.84	0.59
1:L:150:VAL:HG13	1:L:192:TYR:CE1	2.38	0.59
2:H:18:VAL:HG12	2:H:86:LEU:HD11	1.85	0.57
2:H:2:VAL:HG23	2:H:27:TYR:CD2	2.39	0.57
1:L:118:PHE:CD2	2:H:133:LEU:HB3	2.40	0.56
3:R:27:ARG:CB	3:R:30:GLN:HE21	2.19	0.56
2:H:67:LYS:CE	2:H:90:ASP:OD2	2.54	0.55
1:L:61:ARG:HD2	1:L:77:ASN:O	2.07	0.55
2:H:67:LYS:HE3	2:H:90:ASP:OD2	2.08	0.53
2:H:29:PHE:HB2	2:H:77:SER:HB2	1.91	0.53
1:L:32:TYR:CE1	3:R:56:GLU:HG2	2.45	0.52
1:L:108:ARG:HG3	1:L:108:ARG:HH11	1.74	0.52
2:H:2:VAL:HG23	2:H:27:TYR:HD2	1.74	0.52
1:L:136:LEU:HD12	1:L:136:LEU:N	2.24	0.52
1:L:156:SER:O	1:L:158:ASN:N	2.42	0.52
1:L:186:TYR:HA	1:L:192:TYR:OH	2.10	0.51
3:R:27:ARG:HB3	3:R:30:GLN:CG	2.41	0.51
1:L:37:GLN:HG3	1:L:86:TYR:CE1	2.45	0.51
1:L:112:ALA:HB2	1:L:200:GLY:O	2.10	0.51
1:L:124:GLN:HG3	2:H:131:PHE:CE2	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:186:TYR:CD1	1:L:192:TYR:CE2	3.00	0.50
1:L:155:GLN:HE21	1:L:155:GLN:N	2.10	0.50
3:R:47:LEU:HD12	3:R:48:VAL:N	2.27	0.50
2:H:29:PHE:HE2	2:H:72:VAL:CG1	2.25	0.49
1:L:108:ARG:HG3	1:L:108:ARG:NH1	2.27	0.49
1:L:202:SER:N	4:L:301:HOH:O	2.46	0.49
2:H:6:GLN:H	2:H:114:GLN:HE22	1.58	0.49
3:R:92:GLN:HE21	3:R:92:GLN:C	2.16	0.49
3:R:104:THR:HA	3:R:116:CYS:SG	2.53	0.49
3:R:68:LEU:HD22	3:R:77:CYS:HA	1.96	0.48
2:H:51:ILE:HD13	2:H:72:VAL:HG23	1.95	0.47
1:L:153:ALA:O	1:L:155:GLN:NE2	2.48	0.47
2:H:67:LYS:HE2	2:H:90:ASP:OD2	2.15	0.47
3:R:60:LEU:HG	3:R:61:PRO:HD2	1.97	0.46
1:L:117:ILE:HD12	1:L:194:CYS:HB2	1.97	0.46
2:H:6:GLN:HA	2:H:21:SER:O	2.16	0.46
1:L:94:LEU:HD21	3:R:54:PHE:HB3	1.98	0.45
1:L:192:TYR:O	1:L:208:SER:HA	2.16	0.45
2:H:12:VAL:CG2	2:H:86:LEU:HD13	2.46	0.45
2:H:102:TYR:HB3	3:R:23:PRO:HD3	1.98	0.45
2:H:84:ARG:HG3	2:H:85:SER:HB2	1.99	0.45
2:H:6:GLN:N	2:H:114:GLN:HE22	2.15	0.44
3:R:109:TRP:HB3	3:R:119:CYS:HB3	1.99	0.44
2:H:29:PHE:CE2	2:H:72:VAL:CG1	3.01	0.44
2:H:187:LEU:C	2:H:187:LEU:HD23	2.38	0.43
1:L:108:ARG:HH11	1:L:108:ARG:CG	2.32	0.43
2:H:4:LEU:HD12	2:H:4:LEU:N	2.32	0.43
2:H:31:GLU:O	2:H:101:VAL:HG12	2.17	0.43
2:H:60:TYR:CE1	2:H:70:MET:CE	3.02	0.42
1:L:135:LEU:HD22	2:H:190:VAL:HG11	2.00	0.42
1:L:89:GLN:HB2	1:L:98:PHE:CD2	2.55	0.42
2:H:98:ARG:O	2:H:109:LEU:HA	2.19	0.41
2:H:4:LEU:HB3	2:H:22:CYS:SG	2.60	0.41
1:L:116:PHE:CD2	2:H:146:ALA:HB3	2.55	0.41
3:R:99:THR:O	3:R:100:ASP:CB	2.68	0.41
3:R:56:GLU:HG3	3:R:57:THR:N	2.36	0.41
3:R:27:ARG:HB3	3:R:30:GLN:HG3	2.03	0.40
1:L:79:GLU:HB3	1:L:80:PRO:HD2	2.03	0.40
1:L:155:GLN:HB3	1:L:158:ASN:OD1	2.21	0.40
3:R:84:ASP:O	3:R:85:PRO:C	2.60	0.40

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	L	209/214 (98%)	192 (92%)	12 (6%)	5 (2%)	6 29
2	H	212/240 (88%)	197 (93%)	13 (6%)	2 (1%)	17 55
3	R	99/173 (57%)	81 (82%)	14 (14%)	4 (4%)	3 17
All	All	520/627 (83%)	470 (90%)	39 (8%)	11 (2%)	7 33

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	56	SER
1	L	157	GLY
2	H	158	PRO
3	R	64	GLU
3	R	107	GLU
1	L	184	ALA
2	H	213	ASN
1	L	151	ASP
3	R	100	ASP
3	R	25	ALA
1	L	77	ASN

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	L	188/190 (99%)	172 (92%)	16 (8%)	10 38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	H	188/209 (90%)	172 (92%)	16 (8%)	10 38
3	R	94/157 (60%)	83 (88%)	11 (12%)	5 22
All	All	470/556 (84%)	427 (91%)	43 (9%)	9 34

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	15	LEU
1	L	18	ARG
1	L	45	LYS
1	L	60	SER
1	L	69	THR
1	L	93	ASN
1	L	108	ARG
1	L	129	THR
1	L	133	VAL
1	L	142	ARG
1	L	152	ASN
1	L	156	SER
1	L	161	GLU
1	L	185	ASP
1	L	190	LYS
1	L	191	VAL
2	H	20	ILE
2	H	30	THR
2	H	34	MET
2	H	84	ARG
2	H	91	SER
2	H	122	SER
2	H	144	THR
2	H	149	CYS
2	H	159	VAL
2	H	169	THR
2	H	187	LEU
2	H	188	SER
2	H	192	THR
2	H	195	SER
2	H	206	ASN
2	H	223	LYS
3	R	49	SER
3	R	68	LEU

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Mol	Chain	Res	Type
3	R	73	ARG
3	R	83	CYS
3	R	89	LEU
3	R	90	ARG
3	R	92	GLN
3	R	98	GLU
3	R	104	THR
3	R	110	HIS
3	R	120	VAL

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

Mol	Chain	Res	Type
1	L	31	ASN
1	L	93	ASN
1	L	155	GLN
1	L	198	HIS
2	H	54	ASN
2	H	114	GLN
3	R	30	GLN
3	R	92	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)

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

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, 95^{th} 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	L	211/214 (98%)	-0.16	0 100 100	56, 78, 108, 130	0
2	H	216/240 (90%)	-0.09	0 100 100	55, 82, 114, 148	0
3	R	100/173 (57%)	0.54	19 (19%) 1 0	62, 97, 166, 192	0
All	All	527/627 (84%)	-0.00	19 (3%) 42 17	55, 82, 131, 192	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	R	114	GLU	3.7
3	R	109	TRP	3.6
3	R	88	GLY	3.5
3	R	84	ASP	3.5
3	R	108	GLY	3.3
3	R	110	HIS	3.1
3	R	119	CYS	3.1
3	R	112	THR	3.0
3	R	120	VAL	2.7
3	R	118	SER	2.7
3	R	86	ASN	2.5
3	R	89	LEU	2.5
3	R	106	GLU	2.5
3	R	107	GLU	2.4
3	R	117	GLU	2.4
3	R	87	LEU	2.3
3	R	111	CYS	2.3
3	R	115	ALA	2.1
3	R	113	SER	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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.