



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:53 PM GMT

PDB ID : 1VL6
Title : Crystal structure of NAD-dependent malic enzyme (TM0542) from *Thermotoga maritima* at 2.61 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2004-07-13
Resolution : 2.61 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
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) : trunk26865

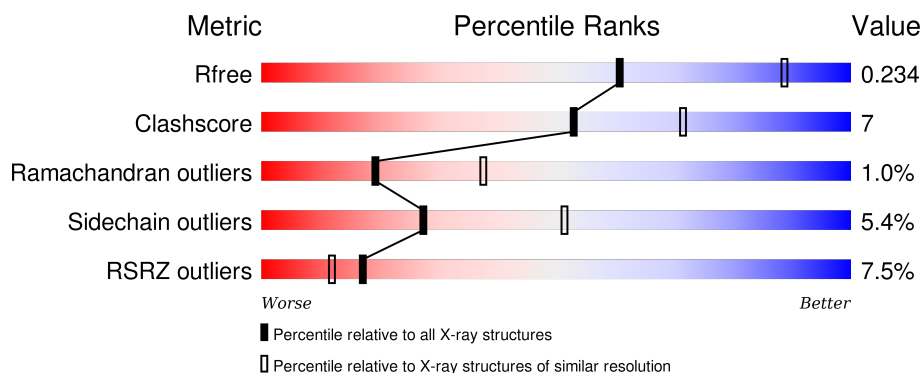
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 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	2700 (2.64-2.60)
Clashscore	102246	3065 (2.64-2.60)
Ramachandran outliers	100387	3015 (2.64-2.60)
Sidechain outliers	100360	3015 (2.64-2.60)
RSRZ outliers	91569	2706 (2.64-2.60)

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 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	A	388	<div> <div>81%</div> <div>14%</div> <div>• • •</div> </div>
1	B	388	<div> <div>13%</div> <div>69%</div> <div>19%</div> <div>• 9%</div> </div>
1	C	388	<div> <div>10%</div> <div>81%</div> <div>15%</div> <div>• •</div> </div>
1	D	388	<div> <div>3%</div> <div>84%</div> <div>11%</div> <div>• •</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11180 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 malate oxidoreductase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	377	Total	C	N	O	S	Se	0	2	0
			2879	1846	481	541	5	6			
1	B	355	Total	C	N	O	S	Se	0	1	0
			2600	1664	434	492	5	5			
1	C	377	Total	C	N	O	S	Se	0	0	0
			2813	1796	468	538	5	6			
1	D	377	Total	C	N	O	S	Se	0	1	0
			2844	1824	470	539	5	6			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MSE	-	LEADER SEQUENCE	UNP Q9WZ12
A	-10	GLY	-	LEADER SEQUENCE	UNP Q9WZ12
A	-9	SER	-	LEADER SEQUENCE	UNP Q9WZ12
A	-8	ASP	-	LEADER SEQUENCE	UNP Q9WZ12
A	-7	LYS	-	LEADER SEQUENCE	UNP Q9WZ12
A	-6	ILE	-	LEADER SEQUENCE	UNP Q9WZ12
A	-5	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
A	-4	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
A	-3	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
A	-2	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
A	-1	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
A	0	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
A	1	VAL	MET	SEE REMARK 999	UNP Q9WZ12
A	6	VAL	ILE	SEE REMARK 999	UNP Q9WZ12
A	84	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
A	147	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
A	272	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
A	322	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
A	336	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
A	362	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
B	-11	MSE	-	LEADER SEQUENCE	UNP Q9WZ12

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-10	GLY	-	LEADER SEQUENCE	UNP Q9WZ12
B	-9	SER	-	LEADER SEQUENCE	UNP Q9WZ12
B	-8	ASP	-	LEADER SEQUENCE	UNP Q9WZ12
B	-7	LYS	-	LEADER SEQUENCE	UNP Q9WZ12
B	-6	ILE	-	LEADER SEQUENCE	UNP Q9WZ12
B	-5	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
B	-4	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
B	-3	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
B	-2	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
B	-1	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
B	0	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
B	1	VAL	MET	SEE REMARK 999	UNP Q9WZ12
B	6	VAL	ILE	SEE REMARK 999	UNP Q9WZ12
B	84	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
B	147	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
B	272	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
B	322	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
B	336	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
B	362	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
C	-11	MSE	-	LEADER SEQUENCE	UNP Q9WZ12
C	-10	GLY	-	LEADER SEQUENCE	UNP Q9WZ12
C	-9	SER	-	LEADER SEQUENCE	UNP Q9WZ12
C	-8	ASP	-	LEADER SEQUENCE	UNP Q9WZ12
C	-7	LYS	-	LEADER SEQUENCE	UNP Q9WZ12
C	-6	ILE	-	LEADER SEQUENCE	UNP Q9WZ12
C	-5	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
C	-4	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
C	-3	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
C	-2	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
C	-1	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
C	0	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
C	1	VAL	MET	SEE REMARK 999	UNP Q9WZ12
C	6	VAL	ILE	SEE REMARK 999	UNP Q9WZ12
C	84	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
C	147	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
C	272	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
C	322	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
C	336	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
C	362	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
D	-11	MSE	-	LEADER SEQUENCE	UNP Q9WZ12
D	-10	GLY	-	LEADER SEQUENCE	UNP Q9WZ12
D	-9	SER	-	LEADER SEQUENCE	UNP Q9WZ12

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-8	ASP	-	LEADER SEQUENCE	UNP Q9WZ12
D	-7	LYS	-	LEADER SEQUENCE	UNP Q9WZ12
D	-6	ILE	-	LEADER SEQUENCE	UNP Q9WZ12
D	-5	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
D	-4	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
D	-3	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
D	-2	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
D	-1	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
D	0	HIS	-	LEADER SEQUENCE	UNP Q9WZ12
D	1	VAL	MET	SEE REMARK 999	UNP Q9WZ12
D	6	VAL	ILE	SEE REMARK 999	UNP Q9WZ12
D	84	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
D	147	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
D	272	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
D	322	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
D	336	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12
D	362	MSE	MET	MODIFIED RESIDUE	UNP Q9WZ12

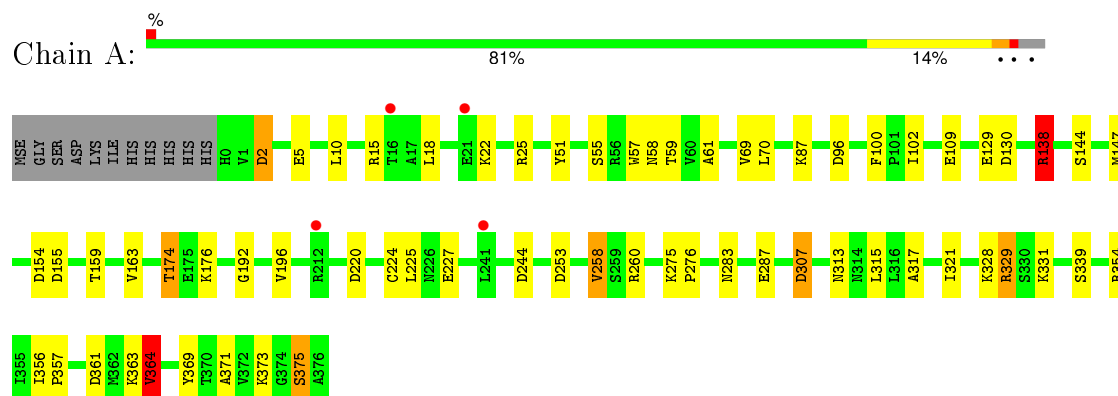
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	29	Total O 29 29	0	0
2	B	1	Total O 1 1	0	0
2	C	2	Total O 2 2	0	0
2	D	12	Total O 12 12	0	0

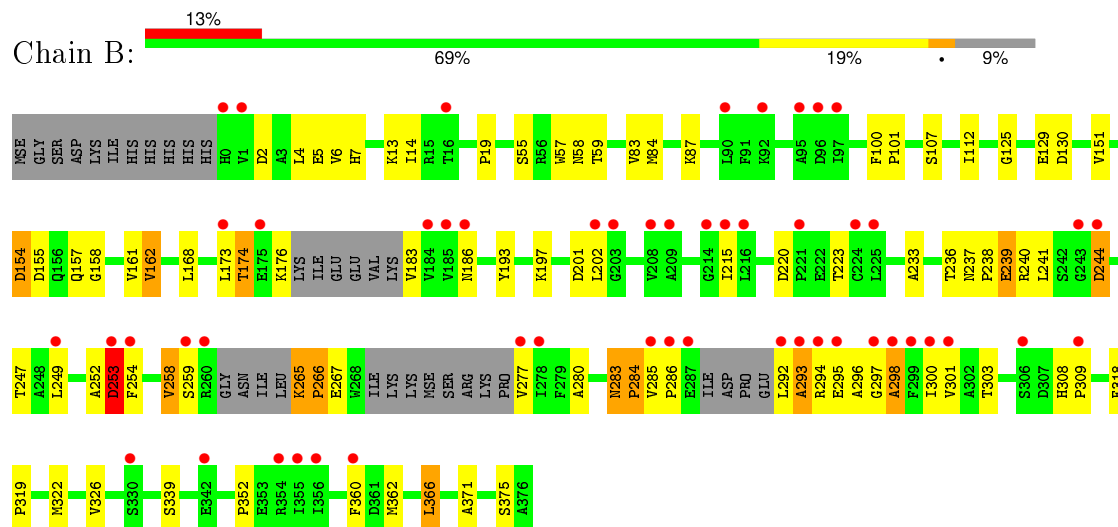
3 Residue-property plots [i](#)

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.

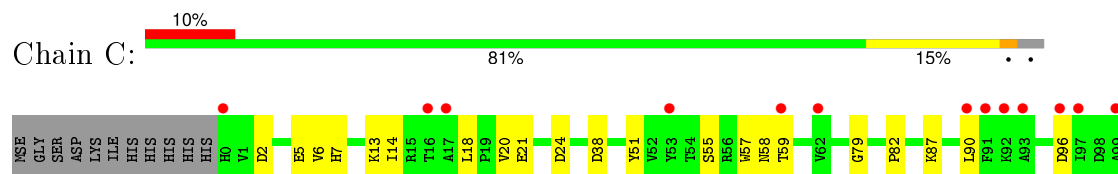
- Molecule 1: malate oxidoreductase

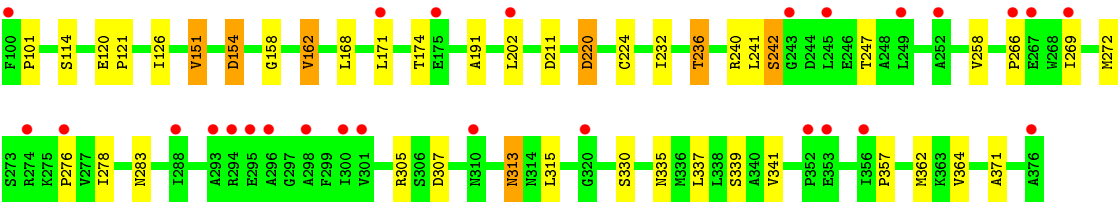


- Molecule 1: malate oxidoreductase

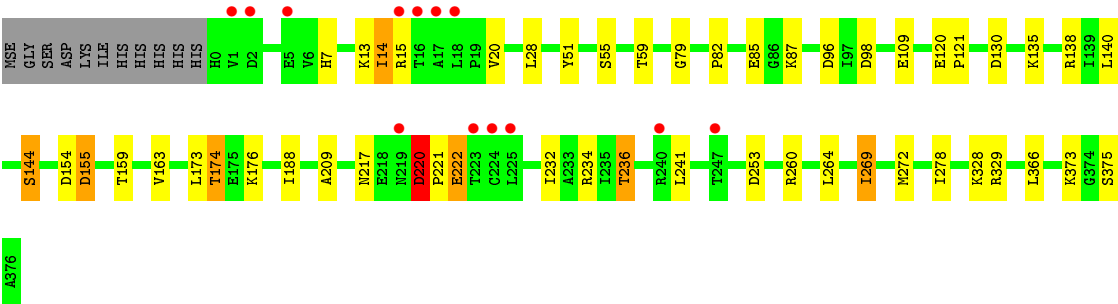
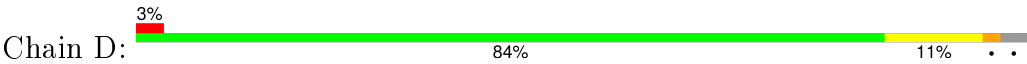


- Molecule 1: malate oxidoreductase





• Molecule 1: malate oxidoreductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	143.96Å 143.96Å 163.43Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.12 – 2.61 47.12 – 2.61	Depositor EDS
% Data completeness (in resolution range)	98.5 (47.12-2.61) 98.5 (47.12-2.61)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.45 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.2.0003	Depositor
R, R_{free}	0.192 , 0.239 0.201 , 0.234	Depositor DCC
R_{free} test set	2904 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	60.8	Xtriage
Anisotropy	0.185	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 67.7	EDS
Estimated twinning fraction	0.022 for h,-h-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Outliers	0 of 57704 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11180	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.29% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	A	0.87	0/2926	0.93	12/3964 (0.3%)
1	B	0.77	1/2640 (0.0%)	0.89	4/3577 (0.1%)
1	C	0.70	1/2860 (0.0%)	0.86	7/3883 (0.2%)
1	D	0.80	0/2890	0.88	6/3917 (0.2%)
All	All	0.79	2/11316 (0.0%)	0.89	29/15341 (0.2%)

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	B	0	2
1	D	0	1
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	253	ASP	CG-OD2	5.88	1.38	1.25
1	C	51	TYR	CD2-CE2	5.50	1.47	1.39

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	155	ASP	CB-CG-OD2	7.85	125.37	118.30
1	A	155	ASP	CB-CG-OD1	-7.66	111.41	118.30
1	C	211	ASP	CB-CG-OD2	7.02	124.62	118.30
1	C	224	CYS	CA-CB-SG	-6.94	101.51	114.00
1	A	307	ASP	CB-CG-OD2	6.58	124.22	118.30
1	A	96	ASP	CB-CG-OD2	6.49	124.14	118.30
1	A	244	ASP	CB-CG-OD2	6.45	124.10	118.30
1	D	155	ASP	CB-CG-OD1	6.38	124.04	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	130	ASP	CB-CG-OD2	6.32	123.99	118.30
1	A	258	VAL	CB-CA-C	6.31	123.40	111.40
1	C	38	ASP	CB-CG-OD2	6.19	123.87	118.30
1	D	98	ASP	CB-CG-OD2	6.13	123.81	118.30
1	B	284	PRO	N-CD-CG	-6.02	94.17	103.20
1	D	220	ASP	CB-CG-OD2	5.99	123.69	118.30
1	C	18	LEU	CA-CB-CG	5.90	128.88	115.30
1	D	96	ASP	CB-CG-OD2	5.86	123.57	118.30
1	A	138	ARG	NE-CZ-NH1	5.66	123.13	120.30
1	A	253	ASP	CB-CG-OD2	5.64	123.38	118.30
1	D	253	ASP	CB-CG-OD2	5.61	123.35	118.30
1	A	130	ASP	CB-CG-OD2	5.54	123.29	118.30
1	C	96	ASP	CB-CG-OD2	5.51	123.26	118.30
1	A	224	CYS	CA-CB-SG	-5.38	104.32	114.00
1	C	24	ASP	CB-CG-OD2	5.37	123.13	118.30
1	B	244	ASP	CB-CG-OD2	5.24	123.02	118.30
1	B	130	ASP	CB-CG-OD2	5.24	123.02	118.30
1	C	307	ASP	CB-CG-OD2	5.20	122.98	118.30
1	B	201	ASP	CB-CG-OD2	5.18	122.96	118.30
1	A	329	ARG	NE-CZ-NH2	-5.11	117.74	120.30
1	A	364	VAL	CB-CA-C	-5.03	101.85	111.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	258	VAL	Peptide
1	B	283	ASN	Peptide
1	D	220	ASP	Peptide

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	A	2879	0	2907	40	0
1	B	2600	0	2550	58	0
1	C	2813	0	2779	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2844	0	2850	29	0
2	A	29	0	0	0	0
2	B	1	0	0	0	0
2	C	2	0	0	0	0
2	D	12	0	0	0	0
All	All	11180	0	11086	146	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 7.

All (146) 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:B:362:MSE:CE	1:B:362:MSE:SE	2.14	1.46
1:A:100[A]:PHE:CE2	1:B:100[A]:PHE:CD1	2.50	0.99
1:A:100[A]:PHE:CE2	1:B:100[A]:PHE:CE1	2.51	0.98
1:A:100[A]:PHE:CD2	1:B:100[A]:PHE:CD1	2.58	0.92
1:C:272:MSE:HE1	1:C:278:ILE:HD11	1.52	0.91
1:A:100[A]:PHE:CD2	1:B:100[A]:PHE:CE1	2.61	0.88
1:A:100[A]:PHE:HE2	1:B:100[A]:PHE:CE1	1.92	0.87
1:C:232:ILE:O	1:C:236:THR:HB	1.76	0.86
1:A:361:ASP:O	1:A:364:VAL:HG23	1.77	0.85
1:D:232:ILE:O	1:D:236:THR:HB	1.84	0.78
1:A:328:LYS:HE3	1:A:375:SER:O	1.84	0.76
1:D:188:ILE:CD1	1:D:209:ALA:HB1	2.17	0.74
1:D:269:ILE:HA	1:D:272:MSE:HE2	1.70	0.74
1:D:272:MSE:HE1	1:D:278:ILE:HD11	1.71	0.71
1:A:100[A]:PHE:CE2	1:B:100[A]:PHE:HD1	2.08	0.70
1:C:269:ILE:HA	1:C:272:MSE:HE2	1.73	0.69
1:C:266:PRO:HA	1:C:269:ILE:HD12	1.75	0.68
1:D:174:THR:HG22	1:D:176:LYS:H	1.58	0.68
1:A:100[A]:PHE:HD2	1:B:100[A]:PHE:CE1	2.12	0.68
1:A:174:THR:HG22	1:A:176:LYS:H	1.58	0.67
1:B:249:LEU:O	1:B:252:ALA:HB2	1.96	0.66
1:B:183:VAL:HG13	1:B:254:PHE:HB2	1.78	0.65
1:A:100[A]:PHE:CE2	1:B:100[A]:PHE:HE1	2.11	0.64
1:A:100[A]:PHE:HE2	1:B:100[A]:PHE:HE1	1.42	0.63
1:C:171:LEU:O	1:C:174:THR:HG22	1.98	0.63
1:D:220:ASP:N	1:D:220:ASP:OD1	2.32	0.63
1:D:7:HIS:NE2	1:D:13:LYS:HE2	2.15	0.62
1:C:191:ALA:HB3	1:C:258:VAL:HG11	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:7:HIS:NE2	1:B:13:LYS:HE2	2.15	0.61
1:C:2:ASP:HB2	1:C:5:GLU:OE1	1.99	0.61
1:B:280:ALA:HB1	1:B:286:PRO:CD	2.31	0.60
1:B:280:ALA:HB1	1:B:286:PRO:HD2	1.84	0.59
1:A:2:ASP:HB3	1:A:5:GLU:H	1.68	0.59
1:D:188:ILE:HD11	1:D:209:ALA:HB1	1.84	0.59
1:B:233:ALA:HA	1:B:236:THR:HG22	1.84	0.59
1:B:293:ALA:O	1:B:301:VAL:HG11	2.01	0.59
1:B:157:GLN:O	1:B:161:VAL:HG23	2.01	0.58
1:D:188:ILE:HG22	1:D:188:ILE:O	2.03	0.58
1:C:14:ILE:HD11	1:C:101:PRO:CD	2.34	0.57
1:B:158:GLY:O	1:B:162:VAL:HG23	2.05	0.57
1:D:7:HIS:NE2	1:D:13:LYS:CE	2.69	0.56
1:D:55:SER:O	1:D:59:THR:HG23	2.06	0.56
1:A:363:LYS:HG3	1:D:366:LEU:HD13	1.88	0.56
1:C:313:ASN:OD1	1:C:313:ASN:C	2.44	0.55
1:C:158:GLY:O	1:C:162:VAL:HG23	2.05	0.55
1:A:147:MSE:O	1:A:331:LYS:NZ	2.39	0.54
1:B:366:LEU:HD21	1:C:362:MSE:HB2	1.90	0.54
1:A:109:GLU:OE2	1:A:138:ARG:HD2	2.07	0.53
1:C:168:LEU:HD21	1:C:202:LEU:HD13	1.91	0.53
1:B:174:THR:HG23	1:B:176:LYS:NZ	2.24	0.52
1:B:292:LEU:C	1:B:294:ARG:N	2.61	0.52
1:D:109:GLU:HG2	1:D:138:ARG:NH1	2.25	0.52
1:A:10:LEU:HD22	1:B:19:PRO:HB3	1.92	0.51
1:D:217:ASN:ND2	1:D:241:LEU:O	2.43	0.51
1:B:339:SER:HB3	1:B:371:ALA:HB1	1.93	0.51
1:D:328:LYS:HE2	1:D:375:SER:O	2.10	0.51
1:B:215:ILE:O	1:B:223:THR:HG21	2.10	0.51
1:D:328:LYS:NZ	1:D:373:LYS:O	2.43	0.51
1:A:260:ARG:O	1:A:287:GLU:HG3	2.11	0.51
1:B:308:HIS:HB3	1:B:309:PRO:HD2	1.92	0.50
1:C:14:ILE:HD11	1:C:101:PRO:HD3	1.93	0.50
1:B:239:GLU:O	1:B:241:LEU:N	2.45	0.50
1:B:107:SER:HA	1:B:112:ILE:HD11	1.93	0.50
1:A:87:LYS:NZ	1:A:154:ASP:OD1	2.39	0.49
1:B:2:ASP:OD1	1:B:4:LEU:HB2	2.12	0.49
1:A:328:LYS:CE	1:A:375:SER:O	2.57	0.49
1:C:313:ASN:OD1	1:C:315:LEU:HB3	2.13	0.49
1:B:55:SER:O	1:B:59:THR:HG23	2.13	0.49
1:A:100[A]:PHE:HD2	1:B:100[A]:PHE:CD1	2.25	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:269:ILE:HG23	1:D:272:MSE:CE	2.42	0.48
1:A:339:SER:HB3	1:A:371:ALA:HB1	1.95	0.48
1:C:7:HIS:NE2	1:C:13:LYS:HE3	2.28	0.48
1:A:57:TRP:CE3	1:A:58:ASN:HB2	2.49	0.48
1:C:7:HIS:NE2	1:C:13:LYS:CE	2.77	0.48
1:B:318:PHE:CG	1:B:319:PRO:HD3	2.49	0.48
1:C:339:SER:HB3	1:C:371:ALA:HB1	1.94	0.48
1:B:173:LEU:HD22	1:B:352:PRO:HD3	1.96	0.48
1:B:186:ASN:HD22	1:B:259:SER:HB3	1.79	0.47
1:C:126:ILE:HB	1:C:151:VAL:HB	1.96	0.47
1:D:220:ASP:O	1:D:222:GLU:N	2.48	0.47
1:A:356:ILE:HB	1:A:357:PRO:HD2	1.96	0.47
1:B:294:ARG:O	1:B:296:ALA:N	2.45	0.47
1:B:83:VAL:HB	1:B:84:MSE:HE2	1.97	0.46
1:B:57:TRP:CE3	1:B:58:ASN:HB2	2.51	0.46
1:A:317:ALA:O	1:A:321:ILE:HG13	2.16	0.46
1:A:55:SER:O	1:A:59:THR:HG23	2.16	0.46
1:A:354:ARG:HG3	1:A:354:ARG:HH11	1.80	0.46
1:A:61:ALA:HB1	1:A:102:ILE:HD12	1.97	0.45
1:A:100[A]:PHE:HE2	1:B:100[A]:PHE:CD1	2.09	0.45
1:C:272:MSE:CE	1:C:278:ILE:HD11	2.35	0.45
1:C:2:ASP:HB3	1:C:5:GLU:H	1.82	0.45
1:C:272:MSE:HE3	1:C:276:PRO:HB2	1.98	0.45
1:B:252:ALA:O	1:B:253:ASP:C	2.54	0.45
1:A:51:TYR:CZ	1:A:329:ARG:HD3	2.52	0.45
1:B:193:TYR:OH	1:B:197:LYS:NZ	2.45	0.45
1:C:220:ASP:OD2	1:C:242:SER:OG	2.35	0.45
1:B:168:LEU:HD21	1:B:202:LEU:HD13	1.99	0.44
1:D:120:GLU:N	1:D:121:PRO:CD	2.80	0.44
1:C:87:LYS:NZ	1:C:154:ASP:OD1	2.50	0.44
1:B:100[B]:PHE:CD1	1:B:101:PRO:HD2	2.53	0.44
1:A:87:LYS:HE3	1:A:129:GLU:OE1	2.17	0.44
1:B:2:ASP:HB3	1:B:5:GLU:HB2	1.99	0.44
1:C:313:ASN:OD1	1:C:313:ASN:O	2.36	0.43
1:C:55:SER:O	1:C:59:THR:HG23	2.18	0.43
1:B:277:VAL:HG13	1:B:300:ILE:HB	2.00	0.43
1:B:220:ASP:O	1:B:223:THR:OG1	2.31	0.43
1:C:90:LEU:HD21	1:D:28:LEU:HD22	2.01	0.43
1:B:280:ALA:HB1	1:B:286:PRO:HG2	2.01	0.43
1:B:100[B]:PHE:HA	1:B:101:PRO:HD3	1.93	0.43
1:D:79:GLY:O	1:D:82:PRO:HD2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:357:PRO:HB2	1:C:364:VAL:HG21	2.00	0.43
1:D:14:ILE:HG13	1:D:85:GLU:HG2	1.99	0.43
1:D:174:THR:HG23	1:D:176:LYS:HG3	2.01	0.43
1:A:354:ARG:HG3	1:A:354:ARG:NH1	2.34	0.43
1:D:140:LEU:O	1:D:144:SER:OG	2.35	0.42
1:B:174:THR:CG2	1:B:176:LYS:NZ	2.82	0.42
1:C:337:LEU:O	1:C:341:VAL:HG23	2.19	0.42
1:C:272:MSE:HE3	1:C:276:PRO:CB	2.50	0.42
1:B:129:GLU:OE1	1:B:154:ASP:OD2	2.37	0.42
1:B:303:THR:HG21	1:B:308:HIS:HB2	2.02	0.42
1:B:322:MSE:HE3	1:B:326:VAL:HG23	2.01	0.42
1:A:275:LYS:N	1:A:276:PRO:CD	2.83	0.42
1:B:265:LYS:HB3	1:B:266:PRO:HD2	2.02	0.42
1:B:297:GLY:O	1:B:298:ALA:HB3	2.20	0.42
1:C:171:LEU:HA	1:C:174:THR:HG22	2.02	0.41
1:A:369:TYR:OH	1:A:373:LYS:HD2	2.20	0.41
1:D:159:THR:O	1:D:163:VAL:HG23	2.21	0.41
1:B:125:GLY:HA3	1:B:322:MSE:HE1	2.03	0.41
1:A:313:ASN:HD21	1:A:315:LEU:HB3	1.85	0.41
1:C:79:GLY:O	1:C:82:PRO:HD2	2.21	0.41
1:A:192:GLY:O	1:A:196:VAL:HG23	2.21	0.41
1:B:254:PHE:CD2	1:B:277:VAL:HB	2.55	0.41
1:B:7:HIS:NE2	1:B:13:LYS:CE	2.83	0.41
1:C:20:VAL:HG12	1:C:21:GLU:N	2.36	0.41
1:A:57:TRP:CD2	1:A:58:ASN:HB2	2.56	0.41
1:B:57:TRP:CD2	1:B:58:ASN:HB2	2.56	0.41
1:A:174:THR:CG2	1:A:176:LYS:HD2	2.51	0.41
1:D:51:TYR:CZ	1:D:329:ARG:HD3	2.55	0.41
1:D:269:ILE:CA	1:D:272:MSE:HE2	2.47	0.41
1:D:109:GLU:HG3	1:D:135:LYS:HB2	2.02	0.41
1:B:174:THR:CG2	1:B:176:LYS:CE	2.99	0.40
1:A:159:THR:O	1:A:163:VAL:HG23	2.21	0.40
1:C:120:GLU:N	1:C:121:PRO:CD	2.84	0.40
1:A:69:VAL:O	1:A:70:LEU:C	2.58	0.40
1:D:173:LEU:HA	1:D:173:LEU:HD23	1.83	0.40
1:C:57:TRP:CD2	1:C:58:ASN:HB2	2.57	0.40

There are no symmetry-related clashes.

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	A	377/388 (97%)	361 (96%)	16 (4%)	0	100	100
1	B	346/388 (89%)	311 (90%)	23 (7%)	12 (4%)	4	6
1	C	375/388 (97%)	357 (95%)	18 (5%)	0	100	100
1	D	376/388 (97%)	356 (95%)	18 (5%)	2 (0%)	34	58
All	All	1474/1552 (95%)	1385 (94%)	75 (5%)	14 (1%)	19	41

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	267	GLU
1	B	284	PRO
1	B	238	PRO
1	B	240	ARG
1	B	295	GLU
1	B	239	GLU
1	B	244	ASP
1	B	293	ALA
1	B	266	PRO
1	B	253	ASP
1	B	298	ALA
1	D	222	GLU
1	B	237	ASN
1	D	221	PRO

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	304/316 (96%)	288 (95%)	16 (5%)	28	52
1	B	265/316 (84%)	248 (94%)	17 (6%)	22	42
1	C	294/316 (93%)	278 (95%)	16 (5%)	27	51
1	D	297/316 (94%)	283 (95%)	14 (5%)	32	59
All	All	1160/1264 (92%)	1097 (95%)	63 (5%)	27	51

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ASP
1	A	15	ARG
1	A	18	LEU
1	A	22	LYS
1	A	25	ARG
1	A	138	ARG
1	A	144	SER
1	A	174	THR
1	A	220	ASP
1	A	225	LEU
1	A	227	GLU
1	A	258	VAL
1	A	283	ASN
1	A	307	ASP
1	A	364	VAL
1	A	375	SER
1	B	6	VAL
1	B	14	ILE
1	B	87	LYS
1	B	151	VAL
1	B	154	ASP
1	B	155	ASP
1	B	162	VAL
1	B	174	THR
1	B	247	THR
1	B	253	ASP
1	B	258	VAL
1	B	265	LYS
1	B	283	ASN
1	B	285	VAL
1	B	360	PHE
1	B	366	LEU
1	B	375	SER

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Mol	Chain	Res	Type
1	C	6	VAL
1	C	114	SER
1	C	151	VAL
1	C	154	ASP
1	C	162	VAL
1	C	220	ASP
1	C	236	THR
1	C	240	ARG
1	C	241	LEU
1	C	242	SER
1	C	247	THR
1	C	283	ASN
1	C	305	ARG
1	C	313	ASN
1	C	330	SER
1	C	335	ASN
1	D	14	ILE
1	D	15	ARG
1	D	20	VAL
1	D	87	LYS
1	D	144	SER
1	D	154	ASP
1	D	155	ASP
1	D	174	THR
1	D	220	ASP
1	D	234	ARG
1	D	236	THR
1	D	260	ARG
1	D	264	LEU
1	D	269	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	308	HIS
1	A	313	ASN
1	A	335	ASN
1	B	186	ASN
1	C	194	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 carbohydrates 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, 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	371/388 (95%)	-0.02	4 (1%) 82 79	56, 64, 75, 86	0
1	B	350/388 (90%)	0.68	52 (14%) 3 1	41, 63, 73, 82	0
1	C	371/388 (95%)	0.61	40 (10%) 8 4	54, 63, 72, 90	0
1	D	371/388 (95%)	0.09	13 (3%) 48 40	55, 64, 75, 95	0
All	All	1463/1552 (94%)	0.34	109 (7%) 17 12	41, 64, 75, 95	0

All (109) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	243	GLY	9.9
1	C	0	HIS	7.4
1	B	300	ILE	7.0
1	B	244	ASP	6.0
1	C	269	ILE	5.8
1	C	376	ALA	5.8
1	B	216	LEU	5.1
1	B	306	SER	5.1
1	B	225	LEU	4.6
1	B	295	GLU	4.2
1	D	224	CYS	4.1
1	C	293	ALA	4.0
1	D	16	THR	4.0
1	B	299	PHE	3.9
1	B	297	GLY	3.8
1	B	278	ILE	3.8
1	C	352	PRO	3.7
1	B	298	ALA	3.7
1	B	294	ARG	3.7
1	C	353	GLU	3.6
1	B	286	PRO	3.6

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Mol	Chain	Res	Type	RSRZ
1	C	300	ILE	3.5
1	B	277	VAL	3.5
1	D	223	THR	3.5
1	B	175	GLU	3.5
1	C	93	ALA	3.5
1	D	1	VAL	3.5
1	C	96	ASP	3.5
1	D	17	ALA	3.4
1	A	21	GLU	3.4
1	C	99	ALA	3.4
1	B	292	LEU	3.3
1	B	342	GLU	3.3
1	B	287	GLU	3.3
1	B	184	VAL	3.3
1	C	245	LEU	3.2
1	B	260	ARG	3.1
1	B	355	ILE	3.1
1	C	53	TYR	3.1
1	C	100	PHE	3.1
1	B	209	ALA	3.1
1	B	254	PHE	3.1
1	D	15	ARG	3.1
1	B	293	ALA	3.1
1	B	215	ILE	3.1
1	B	1	VAL	3.1
1	D	18	LEU	3.0
1	C	296	ALA	3.0
1	B	208	VAL	3.0
1	C	356	ILE	3.0
1	B	0	HIS	2.9
1	B	92	LYS	2.9
1	C	252	ALA	2.9
1	C	295	GLU	2.9
1	B	90	LEU	2.8
1	B	221	PRO	2.8
1	D	5	GLU	2.8
1	D	2	ASP	2.8
1	C	16	THR	2.7
1	C	301	VAL	2.7
1	C	92	LYS	2.7
1	B	301	VAL	2.7
1	C	274	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	309	PRO	2.6
1	B	203	GLY	2.6
1	B	202	LEU	2.6
1	B	16	THR	2.5
1	D	247	THR	2.5
1	B	285	VAL	2.5
1	C	298	ALA	2.5
1	B	354	ARG	2.5
1	A	241	LEU	2.4
1	B	186	ASN	2.4
1	C	90	LEU	2.4
1	C	320	GLY	2.4
1	B	259	SER	2.4
1	D	219	ASN	2.4
1	B	185	VAL	2.4
1	B	330	SER	2.4
1	C	310	ASN	2.4
1	C	243	GLY	2.4
1	C	294	ARG	2.3
1	D	240	ARG	2.3
1	C	62	VAL	2.3
1	B	214	GLY	2.3
1	C	17	ALA	2.3
1	C	288	ILE	2.3
1	C	59	THR	2.3
1	C	276	PRO	2.2
1	B	97	ILE	2.2
1	C	97	ILE	2.1
1	C	249	LEU	2.1
1	B	356	ILE	2.1
1	B	360	PHE	2.1
1	C	91	PHE	2.1
1	B	95	ALA	2.1
1	B	224	CYS	2.1
1	A	16	THR	2.1
1	B	249	LEU	2.1
1	C	266	PRO	2.1
1	C	202	LEU	2.1
1	C	267	GLU	2.1
1	B	173	LEU	2.1
1	B	253	ASP	2.1
1	C	175	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	225	LEU	2.0
1	A	212	ARG	2.0
1	B	96	ASP	2.0
1	C	171	LEU	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 carbohydrates 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.