Full wwPDB X-ray Structure Validation Report (i)

Nov 14, 2023 – 09:47 PM JST

PDB ID	:	6AH7
Title	:	D45W/H226G mutant of marine bacterial prolidase
Authors	:	Jian, Y.; Yunzhu, X.; Lijuan, L.
Deposited on	:	2018-08-17
Resolution	:	2.38 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 (i) 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 (i)) were used in the production of this report:

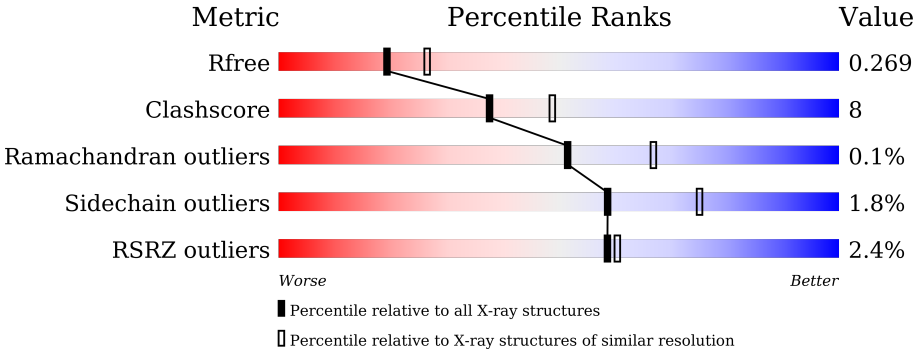
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.38 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	5509 (2.40-2.36)
Clashscore	141614	6082 (2.40-2.36)
Ramachandran outliers	138981	5973 (2.40-2.36)
Sidechain outliers	138945	5975 (2.40-2.36)
RSRZ outliers	127900	5397 (2.40-2.36)

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	A	448	.% 84% 12% • •
1	B	448	2% 83% 14% • •
1	C	448	4% 82% 15% • •
1	D	448	2% 83% 14% • •

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 14924 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 Xaa-Pro dipeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	439	3573	2297	608	654	14	0	1	0
1	B	439	3604	2315	618	657	14	0	4	0
1	C	439	3584	2303	612	655	14	0	2	0
1	D	439	3584	2303	612	655	14	0	2	0

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	45	TRP	ASP	engineered mutation	UNP A0A1I7CHQ2
A	226	GLY	HIS	engineered mutation	UNP A0A1I7CHQ2
A	441	LEU	-	expression tag	UNP A0A1I7CHQ2
A	442	ASP	-	expression tag	UNP A0A1I7CHQ2
A	443	HIS	-	expression tag	UNP A0A1I7CHQ2
A	444	HIS	-	expression tag	UNP A0A1I7CHQ2
A	445	HIS	-	expression tag	UNP A0A1I7CHQ2
A	446	HIS	-	expression tag	UNP A0A1I7CHQ2
A	447	HIS	-	expression tag	UNP A0A1I7CHQ2
A	448	HIS	-	expression tag	UNP A0A1I7CHQ2
B	45	TRP	ASP	engineered mutation	UNP A0A1I7CHQ2
B	226	GLY	HIS	engineered mutation	UNP A0A1I7CHQ2
B	441	LEU	-	expression tag	UNP A0A1I7CHQ2
B	442	ASP	-	expression tag	UNP A0A1I7CHQ2
B	443	HIS	-	expression tag	UNP A0A1I7CHQ2
B	444	HIS	-	expression tag	UNP A0A1I7CHQ2
B	445	HIS	-	expression tag	UNP A0A1I7CHQ2
B	446	HIS	-	expression tag	UNP A0A1I7CHQ2
B	447	HIS	-	expression tag	UNP A0A1I7CHQ2
B	448	HIS	-	expression tag	UNP A0A1I7CHQ2
C	45	TRP	ASP	engineered mutation	UNP A0A1I7CHQ2

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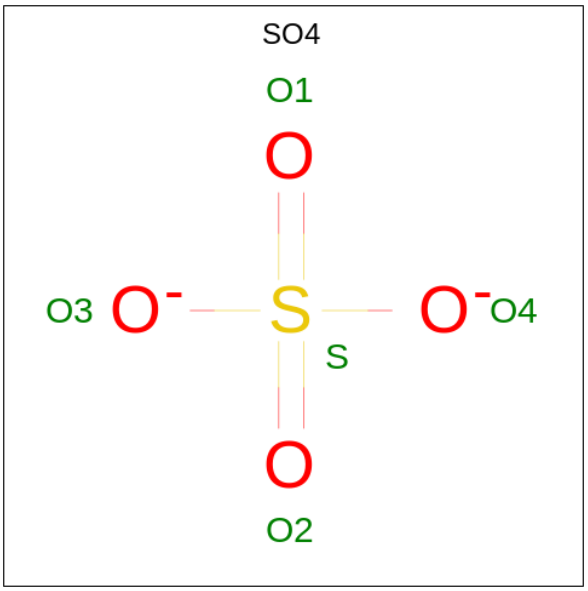
Chain	Residue	Modelled	Actual	Comment	Reference
C	226	GLY	HIS	engineered mutation	UNP A0A1I7CHQ2
C	441	LEU	-	expression tag	UNP A0A1I7CHQ2
C	442	ASP	-	expression tag	UNP A0A1I7CHQ2
C	443	HIS	-	expression tag	UNP A0A1I7CHQ2
C	444	HIS	-	expression tag	UNP A0A1I7CHQ2
C	445	HIS	-	expression tag	UNP A0A1I7CHQ2
C	446	HIS	-	expression tag	UNP A0A1I7CHQ2
C	447	HIS	-	expression tag	UNP A0A1I7CHQ2
C	448	HIS	-	expression tag	UNP A0A1I7CHQ2
D	45	TRP	ASP	engineered mutation	UNP A0A1I7CHQ2
D	226	GLY	HIS	engineered mutation	UNP A0A1I7CHQ2
D	441	LEU	-	expression tag	UNP A0A1I7CHQ2
D	442	ASP	-	expression tag	UNP A0A1I7CHQ2
D	443	HIS	-	expression tag	UNP A0A1I7CHQ2
D	444	HIS	-	expression tag	UNP A0A1I7CHQ2
D	445	HIS	-	expression tag	UNP A0A1I7CHQ2
D	446	HIS	-	expression tag	UNP A0A1I7CHQ2
D	447	HIS	-	expression tag	UNP A0A1I7CHQ2
D	448	HIS	-	expression tag	UNP A0A1I7CHQ2

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mn		
2	A	2	2	2	0	0
2	B	2	2	2	0	0
2	C	2	2	2	0	0
2	D	2	2	2	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Na 1 1	0	0

- Molecule 5 is water.

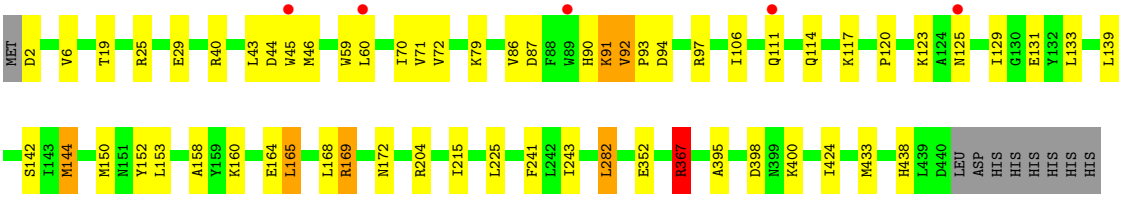
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	156	Total O 156 156	0	0
5	B	160	Total O 160 160	0	0
5	C	110	Total O 110 110	0	0
5	D	139	Total O 139 139	0	0

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.

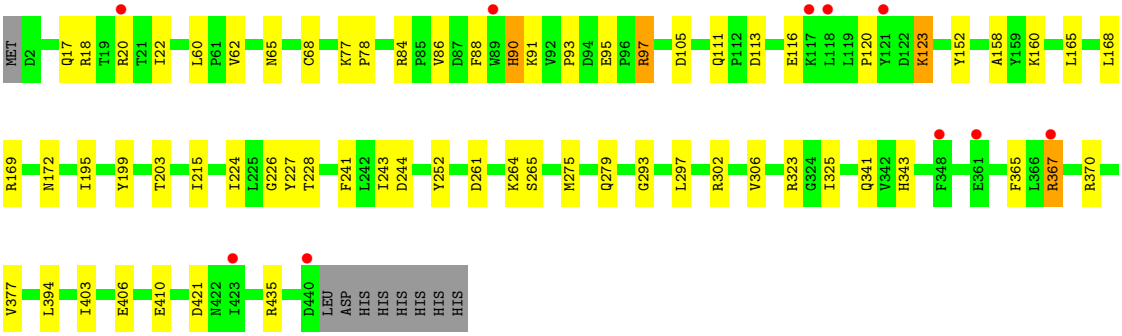
• Molecule 1: Xaa-Pro dipeptidase

Chain A:



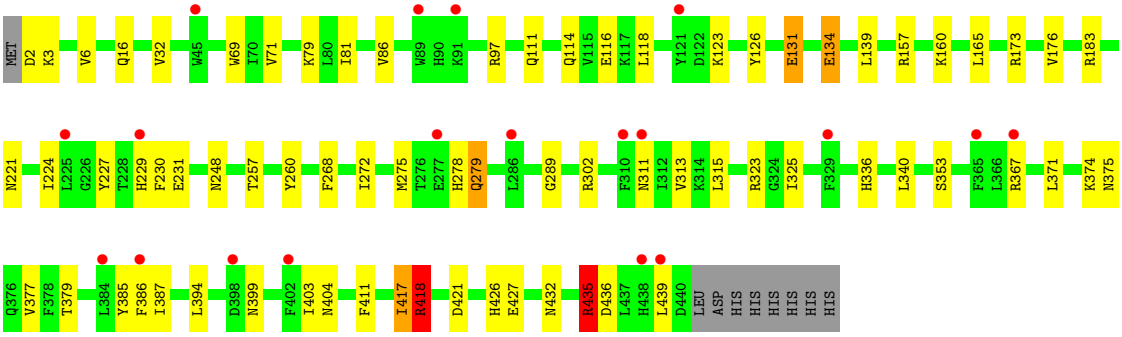
• Molecule 1: Xaa-Pro dipeptidase

Chain B:



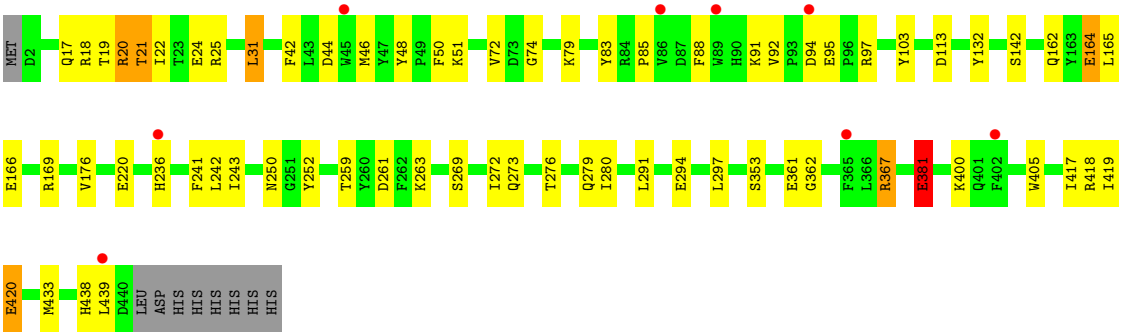
• Molecule 1: Xaa-Pro dipeptidase

Chain C:



• Molecule 1: Xaa-Pro dipeptidase

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α, β, γ	183.63Å 183.63Å 371.31Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	67.29 – 2.38 67.29 – 2.38	Depositor EDS
% Data completeness (in resolution range)	97.8 (67.29-2.38) 94.8 (67.29-2.38)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.21 (at 2.37Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.233 , 0.269 0.236 , 0.269	Depositor DCC
R_{free} test set	4428 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å^2)	41.0	Xtriage
Anisotropy	0.643	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 37.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.53$, $< L^2 > = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	14924	wwPDB-VP
Average B, all atoms (Å^2)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.24% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, MN, NA

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	0.49	1/3677 (0.0%)	0.56	0/4993
1	B	0.39	0/3710	0.53	0/5037
1	C	0.41	1/3688 (0.0%)	0.52	1/5007 (0.0%)
1	D	0.50	6/3688 (0.2%)	0.57	1/5007 (0.0%)
All	All	0.45	8/14763 (0.1%)	0.55	2/20044 (0.0%)

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	A	0	3
1	B	0	4
1	C	0	2
1	D	0	5
All	All	0	14

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	164	GLU	CD-OE1	-8.61	1.16	1.25
1	D	381	GLU	CD-OE2	7.96	1.34	1.25
1	D	420	GLU	CD-OE2	7.31	1.33	1.25
1	D	381	GLU	CD-OE1	-6.64	1.18	1.25
1	A	164	GLU	CD-OE1	-6.63	1.18	1.25
1	D	166	GLU	CD-OE2	-6.60	1.18	1.25
1	D	164	GLU	CD-OE2	-6.22	1.18	1.25
1	C	131	GLU	CD-OE2	-5.58	1.19	1.25

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	21	THR	N-CA-CB	6.26	122.20	110.30
1	C	435	ARG	CB-CA-C	5.07	120.53	110.40

There are no chirality outliers.

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	169	ARG	Sidechain
1	A	367	ARG	Sidechain
1	A	97	ARG	Sidechain
1	B	18	ARG	Sidechain
1	B	367	ARG	Sidechain
1	B	90[B]	HIS	Mainchain
1	B	97	ARG	Sidechain
1	C	367	ARG	Sidechain
1	C	418	ARG	Sidechain
1	D	18	ARG	Sidechain
1	D	20	ARG	Sidechain
1	D	25	ARG	Sidechain
1	D	367	ARG	Sidechain
1	D	418	ARG	Sidechain

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	3573	0	3429	52	0
1	B	3604	0	3453	59	0
1	C	3584	0	3441	58	0
1	D	3584	0	3441	58	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	1	0
3	A	5	0	0	1	0
4	A	1	0	0	0	0
5	A	156	0	0	7	0
5	B	160	0	0	5	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	110	0	0	7	2
5	D	139	0	0	10	1
All	All	14924	0	13764	217	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 8.

All (217) 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:381:GLU:CD	1:D:420:GLU:OE2	1.81	1.18
1:D:381:GLU:HG3	1:D:420:GLU:HG3	1.27	1.15
1:D:381:GLU:HG3	1:D:420:GLU:CG	1.78	1.12
1:D:261:ASP:OD1	1:D:263:LYS:O	1.79	1.00
1:A:19:THR:HG21	1:A:72:VAL:HG12	1.52	0.88
1:D:381:GLU:HG3	1:D:420:GLU:CD	1.94	0.88
1:D:272:ILE:HG12	1:D:417:ILE:HD12	1.58	0.83
1:D:85:PRO:O	1:D:92:VAL:CG1	2.30	0.79
1:D:381:GLU:OE1	5:D:601:HOH:O	1.99	0.78
1:D:17:GLN:O	1:D:20:ARG:O	2.01	0.77
1:D:381:GLU:CG	1:D:420:GLU:CD	2.52	0.77
1:C:71:VAL:HG12	1:C:79:LYS:HB2	1.67	0.75
1:D:85:PRO:O	1:D:92:VAL:HG11	1.87	0.75
1:D:381:GLU:OE2	1:D:420:GLU:OE2	2.03	0.75
1:D:20:ARG:NE	1:D:24:GLU:OE1	2.19	0.73
1:C:32:VAL:HG22	1:C:71:VAL:HG23	1.71	0.73
1:B:394:LEU:HD21	1:B:403:ILE:HD11	1.70	0.72
1:A:131:GLU:OE1	5:A:601:HOH:O	2.06	0.72
1:D:94:ASP:HB3	1:D:97:ARG:NH2	2.03	0.72
1:D:31:LEU:HD12	1:D:72:VAL:HG23	1.70	0.72
1:A:133:LEU:O	1:A:144:MET:HE1	1.90	0.71
1:B:22:ILE:HD13	1:B:152:TYR:CG	2.26	0.70
1:D:94:ASP:HB3	1:D:97:ARG:HH22	1.53	0.70
1:D:44:ASP:OD2	5:D:602:HOH:O	2.09	0.69
1:A:106:ILE:O	5:A:602:HOH:O	2.09	0.69
1:A:398:ASP:OD2	5:A:603:HOH:O	2.11	0.68
1:D:19:THR:HG23	1:D:31:LEU:HD11	1.73	0.68
1:B:168:LEU:HD23	1:B:252:TYR:HB3	1.75	0.68
1:C:2:ASP:OD1	1:C:3:LYS:N	2.27	0.68
1:C:248:ASN:OD1	5:C:601:HOH:O	2.12	0.67
1:C:157:ARG:CZ	1:C:340:LEU:HD12	2.25	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:438:HIS:NE2	1:D:438:HIS:NE2	2.43	0.67
1:C:157:ARG:NE	1:C:340:LEU:HD12	2.10	0.66
1:B:60:LEU:HD13	1:B:62:VAL:CG2	2.25	0.66
1:C:426:HIS:O	5:C:602:HOH:O	2.12	0.66
1:D:48:TYR:OH	5:D:603:HOH:O	2.09	0.65
1:C:71:VAL:CG1	1:C:79:LYS:HD2	2.27	0.65
1:B:265:SER:O	5:B:601:HOH:O	2.13	0.65
1:D:250:ASN:OD1	5:D:604:HOH:O	2.14	0.65
1:D:103:TYR:O	5:D:605:HOH:O	2.15	0.64
1:C:126:TYR:O	5:C:603:HOH:O	2.14	0.64
1:D:420:GLU:OE2	2:D:501:MN:MN	1.55	0.64
1:C:311:ASN:OD1	1:C:404:ASN:ND2	2.30	0.64
1:C:16:GLN:NE2	5:C:606:HOH:O	2.30	0.64
1:D:95:GLU:O	1:D:97:ARG:NH1	2.31	0.64
1:D:85:PRO:O	1:D:92:VAL:HG12	1.98	0.63
1:A:19:THR:HG21	1:A:72:VAL:CG1	2.26	0.63
1:A:87:ASP:HB2	1:A:90:HIS:ND1	2.14	0.62
1:B:60:LEU:HD13	1:B:62:VAL:HG23	1.81	0.62
1:C:221:ASN:HA	1:C:224:ILE:HD12	1.81	0.62
1:A:111:GLN:HB2	1:A:114:GLN:NE2	2.14	0.62
1:A:367:ARG:H	1:A:367:ARG:CD	2.11	0.62
1:A:86:VAL:O	1:A:86:VAL:HG23	1.99	0.62
1:B:90[B]:HIS:ND1	1:B:91:LYS:N	2.45	0.62
1:B:199:TYR:O	1:B:203:THR:HG23	1.99	0.62
1:B:120:PRO:O	1:B:123:LYS:NZ	2.33	0.61
1:B:394:LEU:HD23	1:B:403:ILE:HD13	1.82	0.61
1:D:361:GLU:HG2	1:D:362:GLY:N	2.16	0.61
1:B:111:GLN:NE2	1:B:113:ASP:OD1	2.28	0.61
1:D:269:SER:O	1:D:273:GLN:HG2	2.00	0.61
1:A:91:LYS:HE2	1:B:228:THR:H	1.65	0.61
1:B:394:LEU:CD2	1:B:403:ILE:HD11	2.31	0.61
1:A:44:ASP:OD2	5:A:604:HOH:O	2.16	0.60
1:A:133:LEU:HB3	1:A:144:MET:HE2	1.82	0.60
1:C:111:GLN:OE1	1:C:114:GLN:OE1	2.20	0.60
1:D:381:GLU:CD	1:D:420:GLU:CD	2.61	0.60
1:B:394:LEU:CD2	1:B:403:ILE:CD1	2.80	0.59
1:C:421:ASP:OD2	1:C:435:ARG:NE	2.35	0.59
1:B:86:VAL:HG22	1:B:86:VAL:O	2.02	0.59
1:B:323:ARG:HB2	1:B:325:ILE:HD12	1.86	0.58
1:A:92:VAL:HG12	1:A:92:VAL:O	2.04	0.58
1:C:435:ARG:HG2	1:C:435:ARG:HH21	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:381:GLU:CG	1:D:420:GLU:OE2	2.51	0.58
1:C:375:ASN:OD1	5:C:604:HOH:O	2.18	0.57
1:B:95:GLU:O	1:B:97:ARG:HG3	2.04	0.57
1:C:394:LEU:HD11	1:C:403:ILE:HD11	1.85	0.57
1:C:435:ARG:HH21	1:C:435:ARG:CG	2.16	0.57
1:A:29:GLU:HG3	1:A:125:ASN:HB2	1.87	0.56
1:A:367:ARG:NH1	5:A:607:HOH:O	2.39	0.56
1:D:31:LEU:HD12	1:D:72:VAL:CG2	2.35	0.56
1:A:2:ASP:O	1:A:6:VAL:HG23	2.06	0.56
1:C:116:GLU:OE2	1:C:123:LYS:NZ	2.37	0.56
1:C:257:THR:HG21	1:C:418:ARG:HG2	1.88	0.56
1:D:279:GLN:HG3	1:D:419:ILE:HB	1.88	0.55
1:B:158:ALA:HA	5:B:634:HOH:O	2.07	0.55
1:D:20:ARG:HB2	1:D:74:GLY:HA3	1.88	0.54
1:B:22:ILE:HD13	1:B:152:TYR:CB	2.37	0.54
1:B:160:LYS:HD2	5:B:647:HOH:O	2.08	0.54
1:C:374:LYS:HD3	1:C:427:GLU:HB2	1.90	0.54
1:A:424:ILE:HD11	1:A:433:MET:HE3	1.89	0.54
1:B:172:ASN:ND2	5:B:606:HOH:O	2.39	0.54
1:C:313:VAL:HG12	1:C:315:LEU:HB2	1.90	0.53
1:D:291:LEU:HB3	5:D:625:HOH:O	2.09	0.53
1:D:294:GLU:HA	1:D:297:LEU:HD12	1.90	0.53
1:D:276:THR:O	1:D:280:ILE:HG13	2.08	0.53
1:D:164:GLU:HG2	1:D:252:TYR:OH	2.09	0.53
1:A:169:ARG:N	1:A:433:MET:HE2	2.24	0.53
1:A:59:TRP:CZ2	1:A:72:VAL:HG11	2.43	0.53
1:B:111:GLN:HE21	1:B:113:ASP:CG	2.12	0.53
1:D:164:GLU:HG2	1:D:252:TYR:CZ	2.44	0.52
1:A:43:LEU:O	1:B:341:GLN:NE2	2.41	0.52
1:A:367:ARG:H	1:A:367:ARG:HD2	1.73	0.52
1:C:71:VAL:HG11	1:C:79:LYS:HD2	1.91	0.52
1:D:132:TYR:OH	5:D:606:HOH:O	2.17	0.52
1:A:60:LEU:HD21	1:A:70:ILE:HD11	1.91	0.52
1:A:152:TYR:HD2	1:A:153:LEU:HD12	1.74	0.51
1:C:229:HIS:NE2	1:C:231:GLU:OE1	2.37	0.51
1:A:133:LEU:HB3	1:A:144:MET:CE	2.40	0.51
1:D:51:LYS:HA	5:D:614:HOH:O	2.09	0.51
1:D:400:LYS:HG2	1:D:405:TRP:HE1	1.75	0.51
1:B:275:MET:HE1	1:B:306:VAL:HG21	1.93	0.51
1:C:229:HIS:ND1	1:C:230:PHE:N	2.58	0.51
1:A:395:ALA:O	1:A:400:LYS:HE2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:77:LYS:HG3	1:B:78:PRO:HD2	1.94	0.50
1:B:394:LEU:HD21	1:B:403:ILE:CD1	2.40	0.50
1:C:2:ASP:O	1:C:6:VAL:HG13	2.11	0.50
1:B:60:LEU:CD1	1:B:62:VAL:HB	2.42	0.50
1:B:261:ASP:OD2	1:B:264:LYS:N	2.46	0.49
1:C:173:ARG:NH2	1:C:173:ARG:HB2	2.28	0.49
1:C:221:ASN:OD1	1:D:91:LYS:NZ	2.35	0.48
1:C:435:ARG:CG	1:C:435:ARG:NH2	2.73	0.48
1:A:91:LYS:HE3	1:B:227:TYR:HA	1.95	0.48
1:C:323:ARG:HD2	1:C:399:ASN:OD1	2.13	0.48
1:C:385:TYR:OH	1:C:418:ARG:HD3	2.13	0.48
1:C:69:TRP:HB2	1:C:81:ILE:HB	1.96	0.48
1:C:131:GLU:HB2	1:D:42:PHE:CD1	2.49	0.48
1:C:176:VAL:HG13	1:C:439:LEU:HD13	1.94	0.48
1:A:120:PRO:O	1:A:123:LYS:HE3	2.13	0.48
1:C:279:GLN:HE21	1:C:279:GLN:HB2	1.49	0.48
1:A:6:VAL:HG21	1:D:162:GLN:HG3	1.95	0.48
1:B:215:ILE:HB	1:B:244:ASP:HB3	1.96	0.48
1:C:323:ARG:HB2	1:C:325:ILE:HD13	1.96	0.47
1:D:241:PHE:CZ	1:D:243:ILE:HB	2.49	0.47
1:A:123:LYS:NZ	1:A:139:LEU:O	2.36	0.47
1:A:215:ILE:HA	5:A:640:HOH:O	2.12	0.47
1:D:83:TYR:CZ	1:D:85:PRO:HG3	2.49	0.47
1:B:394:LEU:HD23	1:B:403:ILE:CD1	2.45	0.47
1:C:173:ARG:HB2	1:C:173:ARG:HH21	1.80	0.47
1:A:160:LYS:HB2	1:A:165:LEU:HD13	1.95	0.47
1:C:289:GLY:C	1:C:371:LEU:HD11	2.35	0.47
1:D:242:LEU:HD23	1:D:259:THR:OG1	2.15	0.46
1:C:116:GLU:C	1:C:118:LEU:H	2.18	0.46
1:C:268:PHE:CE2	1:C:272:ILE:HD11	2.50	0.46
1:D:361:GLU:HG2	1:D:362:GLY:H	1.79	0.46
1:C:387:ILE:HG21	1:D:88:PHE:HB2	1.96	0.46
1:D:381:GLU:OE1	1:D:420:GLU:OE2	2.28	0.46
1:C:3:LYS:O	1:C:6:VAL:HG22	2.16	0.46
1:B:168:LEU:HD12	1:B:377:VAL:HG21	1.98	0.46
1:D:169:ARG:N	1:D:433:MET:HE1	2.31	0.45
1:D:176:VAL:HG13	1:D:439:LEU:HB2	1.99	0.45
1:A:91:LYS:O	1:A:93:PRO:HD3	2.17	0.45
1:C:160:LYS:HG3	1:C:377:VAL:HG23	1.99	0.45
1:B:84:ARG:NH1	1:B:84:ARG:HG2	2.31	0.45
1:B:302:ARG:O	1:B:306:VAL:HG23	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:394:LEU:CD2	1:B:403:ILE:HD13	2.45	0.45
1:C:123:LYS:O	5:C:603:HOH:O	2.20	0.45
1:D:50:PHE:HA	5:D:624:HOH:O	2.17	0.45
1:A:424:ILE:HD11	1:A:433:MET:CE	2.47	0.45
1:A:133:LEU:HA	1:A:144:MET:HE3	1.99	0.44
1:C:160:LYS:HB2	1:C:165:LEU:CD1	2.47	0.44
1:B:406:GLU:O	1:B:410:GLU:HG3	2.17	0.44
1:C:116:GLU:HG2	1:C:139:LEU:HD22	1.99	0.44
1:C:183:ARG:HG3	1:C:260:TYR:CE2	2.52	0.44
1:D:22:ILE:HD12	1:D:22:ILE:HA	1.85	0.44
1:A:129:ILE:HD12	1:A:150:MET:HE3	1.99	0.44
1:B:195:ILE:HG21	1:B:241:PHE:CZ	2.53	0.44
1:C:275:MET:HG2	1:C:417:ILE:HD11	2.00	0.44
1:A:225:LEU:HD12	1:B:88:PHE:HE1	1.83	0.44
1:C:386:PHE:CE2	1:C:411:PHE:HB3	2.53	0.44
1:A:45:TRP:CZ3	1:B:343[B]:HIS:HB3	2.53	0.43
1:C:353:SER:HA	5:C:607:HOH:O	2.18	0.43
1:B:84:ARG:HG3	1:B:93:PRO:HG2	2.00	0.43
1:B:84:ARG:CG	1:B:84:ARG:HH11	2.31	0.43
1:C:227:TYR:CZ	1:C:229:HIS:HB3	2.53	0.43
1:A:168:LEU:C	1:A:433:MET:HE2	2.39	0.43
1:B:60:LEU:HD13	1:B:62:VAL:HB	2.01	0.43
1:A:215:ILE:O	1:A:243:ILE:HA	2.18	0.43
1:C:403:ILE:HD12	1:C:403:ILE:N	2.34	0.43
1:D:353:SER:O	5:D:609:HOH:O	2.22	0.43
1:C:336:HIS:CE1	1:C:379:THR:HG21	2.54	0.42
1:A:165:LEU:HD12	1:A:165:LEU:HA	1.89	0.42
1:A:158:ALA:HA	5:A:626:HOH:O	2.20	0.42
1:A:241:PHE:CZ	1:A:243:ILE:HB	2.54	0.42
1:B:279:GLN:OE1	1:B:435:ARG:NH1	2.49	0.42
1:A:40:ARG:NH2	3:A:503:SO4:O1	2.53	0.42
1:B:65:ASN:ND2	1:B:68:CYS:SG	2.93	0.42
1:B:226:GLY:O	1:B:228:THR:HG23	2.20	0.42
1:B:323:ARG:HB2	1:B:325:ILE:CD1	2.48	0.42
1:A:91:LYS:H	1:A:91:LYS:HG2	1.29	0.42
1:B:168:LEU:CD2	1:B:252:TYR:HB3	2.47	0.41
1:B:293:GLY:O	1:B:297:LEU:HD13	2.20	0.41
1:C:315:LEU:HD12	1:C:315:LEU:HA	1.86	0.41
1:D:220:GLU:CD	1:D:220:GLU:H	2.23	0.41
1:B:88:PHE:CD1	1:B:88:PHE:C	2.94	0.41
1:A:165:LEU:HG	1:A:424:ILE:HD13	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:77:LYS:HE3	1:B:105:ASP:OD2	2.21	0.41
1:B:165:LEU:O	1:B:169:ARG:HG3	2.20	0.41
1:C:278:HIS:ND1	1:C:302:ARG:HD3	2.35	0.41
1:A:117:LYS:HD3	1:A:117:LYS:HA	1.81	0.41
1:B:241:PHE:CZ	1:B:243:ILE:HB	2.56	0.41
1:D:95:GLU:H	1:D:95:GLU:HG3	1.60	0.41
1:B:17:GLN:CD	1:B:20:ARG:HH21	2.25	0.41
1:B:116:GLU:O	1:B:116:GLU:CG	2.69	0.41
1:B:224:ILE:HB	1:B:227:TYR:HB2	2.02	0.41
1:B:279:GLN:HE22	1:B:421:ASP:CG	2.25	0.41
1:C:116:GLU:C	1:C:118:LEU:N	2.74	0.41
1:B:370:ARG:HB3	5:B:653:HOH:O	2.21	0.40
1:B:365:PHE:O	1:B:367:ARG:HG3	2.21	0.40
1:D:83:TYR:CE2	1:D:85:PRO:HG3	2.56	0.40
1:A:25:ARG:NH1	1:A:352:GLU:OE1	2.43	0.40
1:A:282:LEU:HD12	1:A:282:LEU:HA	1.85	0.40
1:C:134:GLU:H	1:C:134:GLU:CD	2.25	0.40
1:A:204:ARG:HG2	1:A:204:ARG:HH11	1.86	0.40
1:D:79:LYS:HE3	1:D:79:LYS:HB2	1.51	0.40
1:A:71:VAL:HB	1:A:79:LYS:HB3	2.02	0.40
1:B:60:LEU:HD13	1:B:62:VAL:CB	2.51	0.40
1:C:432:ASN:CG	1:C:435:ARG:HB2	2.41	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)
5:B:742:HOH:O	5:C:687:HOH:O[15_544]	1.90	0.30
5:C:678:HOH:O	5:D:714:HOH:O[4_555]	1.94	0.26

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	438/448 (98%)	431 (98%)	7 (2%)	0	100	100
1	B	441/448 (98%)	435 (99%)	6 (1%)	0	100	100
1	C	439/448 (98%)	422 (96%)	17 (4%)	0	100	100
1	D	439/448 (98%)	425 (97%)	13 (3%)	1 (0%)	47	61
All	All	1757/1792 (98%)	1713 (98%)	43 (2%)	1 (0%)	51	67

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	21	THR

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	378/386 (98%)	368 (97%)	10 (3%)	46	64
1	B	381/386 (99%)	380 (100%)	1 (0%)	92	97
1	C	379/386 (98%)	371 (98%)	8 (2%)	53	70
1	D	379/386 (98%)	371 (98%)	8 (2%)	53	70
All	All	1517/1544 (98%)	1490 (98%)	27 (2%)	59	75

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	MET
1	A	91	LYS
1	A	92	VAL
1	A	94	ASP
1	A	142	SER
1	A	144	MET
1	A	165	LEU
1	A	172	ASN
1	A	282	LEU
1	A	367	ARG

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Mol	Chain	Res	Type
1	B	123	LYS
1	C	86	VAL
1	C	97	ARG
1	C	134	GLU
1	C	279	GLN
1	C	417	ILE
1	C	418	ARG
1	C	435	ARG
1	C	436	ASP
1	D	31	LEU
1	D	46	MET
1	D	113	ASP
1	D	142	SER
1	D	165	LEU
1	D	236	HIS
1	D	367	ARG
1	D	381	GLU

Sometimes 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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 10 ligands modelled in this entry, 9 are monoatomic - leaving 1 for Mogul analysis.

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	SO4	A	503	-	4,4,4	0.42	0	6,6,6	0.38	0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	503	SO4	1	0

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	439/448 (97%)	0.19	5 (1%)	80	81	29, 42, 63, 78	0
1	B	439/448 (97%)	0.26	10 (2%)	60	62	33, 44, 66, 79	0
1	C	439/448 (97%)	0.45	19 (4%)	35	38	37, 54, 77, 97	0
1	D	439/448 (97%)	0.33	8 (1%)	68	70	33, 46, 70, 93	0
All	All	1756/1792 (97%)	0.31	42 (2%)	59	60	29, 46, 70, 97	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	365	PHE	4.9
1	C	367	ARG	4.7
1	C	402	PHE	4.3
1	C	89	TRP	3.2
1	A	89	TRP	3.1
1	C	439	LEU	3.0
1	D	45	TRP	2.9
1	C	365	PHE	2.9
1	B	348	PHE	2.9
1	A	45	TRP	2.9
1	D	89	TRP	2.9
1	D	439	LEU	2.8
1	C	398	ASP	2.8
1	C	311	ASN	2.7
1	B	117	LYS	2.7
1	C	229	HIS	2.7
1	C	384	LEU	2.7
1	A	111	GLN	2.6
1	D	236	HIS	2.6
1	C	286	LEU	2.5
1	C	91	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	121	TYR	2.5
1	A	125	ASN	2.5
1	B	89	TRP	2.4
1	B	367	ARG	2.4
1	C	386	PHE	2.4
1	C	329	PHE	2.4
1	B	361	GLU	2.3
1	C	277	GLU	2.3
1	B	423	ILE	2.3
1	C	438	HIS	2.3
1	C	45	TRP	2.2
1	D	402	PHE	2.2
1	B	20	ARG	2.2
1	C	225	LEU	2.2
1	C	121	TYR	2.1
1	B	440	ASP	2.1
1	C	310	PHE	2.1
1	D	94	ASP	2.0
1	A	60	LEU	2.0
1	D	86	VAL	2.0
1	B	118	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 monosaccharides 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
4	NA	A	504	1/1	0.85	0.17	30,30,30,30	0
2	MN	B	501	1/1	0.90	0.11	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	MN	C	501	1/1	0.93	0.12	52,52,52,52	0
2	MN	D	501	1/1	0.94	0.08	44,44,44,44	0
2	MN	A	501	1/1	0.94	0.17	46,46,46,46	0
2	MN	D	502	1/1	0.95	0.05	50,50,50,50	0
2	MN	C	502	1/1	0.95	0.09	53,53,53,53	0
3	SO4	A	503	5/5	0.97	0.38	30,30,30,30	0
2	MN	A	502	1/1	0.98	0.12	50,50,50,50	0
2	MN	B	502	1/1	0.98	0.05	48,48,48,48	0

6.5 Other polymers (i)

There are no such residues in this entry.