



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 08:15 PM GMT

PDB ID : 4XM2
Title : N,N'-diacetylchitobiose deacetylase from *Pyrococcus furiosus* in the absence of cadmium
Authors : Nakamura, T.; Niiyama, M.; Hashimoto, W.; Ida, K.; Uegaki, K.
Deposited on : 2015-01-14
Resolution : 2.30 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 : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
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) : rb-20026982

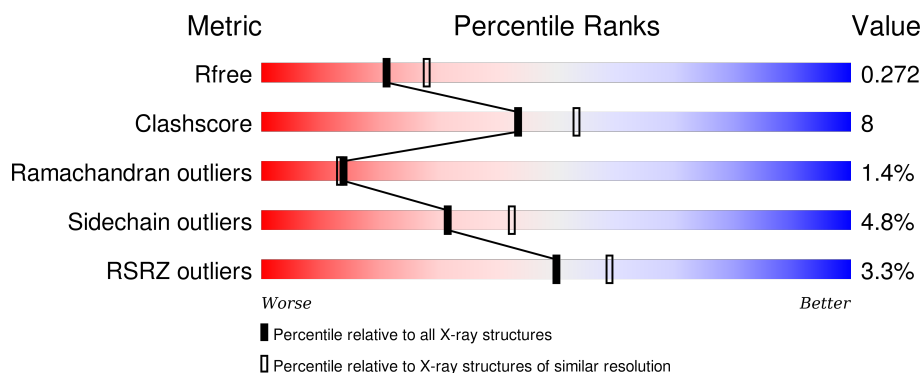
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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	267	<div> <div>3%</div> <div>79% 18% .</div> </div>
1	B	267	<div> <div>5%</div> <div>78% 16% . .</div> </div>
1	C	267	<div> <div>7%</div> <div>72% 24% .</div> </div>
1	D	267	<div> <div>%</div> <div>82% 16% .</div> </div>
1	E	267	<div> <div>3%</div> <div>77% 21% .</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	267	 A horizontal bar chart showing the quality of the chain. The bar is divided into two segments: a green segment representing 79% and a yellow segment representing 19%. A small black dot is located at the end of the yellow segment.

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13177 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 Uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	266	Total	C	N	O	S	0	0	0
			2182	1411	359	403	9			
1	B	259	Total	C	N	O	S	0	0	0
			2123	1372	351	391	9			
1	C	266	Total	C	N	O	S	0	0	0
			2182	1411	359	403	9			
1	D	267	Total	C	N	O	S	0	0	0
			2190	1416	360	404	10			
1	E	267	Total	C	N	O	S	0	0	0
			2190	1416	360	404	10			
1	F	267	Total	C	N	O	S	0	0	0
			2190	1416	360	404	10			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total	Zn	0	0
			1	1		
2	E	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		
2	F	1	Total	Zn	0	0
			1	1		

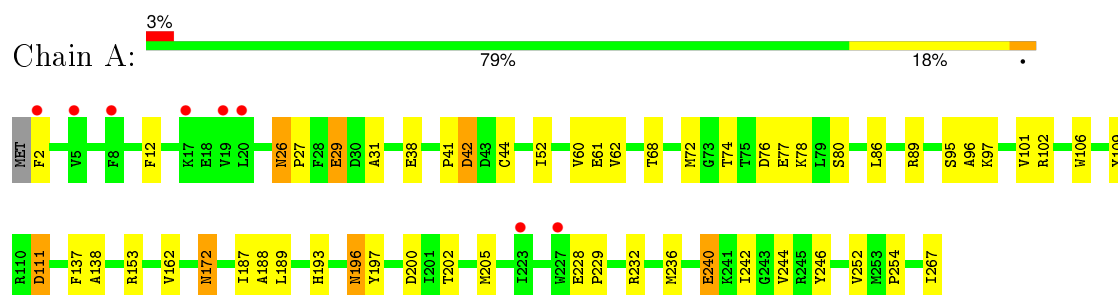
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	17	Total 17	O 17	0	0
3	B	16	Total 16	O 16	0	0
3	C	18	Total 18	O 18	0	0
3	D	24	Total 24	O 24	0	0
3	E	18	Total 18	O 18	0	0
3	F	21	Total 21	O 21	0	0

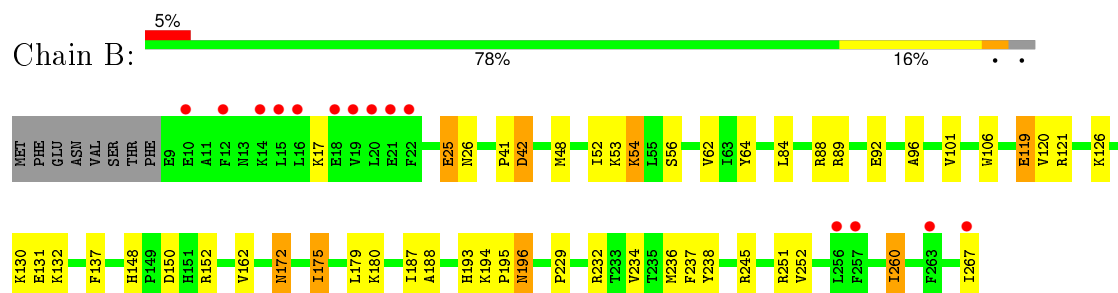
3 Residue-property plots [i](#)

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.

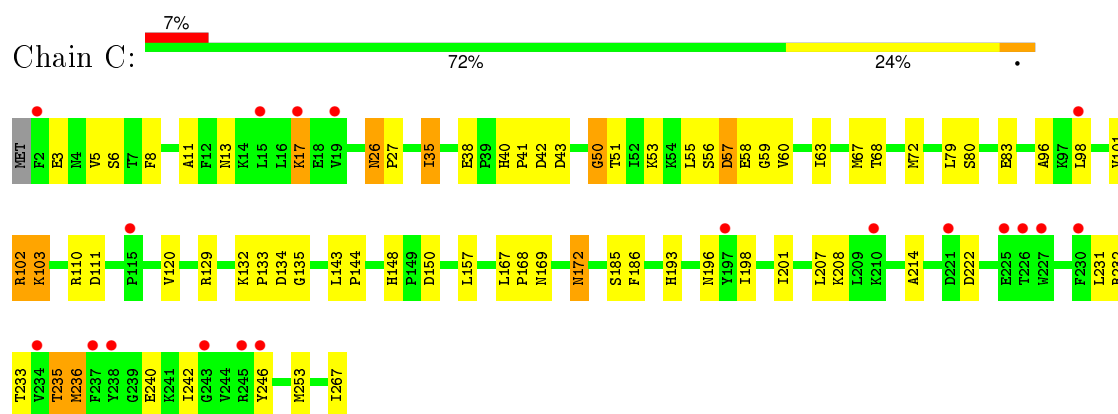
• Molecule 1: Uncharacterized protein



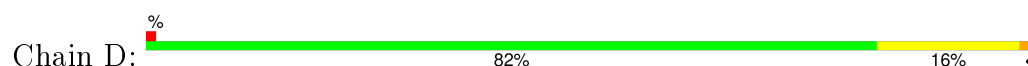
• Molecule 1: Uncharacterized protein

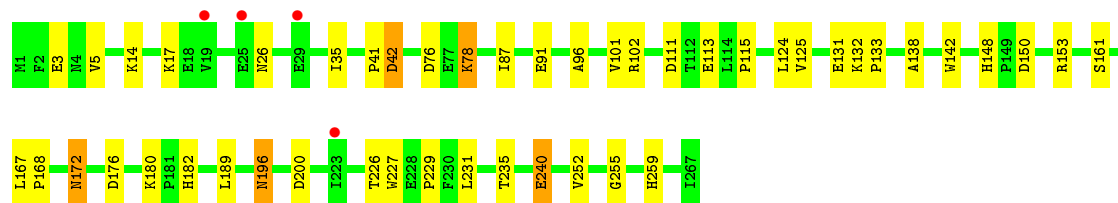


• Molecule 1: Uncharacterized protein

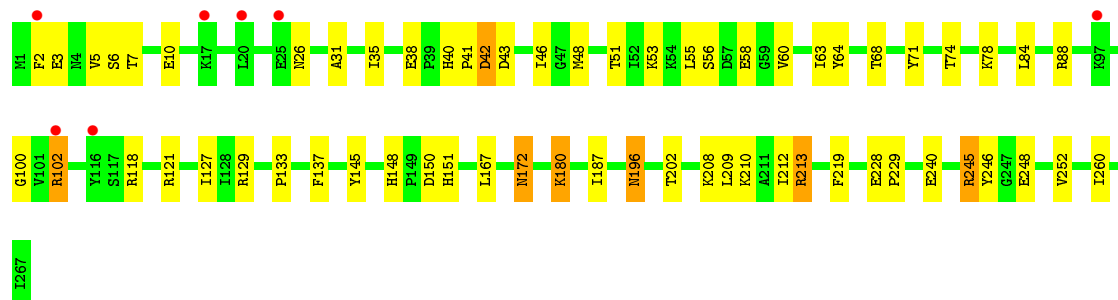
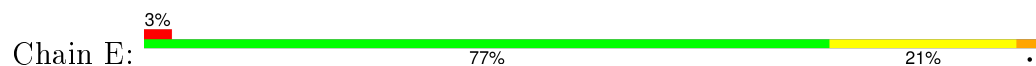


• Molecule 1: Uncharacterized protein

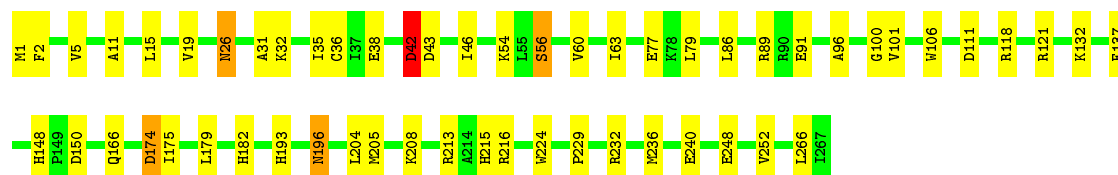
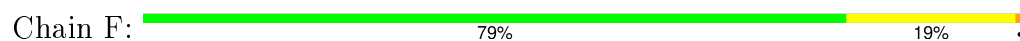




• Molecule 1: Uncharacterized protein



• Molecule 1: Uncharacterized protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	81.63Å 121.83Å 92.13Å 90.00° 113.88° 90.00°	Depositor
Resolution (Å)	46.57 – 2.30 46.57 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.5 (46.57-2.30) 99.5 (46.57-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.22 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.209 , 0.276 0.207 , 0.272	Depositor DCC
R_{free} test set	3668 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	42.0	Xtriage
Anisotropy	0.073	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 45.2	EDS
Estimated twinning fraction	0.020 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 72783 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13177	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 4.80% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.84	0/2240	0.83	3/3031 (0.1%)
1	B	0.83	1/2179 (0.0%)	0.83	1/2948 (0.0%)
1	C	0.84	0/2240	0.85	1/3031 (0.0%)
1	D	0.84	0/2248	0.85	2/3041 (0.1%)
1	E	0.84	0/2248	0.86	1/3041 (0.0%)
1	F	0.90	0/2248	0.90	7/3041 (0.2%)
All	All	0.85	1/13403 (0.0%)	0.86	15/18133 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	119	GLU	CB-CG	6.05	1.63	1.52

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	F	121	ARG	NE-CZ-NH1	7.62	124.11	120.30
1	F	121	ARG	NE-CZ-NH2	-7.40	116.60	120.30
1	F	111	ASP	CB-CG-OD2	-7.21	111.81	118.30
1	F	111	ASP	CB-CG-OD1	5.99	123.69	118.30
1	F	42	ASP	CB-CG-OD1	5.67	123.40	118.30
1	A	111	ASP	CB-CG-OD1	5.55	123.30	118.30
1	A	153	ARG	NE-CZ-NH2	-5.19	117.71	120.30
1	D	153	ARG	NE-CZ-NH2	-5.17	117.72	120.30
1	F	166	GLN	CB-CA-C	-5.15	100.10	110.40
1	F	174	ASP	CB-CG-OD2	-5.11	113.70	118.30
1	E	64	TYR	CB-CG-CD2	-5.11	117.94	121.00
1	A	111	ASP	CB-CG-OD2	-5.08	113.72	118.30
1	D	111	ASP	CB-CG-OD1	5.08	122.87	118.30
1	B	152	ARG	NE-CZ-NH2	5.05	122.83	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	C	67	MET	CG-SD-CE	5.03	108.24	100.20

There are no chirality outliers.

There are no planarity outliers.

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	2182	0	2149	34	0
1	B	2123	0	2098	45	0
1	C	2182	0	2149	46	0
1	D	2190	0	2161	30	0
1	E	2190	0	2161	36	0
1	F	2190	0	2161	31	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	17	0	0	0	0
3	B	16	0	0	0	0
3	C	18	0	0	0	0
3	D	24	0	0	2	0
3	E	18	0	0	1	0
3	F	21	0	0	0	0
All	All	13177	0	12879	210	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 (210) 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:162:VAL:HG11	1:B:187:ILE:HD11	1.09	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:162:VAL:HG11	1:B:187:ILE:CD1	1.83	1.07
1:B:196:ASN:HD22	1:B:196:ASN:H	1.05	0.97
1:B:162:VAL:CG1	1:B:187:ILE:HD11	1.98	0.94
1:E:31:ALA:O	1:E:60:VAL:HG22	1.72	0.90
1:E:35:ILE:HD12	1:E:133:PRO:HG3	1.54	0.90
1:D:78:LYS:HB2	1:D:78:LYS:NZ	1.92	0.85
1:E:51:THR:O	1:E:55:LEU:HG	1.77	0.83
1:A:196:ASN:HD21	1:A:252:VAL:H	1.28	0.81
1:F:196:ASN:HD21	1:F:252:VAL:H	1.30	0.80
1:C:51:THR:HG22	1:C:55:LEU:HD11	1.65	0.77
1:B:89:ARG:HG3	1:B:106:TRP:CZ2	2.20	0.76
1:A:232:ARG:O	1:A:236:MET:HG3	1.85	0.76
1:B:196:ASN:HD22	1:B:196:ASN:N	1.75	0.76
1:D:78:LYS:HB2	1:D:78:LYS:HZ3	1.48	0.75
1:F:216:ARG:HH21	1:F:216:ARG:HG3	1.51	0.74
1:B:175:ILE:H	1:B:175:ILE:CD1	2.00	0.73
1:B:148:HIS:HD2	1:B:150:ASP:H	1.34	0.73
1:C:172:ASN:HD22	1:C:172:ASN:H	1.35	0.72
1:B:175:ILE:HD12	1:B:175:ILE:N	2.05	0.72
1:B:196:ASN:ND2	1:B:251:ARG:HA	2.06	0.69
1:D:96:ALA:HB1	1:D:101:VAL:HB	1.75	0.69
1:B:196:ASN:ND2	1:B:196:ASN:H	1.87	0.68
1:F:96:ALA:HB1	1:F:101:VAL:HB	1.75	0.68
1:C:172:ASN:HD22	1:C:172:ASN:N	1.92	0.68
1:F:15:LEU:HA	1:F:19:VAL:HG23	1.74	0.68
1:C:148:HIS:HD2	1:C:150:ASP:H	1.42	0.68
1:F:42:ASP:O	1:F:46:ILE:HG13	1.95	0.66
1:F:15:LEU:HA	1:F:19:VAL:CG2	2.25	0.66
1:B:175:ILE:H	1:B:175:ILE:HD12	1.59	0.65
1:E:187:ILE:O	3:E:417:HOH:O	2.14	0.64
1:A:80:SER:HA	1:C:169:ASN:HD21	1.63	0.64
1:C:13:ASN:O	1:C:17:LYS:HB2	1.98	0.64
1:F:208:LYS:NZ	1:F:248:GLU:OE2	2.20	0.63
1:C:51:THR:HG22	1:C:55:LEU:CD1	2.29	0.62
1:B:175:ILE:CD1	1:B:175:ILE:N	2.63	0.62
1:A:31:ALA:O	1:A:60:VAL:HG22	2.00	0.62
1:B:196:ASN:HD21	1:B:252:VAL:H	1.47	0.62
1:B:196:ASN:HD21	1:B:251:ARG:HA	1.63	0.62
1:E:38:GLU:HB2	1:E:43:ASP:HB2	1.81	0.62
1:E:74:THR:HG22	1:E:84:LEU:HD22	1.83	0.61
1:B:96:ALA:HB1	1:B:101:VAL:HB	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:172:ASN:H	1:E:172:ASN:HD22	1.47	0.60
1:B:172:ASN:HD22	1:B:172:ASN:H	1.48	0.60
1:A:2:PHE:HB3	1:B:232:ARG:HD2	1.84	0.60
1:F:38:GLU:HB2	1:F:43:ASP:HB2	1.83	0.60
1:A:242:ILE:HG13	1:A:244:VAL:HG22	1.83	0.58
1:A:38:GLU:HG2	1:A:44:CYS:SG	2.43	0.58
1:C:53:LYS:HG2	1:C:207:LEU:HD23	1.86	0.58
1:E:46:ILE:HD11	1:E:219:PHE:HZ	1.69	0.58
1:A:162:VAL:HG11	1:A:187:ILE:HD11	1.87	0.57
1:D:226:THR:O	1:D:229:PRO:HD2	2.05	0.57
1:F:5:VAL:HG21	1:F:11:ALA:HB2	1.86	0.57
1:A:137:PHE:CD1	1:A:188:ALA:HB3	2.39	0.57
1:F:216:ARG:HG3	1:F:216:ARG:NH2	2.20	0.57
1:C:35:ILE:HG13	1:C:133:PRO:HG3	1.86	0.57
1:C:51:THR:O	1:C:55:LEU:HD12	2.05	0.56
1:A:61:GLU:HG3	1:A:102:ARG:HG3	1.87	0.56
1:E:212:ILE:HG23	1:E:219:PHE:CE2	2.40	0.56
1:D:196:ASN:HD21	1:D:252:VAL:H	1.53	0.56
1:A:202:THR:HA	1:A:246:TYR:HB2	1.87	0.56
1:C:57:ASP:O	1:C:59:GLY:N	2.39	0.56
1:E:84:LEU:O	1:E:88:ARG:HG3	2.06	0.56
1:D:5:VAL:HG11	1:D:14:LYS:HD3	1.88	0.56
1:C:50:GLY:H	1:C:208:LYS:HD2	1.70	0.55
1:B:48:MET:O	1:B:52:ILE:HG13	2.06	0.55
1:A:172:ASN:HD22	1:A:172:ASN:H	1.55	0.55
1:A:26:ASN:ND2	1:A:29:GLU:OE2	2.40	0.55
1:C:232:ARG:O	1:C:236:MET:HG2	2.07	0.54
1:B:126:LYS:NZ	1:F:174:ASP:OD1	2.39	0.54
1:C:55:LEU:O	1:C:60:VAL:HB	2.08	0.54
1:E:202:THR:HA	1:E:246:TYR:HB2	1.89	0.53
1:D:172:ASN:HD22	1:D:172:ASN:H	1.54	0.53
1:E:196:ASN:HD21	1:E:252:VAL:H	1.56	0.53
1:F:132:LYS:HB3	1:F:182:HIS:CE1	2.44	0.53
1:D:35:ILE:HD12	1:D:133:PRO:HG3	1.88	0.53
1:B:196:ASN:ND2	1:B:196:ASN:N	2.46	0.53
1:D:87:ILE:O	1:D:91:GLU:HG3	2.09	0.52
1:F:148:HIS:HD2	1:F:150:ASP:H	1.56	0.52
1:E:55:LEU:O	1:E:60:VAL:HB	2.09	0.52
1:C:35:ILE:HA	1:C:63:ILE:O	2.09	0.52
1:B:148:HIS:CD2	1:B:150:ASP:H	2.23	0.52
1:C:231:LEU:O	1:C:235:THR:OG1	2.27	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:205:MET:HG2	1:A:246:TYR:CD2	2.46	0.51
1:E:40:HIS:HD2	1:E:68:THR:OG1	1.93	0.51
1:E:35:ILE:HA	1:E:63:ILE:O	2.10	0.51
1:F:148:HIS:CD2	1:F:150:ASP:HB2	2.46	0.51
1:F:213:ARG:HD2	1:F:224:TRP:CE2	2.46	0.51
1:A:52:ILE:HG23	1:A:62:VAL:HG11	1.92	0.51
1:A:41:PRO:O	1:A:42:ASP:CG	2.49	0.51
1:D:41:PRO:O	1:D:42:ASP:CB	2.60	0.50
1:B:41:PRO:HA	1:B:92:GLU:OE2	2.12	0.49
1:F:175:ILE:HD12	1:F:179:LEU:O	2.11	0.49
1:C:172:ASN:ND2	1:C:172:ASN:N	2.60	0.49
1:A:240:GLU:O	1:A:240:GLU:HG3	2.12	0.49
1:D:227:TRP:O	1:D:231:LEU:HG	2.12	0.49
1:C:253:MET:HG2	1:C:267:ILE:HD11	1.95	0.49
1:A:96:ALA:HB1	1:A:101:VAL:HB	1.95	0.48
1:B:64:TYR:CE1	1:B:101:VAL:HG21	2.48	0.48
1:B:84:LEU:O	1:B:88:ARG:HG3	2.13	0.48
1:D:138:ALA:O	1:D:189:LEU:HA	2.14	0.48
1:F:89:ARG:HG3	1:F:106:TRP:CZ2	2.49	0.48
1:D:148:HIS:HE1	3:D:403:HOH:O	1.97	0.48
1:C:198:ILE:HG13	1:C:242:ILE:HG23	1.95	0.48
1:C:148:HIS:HD2	1:C:150:ASP:N	2.10	0.48
1:B:232:ARG:O	1:B:236:MET:HG3	2.14	0.47
1:C:5:VAL:HG21	1:C:11:ALA:HB2	1.96	0.47
1:C:72:MET:HB2	1:C:111:ASP:OD2	2.14	0.47
1:C:96:ALA:HB1	1:C:101:VAL:HB	1.96	0.47
1:F:91:GLU:HB3	1:F:215:HIS:HA	1.96	0.47
1:C:79:LEU:HD12	1:C:83:GLU:HB3	1.95	0.47
1:F:31:ALA:O	1:F:60:VAL:HG22	2.14	0.47
1:B:193:HIS:CE1	1:B:194:LYS:HG2	2.50	0.47
1:C:57:ASP:C	1:C:59:GLY:H	2.18	0.47
1:E:148:HIS:HD2	1:E:150:ASP:H	1.62	0.47
1:D:200:ASP:HB3	3:D:414:HOH:O	2.15	0.47
1:C:38:GLU:HB2	1:C:43:ASP:HB2	1.95	0.47
1:E:74:THR:CG2	1:E:84:LEU:HD22	2.45	0.46
1:B:195:PRO:HG3	1:B:238:TYR:HE1	1.80	0.46
1:D:148:HIS:HD2	1:D:150:ASP:H	1.64	0.46
1:F:232:ARG:O	1:F:236:MET:HG3	2.16	0.46
1:C:41:PRO:O	1:C:42:ASP:CG	2.54	0.46
1:D:226:THR:C	1:D:229:PRO:HD2	2.36	0.46
1:B:120:VAL:O	1:B:121:ARG:C	2.54	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:76:ASP:OD2	1:D:78:LYS:HB2	2.15	0.46
1:D:229:PRO:HB3	1:F:2:PHE:CE2	2.51	0.46
1:C:26:ASN:N	1:C:26:ASN:HD22	2.13	0.46
1:C:172:ASN:ND2	1:C:172:ASN:H	2.09	0.46
1:A:12:PHE:HZ	1:A:267:ILE:HG23	1.81	0.46
1:E:228:GLU:HB3	1:E:229:PRO:HD3	1.98	0.45
1:E:129:ARG:NH2	1:E:167:LEU:O	2.49	0.45
1:E:208:LYS:HD2	1:E:248:GLU:OE2	2.15	0.45
1:D:113:GLU:O	1:D:115:PRO:HD3	2.16	0.45
1:E:180:LYS:HB2	1:E:180:LYS:NZ	2.31	0.45
1:A:76:ASP:C	1:A:78:LYS:H	2.20	0.45
1:E:48:MET:HE1	1:E:137:PHE:CG	2.52	0.45
1:E:100:GLY:O	1:E:102:ARG:NH1	2.50	0.45
1:C:144:PRO:HD3	1:C:193:HIS:CE1	2.51	0.44
1:F:26:ASN:N	1:F:26:ASN:HD22	2.16	0.44
1:A:254:PRO:HD2	1:A:267:ILE:CD1	2.48	0.44
1:A:27:PRO:HD2	1:A:197:TYR:CE1	2.52	0.44
1:A:196:ASN:ND2	1:A:252:VAL:H	2.07	0.44
1:B:148:HIS:CD2	1:B:150:ASP:HB2	2.52	0.44
1:E:172:ASN:HD22	1:E:172:ASN:N	2.15	0.44
1:B:137:PHE:CD1	1:B:188:ALA:HB3	2.52	0.44
1:E:148:HIS:CD2	1:E:150:ASP:HB2	2.53	0.44
1:A:200:ASP:OD2	1:A:244:VAL:HG11	2.17	0.44
1:A:86:LEU:HD12	1:A:86:LEU:HA	1.70	0.44
1:E:2:PHE:CD2	1:F:229:PRO:HB3	2.53	0.44
1:B:195:PRO:HG3	1:B:238:TYR:CE1	2.53	0.43
1:D:125:VAL:HG23	1:D:161:SER:HB3	2.00	0.43
1:C:135:GLY:HA2	1:C:186:PHE:O	2.18	0.43
1:F:56:SER:OG	1:F:100:GLY:HA3	2.19	0.43
1:C:53:LYS:HG2	1:C:207:LEU:CD2	2.47	0.43
1:D:132:LYS:HA	1:D:182:HIS:CD2	2.54	0.43
1:F:35:ILE:HA	1:F:63:ILE:O	2.19	0.43
1:C:120:VAL:CG1	1:C:157:LEU:HD13	2.49	0.43
1:A:2:PHE:CE2	1:B:229:PRO:HB3	2.54	0.42
1:D:131:GLU:O	1:D:132:LYS:C	2.57	0.42
1:F:266:LEU:HA	1:F:266:LEU:HD23	1.79	0.42
1:E:209:LEU:O	1:E:213:ARG:HG3	2.19	0.42
1:C:79:LEU:CD1	1:C:83:GLU:HB3	2.49	0.42
1:A:89:ARG:HG3	1:A:106:TRP:CZ2	2.53	0.42
1:A:74:THR:O	1:C:168:PRO:HD2	2.19	0.42
1:A:228:GLU:HB3	1:A:229:PRO:HD3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:172:ASN:HA	1:B:175:ILE:HD13	2.02	0.42
1:A:240:GLU:O	1:A:240:GLU:CG	2.67	0.42
1:C:129:ARG:NH2	1:C:167:LEU:O	2.52	0.42
1:E:7:THR:OG1	1:E:10:GLU:HG3	2.19	0.42
1:D:142:TRP:CZ2	1:E:145:TYR:HA	2.54	0.42
1:D:167:LEU:HA	1:D:168:PRO:HD2	1.80	0.42
1:C:40:HIS:HD2	1:C:68:THR:OG1	2.03	0.42
1:A:138:ALA:O	1:A:189:LEU:HA	2.20	0.42
1:D:5:VAL:O	1:E:245:ARG:NH2	2.53	0.42
1:D:148:HIS:CD2	1:D:150:ASP:HB2	2.55	0.42
1:C:148:HIS:CD2	1:C:150:ASP:H	2.30	0.42
1:B:41:PRO:O	1:B:42:ASP:CG	2.58	0.42
1:B:130:LYS:HA	1:B:179:LEU:HD22	2.02	0.42
1:F:204:LEU:O	1:F:205:MET:C	2.58	0.42
1:E:127:ILE:O	1:E:127:ILE:HG22	2.19	0.42
1:F:79:LEU:HD12	1:F:79:LEU:HA	1.92	0.42
1:C:102:ARG:O	1:C:103:LYS:HB2	2.20	0.42
1:B:234:VAL:O	1:B:237:PHE:HB3	2.21	0.41
1:F:36:CYS:HA	1:F:137:PHE:HB2	2.02	0.41
1:B:119:GLU:OE2	1:F:118:ARG:NE	2.47	0.41
1:D:78:LYS:CB	1:D:78:LYS:NZ	2.74	0.41
1:E:53:LYS:HA	1:E:53:LYS:HD2	1.89	0.41
1:B:131:GLU:O	1:B:132:LYS:C	2.58	0.41
1:E:41:PRO:O	1:E:42:ASP:CB	2.69	0.41
1:E:118:ARG:O	1:E:121:ARG:HB2	2.20	0.41
1:C:235:THR:HB	1:C:246:TYR:CD1	2.56	0.41
1:C:233:THR:HA	1:C:236:MET:HG3	2.03	0.41
1:C:132:LYS:HB3	1:C:132:LYS:HE3	1.50	0.41
1:B:148:HIS:HD2	1:B:150:ASP:N	2.11	0.41
1:F:15:LEU:HD12	1:F:19:VAL:HB	2.03	0.41
1:A:172:ASN:HD22	1:A:172:ASN:N	2.17	0.41
1:C:110:ARG:O	1:C:111:ASP:C	2.59	0.41
1:E:102:ARG:CZ	1:E:102:ARG:HB2	2.50	0.41
1:A:72:MET:HB2	1:A:111:ASP:OD2	2.20	0.41
1:D:259:HIS:HE1	1:E:151:HIS:CD2	2.38	0.41
1:C:134:ASP:O	1:C:185:SER:HB2	2.20	0.41
1:B:130:LYS:HA	1:B:179:LEU:CD2	2.51	0.41
1:B:52:ILE:HG23	1:B:62:VAL:HG11	2.02	0.40
1:D:41:PRO:O	1:D:42:ASP:HB3	2.21	0.40
1:B:260:ILE:HA	1:C:143:LEU:HD21	2.03	0.40
1:B:53:LYS:O	1:B:54:LYS:C	2.60	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:193:HIS:C	1:B:195:PRO:HD3	2.41	0.40
1:C:26:ASN:HA	1:C:27:PRO:HD2	1.89	0.40
1:D:124:LEU:HA	1:D:124:LEU:HD23	1.91	0.40
1:A:68:THR:HA	1:A:109:TYR:O	2.21	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	264/267 (99%)	248 (94%)	14 (5%)	2 (1%)	24	27
1	B	257/267 (96%)	238 (93%)	15 (6%)	4 (2%)	12	11
1	C	264/267 (99%)	234 (89%)	23 (9%)	7 (3%)	6	4
1	D	265/267 (99%)	242 (91%)	19 (7%)	4 (2%)	13	12
1	E	265/267 (99%)	250 (94%)	12 (4%)	3 (1%)	17	18
1	F	265/267 (99%)	256 (97%)	7 (3%)	2 (1%)	24	27
All	All	1580/1602 (99%)	1468 (93%)	90 (6%)	22 (1%)	14	13

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	3	GLU
1	C	58	GLU
1	E	42	ASP
1	A	77	GLU
1	B	42	ASP
1	C	98	LEU
1	D	42	ASP
1	D	176	ASP

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Mol	Chain	Res	Type
1	F	42	ASP
1	A	42	ASP
1	B	54	LYS
1	C	103	LYS
1	E	71	TYR
1	F	77	GLU
1	D	255	GLY
1	B	25	GLU
1	B	260	ILE
1	C	57	ASP
1	C	214	ALA
1	D	240	GLU
1	C	50	GLY
1	E	260	ILE

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	238/239 (100%)	230 (97%)	8 (3%)	44	59
1	B	231/239 (97%)	221 (96%)	10 (4%)	35	47
1	C	238/239 (100%)	223 (94%)	15 (6%)	22	29
1	D	239/239 (100%)	229 (96%)	10 (4%)	36	49
1	E	239/239 (100%)	224 (94%)	15 (6%)	22	29
1	F	239/239 (100%)	229 (96%)	10 (4%)	36	49
All	All	1424/1434 (99%)	1356 (95%)	68 (5%)	31	42

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	ASN
1	A	29	GLU
1	A	95	SER
1	A	97	LYS

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Mol	Chain	Res	Type
1	A	172	ASN
1	A	193	HIS
1	A	196	ASN
1	A	240	GLU
1	B	17	LYS
1	B	25	GLU
1	B	26	ASN
1	B	56	SER
1	B	172	ASN
1	B	175	ILE
1	B	180	LYS
1	B	196	ASN
1	B	245	ARG
1	B	267	ILE
1	C	6	SER
1	C	8	PHE
1	C	17	LYS
1	C	26	ASN
1	C	35	ILE
1	C	56	SER
1	C	80	SER
1	C	102	ARG
1	C	172	ASN
1	C	196	ASN
1	C	201	ILE
1	C	222	ASP
1	C	235	THR
1	C	236	MET
1	C	240	GLU
1	D	3	GLU
1	D	17	LYS
1	D	26	ASN
1	D	78	LYS
1	D	102	ARG
1	D	172	ASN
1	D	180	LYS
1	D	196	ASN
1	D	235	THR
1	D	240	GLU
1	E	3	GLU
1	E	5	VAL
1	E	6	SER

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Mol	Chain	Res	Type
1	E	26	ASN
1	E	56	SER
1	E	58	GLU
1	E	78	LYS
1	E	102	ARG
1	E	172	ASN
1	E	180	LYS
1	E	196	ASN
1	E	210	LYS
1	E	213	ARG
1	E	240	GLU
1	E	245	ARG
1	F	1	MET
1	F	26	ASN
1	F	32	LYS
1	F	42	ASP
1	F	54	LYS
1	F	56	SER
1	F	86	LEU
1	F	193	HIS
1	F	196	ASN
1	F	240	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	108	ASN
1	A	148	HIS
1	A	169	ASN
1	A	172	ASN
1	A	196	ASN
1	B	108	ASN
1	B	148	HIS
1	B	172	ASN
1	B	196	ASN
1	B	218	GLN
1	C	13	ASN
1	C	148	HIS
1	C	169	ASN
1	C	172	ASN
1	C	196	ASN
1	D	13	ASN

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Mol	Chain	Res	Type
1	D	82	HIS
1	D	108	ASN
1	D	148	HIS
1	D	169	ASN
1	D	172	ASN
1	D	196	ASN
1	D	218	GLN
1	E	108	ASN
1	E	148	HIS
1	E	169	ASN
1	E	172	ASN
1	E	196	ASN
1	F	26	ASN
1	F	108	ASN
1	F	148	HIS
1	F	172	ASN
1	F	196	ASN
1	F	218	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 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

There are no such residues in this entry.

5.8 Polymer linkage issues

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	266/267 (99%)	0.19	8 (3%) 54 63	26, 48, 73, 83	0
1	B	259/267 (97%)	0.28	14 (5%) 29 38	24, 49, 94, 105	0
1	C	266/267 (99%)	0.49	19 (7%) 19 26	26, 54, 82, 88	0
1	D	267/267 (100%)	0.00	4 (1%) 76 81	23, 47, 70, 78	0
1	E	267/267 (100%)	0.14	7 (2%) 59 68	25, 52, 75, 83	0
1	F	267/267 (100%)	-0.14	0 100 100	21, 43, 64, 72	0
All	All	1592/1602 (99%)	0.16	52 (3%) 50 59	21, 49, 76, 105	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	12	PHE	4.8
1	B	19	VAL	4.4
1	C	230	PHE	4.1
1	A	5	VAL	3.6
1	E	20	LEU	3.5
1	B	21	GLU	3.5
1	B	256	LEU	3.2
1	B	263	PHE	3.2
1	B	15	LEU	3.2
1	C	17	LYS	3.1
1	B	267	ILE	3.1
1	E	102	ARG	3.0
1	B	18	GLU	3.0
1	C	245	ARG	2.9
1	C	227	TRP	2.8
1	E	97	LYS	2.8
1	B	22	PHE	2.7
1	B	14	LYS	2.7
1	C	237	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	223	ILE	2.6
1	A	2	PHE	2.6
1	C	2	PHE	2.6
1	B	16	LEU	2.5
1	C	226	THR	2.5
1	B	20	LEU	2.5
1	C	98	LEU	2.5
1	B	10	GLU	2.4
1	C	115	PRO	2.4
1	A	223	ILE	2.4
1	C	238	TYR	2.4
1	C	246	TYR	2.4
1	C	243	GLY	2.4
1	B	257	PHE	2.4
1	C	210	LYS	2.3
1	C	19	VAL	2.3
1	E	116	TYR	2.3
1	C	225	GLU	2.3
1	E	2	PHE	2.3
1	A	8	PHE	2.3
1	A	227	TRP	2.3
1	E	17	LYS	2.2
1	C	234	VAL	2.2
1	D	29	GLU	2.2
1	C	15	LEU	2.2
1	D	19	VAL	2.2
1	C	221	ASP	2.1
1	A	19	VAL	2.1
1	D	25	GLU	2.1
1	E	25	GLU	2.1
1	A	17	LYS	2.1
1	C	197	TYR	2.0
1	A	20	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	ZN	E	301	1/1	0.99	0.11	-0.61	53,53,53,53	0
2	ZN	C	301	1/1	0.97	0.10	-1.09	62,62,62,62	0
2	ZN	B	301	1/1	0.98	0.10	-1.29	54,54,54,54	0
2	ZN	A	301	1/1	0.99	0.09	-1.29	50,50,50,50	0
2	ZN	F	301	1/1	1.00	0.06	-2.42	47,47,47,47	0
2	ZN	D	301	1/1	0.99	0.07	-3.28	47,47,47,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.