Full wwPDB X-ray Structure Validation Report (i)

Oct 31, 2023 – 05:29 PM JST

PDB ID	:	5GN9
Title	:	Crystal structure of alternative oxidase from Trypanosoma brucei brucei complexed with cumarin derivative-17b
Authors	:	Balogun, E.O.; Inaoka, D.K.; Shiba, T.; Tsuge, T.; May, B.; Sato, T.; Kido, Y.; Takeshi, N.; Aoki, T.; Honma, T.; Tanaka, A.; Inoue, M.; Matsuoka, S.; Michels, P.A.M.; Watanabe, Y.; Moore, A.L.; Harada, S.; Kita, K.
Deposited on	:	2016-07-19
Resolution	:	3.20 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:

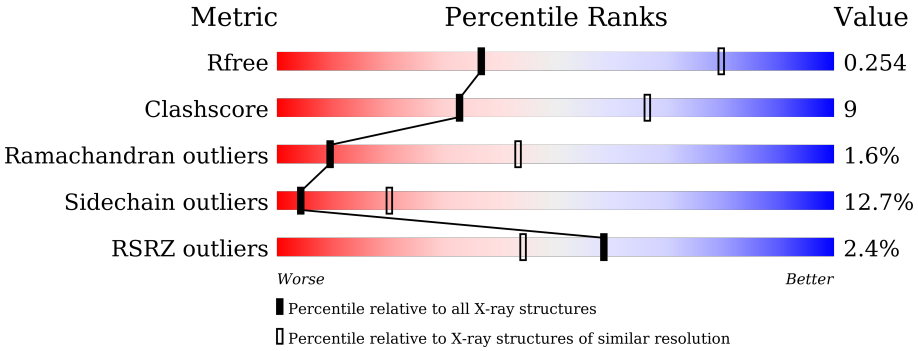
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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	329	55% 20% 5% 20%
1	B	329	% 53% 24% • • 20%
1	C	329	4% 57% 20% • • 20%
1	D	329	3% 60% 18% • 20%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 8660 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.

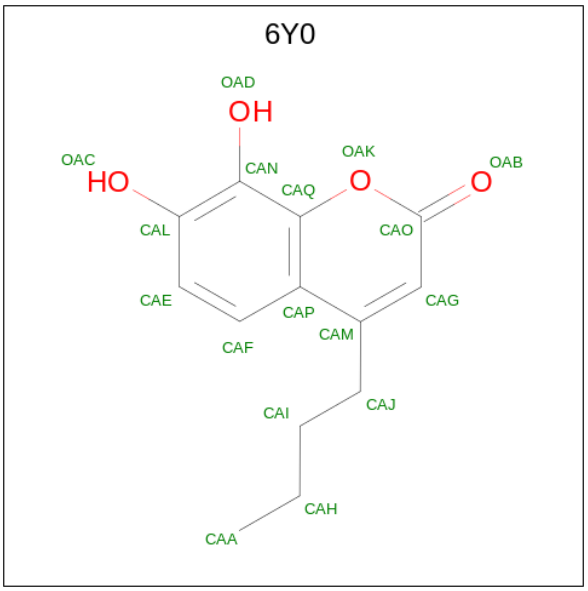
- Molecule 1 is a protein called Alternative oxidase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	264	2146	1375	381	380	10	0	0	0
1	B	264	2146	1375	381	380	10	0	0	0
1	C	264	2146	1375	381	380	10	0	0	0
1	D	264	2146	1375	381	380	10	0	0	0

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Fe		
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 4-butyl-7,8-bis(oxidanyl)chromen-2-one (three-letter code: 6Y0) (formula: $C_{13}H_{14}O_4$).



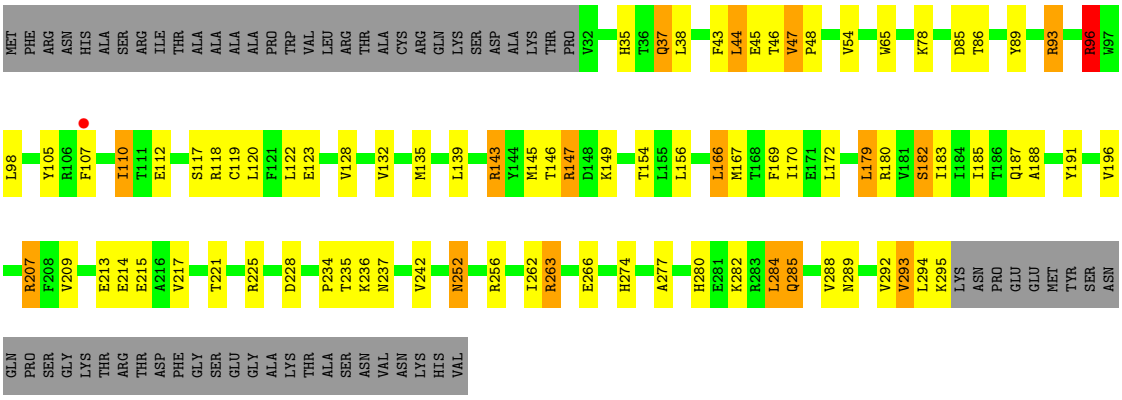
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	17	13	4	0	0
			Total	C	O		
3	B	1	17	13	4	0	0
			Total	C	O		
3	C	1	17	13	4	0	0
			Total	C	O		
3	D	1	17	13	4	0	0

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.

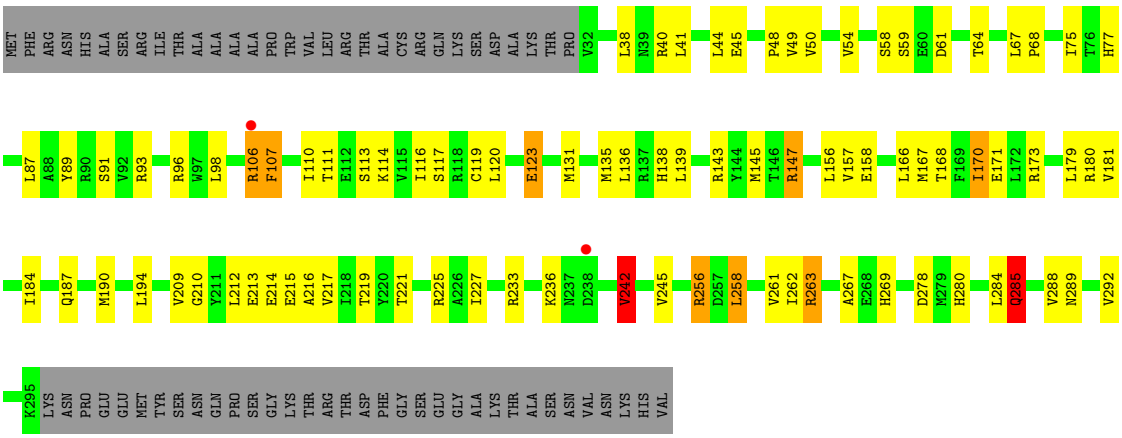
• Molecule 1: Alternative oxidase, mitochondrial

Chain A: 55% 20% 5% 20%



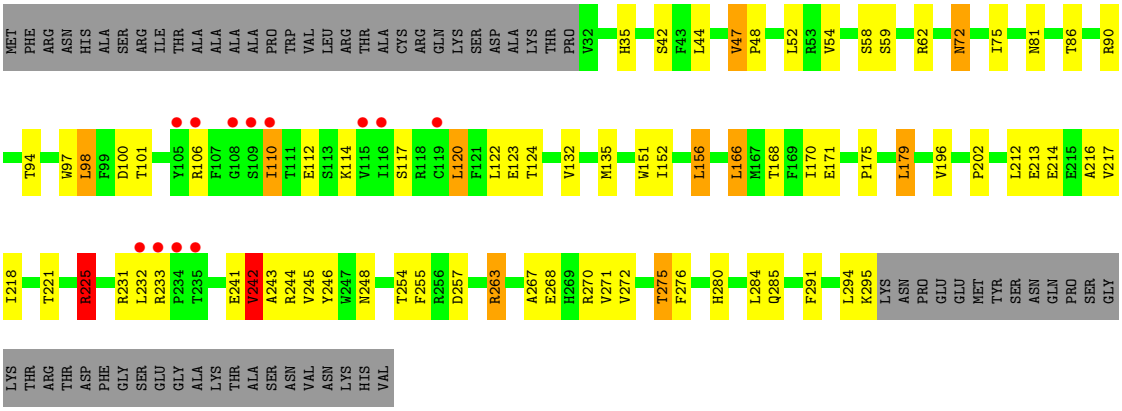
• Molecule 1: Alternative oxidase, mitochondrial

Chain B: % 53% 24% • • 20%



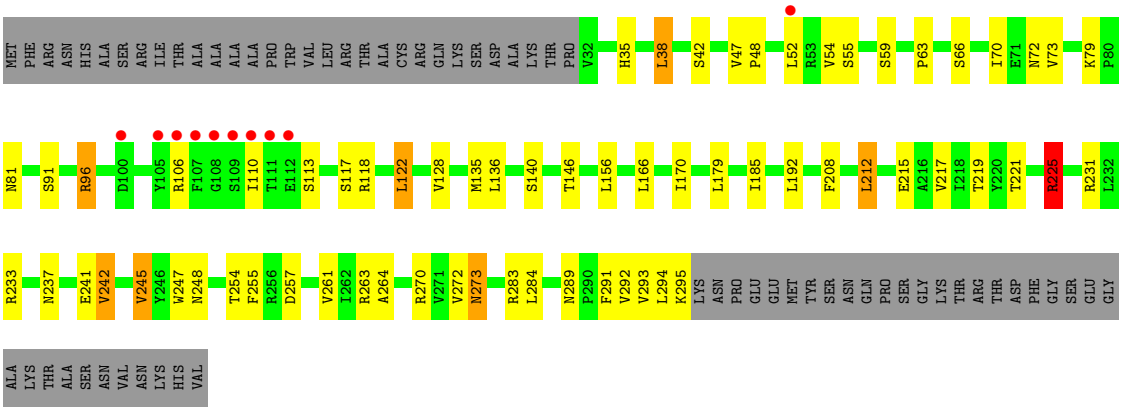
• Molecule 1: Alternative oxidase, mitochondrial

Chain C: 4% 57% 20% • • 20%



- Molecule 1: Alternative oxidase, mitochondrial

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	150.22Å 221.81Å 62.61Å 90.00° 114.64° 90.00°	Depositor
Resolution (Å)	42.19 – 3.20 42.19 – 3.20	Depositor EDS
% Data completeness (in resolution range)	90.9 (42.19-3.20) 94.9 (42.19-3.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.47 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.192 , 0.252 0.195 , 0.254	Depositor DCC
R_{free} test set	1476 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	71.1	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 41.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.280 for -h-2*l,-k,l	Xtriage
Reported twinning fraction	0.600 for H, K, L 0.400 for H+4/2L, -K, -L	Depositor
Outliers	0 of 29084 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	8660	wwPDB-VP
Average B, all atoms (Å^2)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.16% 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: 6Y0, FE

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	0.71	0/2195	0.97	5/2982 (0.2%)
1	B	0.70	0/2195	0.95	6/2982 (0.2%)
1	C	0.64	0/2195	0.87	1/2982 (0.0%)
1	D	0.63	0/2195	0.87	2/2982 (0.1%)
All	All	0.67	0/8780	0.92	14/11928 (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
1	A	0	1
1	D	0	1
All	All	0	2

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	143	ARG	NE-CZ-NH1	7.79	124.19	120.30
1	B	263	ARG	NE-CZ-NH1	5.81	123.21	120.30
1	B	263	ARG	NE-CZ-NH2	-5.77	117.42	120.30
1	B	147	ARG	NE-CZ-NH1	-5.61	117.50	120.30
1	B	233	ARG	NE-CZ-NH1	5.59	123.09	120.30
1	D	225	ARG	NE-CZ-NH2	-5.37	117.62	120.30
1	D	231	ARG	NE-CZ-NH2	5.30	122.95	120.30
1	A	96	ARG	NE-CZ-NH1	5.26	122.93	120.30
1	A	207	ARG	NE-CZ-NH2	-5.23	117.69	120.30
1	B	256	ARG	NE-CZ-NH2	5.19	122.89	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	242	VAL	CB-CA-C	-5.17	101.59	111.40
1	A	93	ARG	NE-CZ-NH1	-5.11	117.75	120.30
1	A	147	ARG	NE-CZ-NH1	-5.10	117.75	120.30
1	C	225	ARG	NE-CZ-NH1	5.08	122.84	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	237	ASN	Peptide
1	D	237	ASN	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	A	2146	0	2175	55	0
1	B	2146	0	2175	55	0
1	C	2146	0	2175	34	0
1	D	2146	0	2175	27	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	0	0
3	A	17	0	0	0	0
3	B	17	0	0	3	0
3	C	17	0	0	2	0
3	D	17	0	0	2	0
All	All	8660	0	8700	151	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 9.

All (151) 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:A:221:THR:HG22	1:A:263:ARG:HE	1.43	0.80
1:B:221:THR:HG22	1:B:263:ARG:HE	1.50	0.77
1:A:221:THR:HG22	1:A:263:ARG:NE	1.99	0.76
1:D:221:THR:HG22	1:D:263:ARG:HE	1.54	0.72
1:A:167:MET:HE2	1:B:147:ARG:HA	1.73	0.70
1:D:54:VAL:CG1	1:D:242:VAL:HA	2.22	0.69
1:D:96:ARG:NH1	1:D:215:GLU:OE1	2.28	0.66
1:C:216:ALA:HB2	3:C:503:6Y0:CAE	2.26	0.66
1:A:172:LEU:HD22	1:A:236:LYS:HD2	1.78	0.66
1:A:214:GLU:OE1	1:A:274:HIS:HE1	1.80	0.65
1:D:221:THR:HG22	1:D:263:ARG:NE	2.10	0.65
1:A:221:THR:CG2	1:A:263:ARG:HE	2.09	0.65
1:B:289:ASN:O	1:B:292:VAL:HG22	1.98	0.62
1:B:111:THR:HG1	1:B:114:LYS:H	1.48	0.62
1:C:47:VAL:HG22	1:C:48:PRO:HD3	1.80	0.62
1:B:221:THR:HG22	1:B:263:ARG:NE	2.14	0.61
1:A:289:ASN:O	1:A:292:VAL:HG22	2.01	0.60
1:B:168:THR:HG21	1:B:258:LEU:HD11	1.82	0.60
1:B:217:VAL:O	1:B:221:THR:HG23	2.02	0.60
1:B:116:ILE:HG21	1:B:173:ARG:HB3	1.86	0.58
1:D:241:GLU:O	1:D:245:VAL:HG13	2.03	0.58
1:D:122:LEU:HD13	3:D:503:6Y0:CAG	2.34	0.57
1:D:272:VAL:HG22	1:D:291:PHE:CD2	2.40	0.56
1:C:152:ILE:HG22	1:C:156:LEU:HD22	1.86	0.56
1:D:217:VAL:O	1:D:221:THR:HG23	2.05	0.56
1:A:166:LEU:HD21	1:B:145:MET:HG2	1.88	0.56
1:D:63:PRO:HG2	1:D:247:TRP:CD1	2.41	0.56
1:D:110:ILE:HG23	1:D:110:ILE:O	2.07	0.55
1:A:145:MET:HG2	1:B:166:LEU:HD21	1.89	0.55
1:A:37:GLN:CD	1:A:37:GLN:N	2.59	0.55
1:B:77:HIS:HA	1:B:214:GLU:OE1	2.07	0.55
1:A:172:LEU:O	1:A:236:LYS:NZ	2.40	0.55
1:C:241:GLU:OE1	1:C:244:ARG:NH2	2.39	0.54
1:B:58:SER:OG	1:B:59:SER:O	2.20	0.54
1:D:292:VAL:HG23	1:D:293:VAL:HG23	1.88	0.54
1:D:54:VAL:HG13	1:D:242:VAL:HA	1.88	0.54
1:D:219:THR:HG21	3:D:503:6Y0:OAB	2.08	0.54
1:A:143:ARG:HD3	1:B:187:GLN:HE21	1.73	0.54
1:A:105:TYR:CE1	1:A:118:ARG:HD2	2.44	0.53
1:D:272:VAL:HA	1:D:291:PHE:CE2	2.43	0.53
1:C:272:VAL:HA	1:C:291:PHE:CE2	2.44	0.53
1:A:217:VAL:O	1:A:221:THR:HG23	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:280:HIS:CE1	1:B:285:GLN:HB3	2.44	0.52
1:A:282:LYS:HB2	1:A:284:LEU:HD22	1.92	0.52
1:D:272:VAL:HG22	1:D:291:PHE:CE2	2.45	0.52
1:C:54:VAL:HG13	1:C:242:VAL:HA	1.93	0.51
1:B:216:ALA:HB2	3:B:503:6Y0:CAE	2.41	0.51
1:A:209:VAL:O	1:A:213:GLU:HG2	2.11	0.51
1:A:187:GLN:HE21	1:B:143:ARG:HH11	1.58	0.51
1:A:96:ARG:NE	1:A:215:GLU:OE1	2.28	0.51
1:A:89:TYR:OH	1:D:225:ARG:HG3	2.11	0.50
1:D:217:VAL:HG21	1:D:270:ARG:NH1	2.26	0.50
1:C:62:ARG:HD3	1:C:246:TYR:HA	1.93	0.50
1:C:217:VAL:HG13	1:C:263:ARG:HD3	1.93	0.50
1:C:275:THR:HG21	1:C:291:PHE:CE2	2.47	0.50
1:C:268:GLU:O	1:C:272:VAL:HG23	2.12	0.50
1:A:44:LEU:HD22	1:A:44:LEU:O	2.11	0.49
1:A:145:MET:HB3	1:B:170:ILE:HG13	1.95	0.49
1:B:113:SER:OG	1:B:173:ARG:NH2	2.46	0.49
1:C:120:LEU:HD21	1:C:175:PRO:HG3	1.94	0.49
1:A:185:ILE:O	1:A:188:ALA:HB3	2.13	0.49
1:A:179:LEU:HA	1:A:182:SER:OG	2.12	0.48
1:D:54:VAL:HG11	1:D:242:VAL:HA	1.96	0.48
1:D:208:PHE:CE2	1:D:212:LEU:HD12	2.49	0.48
1:A:191:TYR:CE2	1:B:139:LEU:HD11	2.49	0.48
1:B:261:VAL:O	1:B:262:ILE:C	2.52	0.48
1:A:123:GLU:OE2	1:A:123:GLU:HA	2.15	0.47
1:A:128:VAL:O	1:A:132:VAL:HG13	2.15	0.47
1:B:123:GLU:HB2	1:B:166:LEU:HB2	1.96	0.47
1:A:228:ASP:OD2	1:A:256:ARG:NH1	2.47	0.47
1:B:61:ASP:OD2	1:B:157:VAL:HG11	2.15	0.47
1:C:124:THR:HG22	1:C:166:LEU:HD11	1.96	0.47
1:B:227:ILE:HD13	1:B:256:ARG:HB2	1.97	0.47
1:A:47:VAL:N	1:A:48:PRO:CD	2.79	0.46
1:C:254:THR:N	1:C:257:ASP:OD2	2.45	0.46
1:C:123:GLU:OE2	1:C:123:GLU:HA	2.16	0.46
1:B:93:ARG:NH2	1:B:215:GLU:OE2	2.49	0.46
1:A:135:MET:HG2	1:B:131:MET:HG3	1.98	0.46
1:D:289:ASN:O	1:D:292:VAL:HG22	2.16	0.46
1:B:217:VAL:HG21	1:B:267:ALA:HB2	1.98	0.45
1:A:288:VAL:CG1	1:B:50:VAL:HG22	2.46	0.45
1:B:110:ILE:O	1:B:110:ILE:HG23	2.16	0.45
1:A:65:TRP:CZ3	1:B:38:LEU:HD11	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:181:VAL:O	1:B:184:ILE:N	2.50	0.45
1:B:49:VAL:HG23	1:B:49:VAL:O	2.18	0.45
1:C:202:PRO:HB2	1:C:280:HIS:NE2	2.32	0.45
1:C:213:GLU:O	1:C:216:ALA:N	2.50	0.45
1:A:89:TYR:CZ	1:A:93:ARG:HD3	2.52	0.44
1:A:119:CYS:HB3	1:A:169:PHE:CE2	2.52	0.44
1:A:147:ARG:NH1	1:B:171:GLU:OE2	2.46	0.44
1:B:190:MET:HE2	1:B:194:LEU:HD11	2.00	0.44
1:B:67:LEU:N	1:B:68:PRO:HD2	2.33	0.44
1:C:271:VAL:O	1:C:275:THR:HB	2.17	0.44
1:A:280:HIS:CD2	1:A:285:GLN:HG2	2.52	0.44
1:C:213:GLU:HA	1:C:213:GLU:OE1	2.17	0.44
1:B:75:ILE:HB	1:C:75:ILE:HB	2.00	0.44
1:B:209:VAL:O	1:B:210:GLY:C	2.56	0.44
1:A:119:CYS:O	1:A:122:LEU:N	2.51	0.44
1:A:143:ARG:HD3	1:B:187:GLN:NE2	2.32	0.43
1:C:175:PRO:CB	1:C:179:LEU:HD12	2.48	0.43
1:A:43:PHE:O	1:A:46:THR:OG1	2.36	0.43
1:A:85:ASP:HA	1:A:207:ARG:HG2	2.00	0.43
1:C:112:GLU:OE1	1:C:232:LEU:HD11	2.19	0.43
1:C:110:ILE:HG23	1:C:110:ILE:O	2.19	0.43
1:C:168:THR:OG1	1:C:243:ALA:HB2	2.19	0.43
1:B:190:MET:CE	1:B:194:LEU:HD11	2.49	0.43
1:D:273:ASN:OD1	1:D:273:ASN:N	2.51	0.43
1:D:35:HIS:HA	1:D:38:LEU:HB2	2.01	0.42
1:C:86:THR:O	1:C:90:ARG:HG3	2.19	0.42
1:A:135:MET:O	1:A:139:LEU:HG	2.19	0.42
1:B:89:TYR:CZ	1:B:93:ARG:HD3	2.55	0.42
1:C:75:ILE:HD11	1:C:218:ILE:HA	2.00	0.42
1:C:94:THR:HG22	1:C:98:LEU:HD13	2.01	0.42
1:C:97:TRP:CZ3	1:C:101:THR:HG21	2.54	0.42
1:A:288:VAL:HG13	1:B:50:VAL:HG22	2.02	0.42
1:D:47:VAL:N	1:D:48:PRO:CD	2.82	0.42
1:A:112:GLU:OE1	1:A:234:PRO:HA	2.19	0.42
1:B:106:ARG:HD3	1:B:107:PHE:N	2.35	0.42
1:B:216:ALA:HB2	3:B:503:6Y0:CAF	2.49	0.42
1:B:89:TYR:OH	1:C:225:ARG:HG3	2.19	0.42
1:D:261:VAL:O	1:D:264:ALA:N	2.52	0.42
1:A:110:ILE:O	1:A:110:ILE:HG23	2.20	0.42
1:B:119:CYS:O	1:B:123:GLU:HG2	2.20	0.42
1:C:175:PRO:HB3	1:C:179:LEU:HD12	2.00	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:254:THR:O	1:D:257:ASP:N	2.53	0.41
1:A:78:LYS:HA	1:B:41:LEU:HD13	2.02	0.41
1:B:135:MET:O	1:B:138:HIS:HB3	2.20	0.41
1:A:44:LEU:HB2	1:B:278:ASP:HB3	2.03	0.41
1:A:147:ARG:NH1	1:B:242:VAL:HG13	2.35	0.41
1:B:120:LEU:HD12	1:B:166:LEU:CD2	2.49	0.41
1:A:35:HIS:HA	1:A:38:LEU:HB2	2.02	0.41
1:A:167:MET:HE2	1:B:147:ARG:HD3	2.03	0.41
1:A:293:VAL:O	1:A:295:LYS:N	2.51	0.41
1:C:213:GLU:O	1:C:214:GLU:C	2.58	0.41
1:C:267:ALA:O	1:C:270:ARG:HB3	2.21	0.41
1:C:151:TRP:CZ3	1:C:276:PHE:CD2	3.08	0.41
1:A:207:ARG:CZ	1:A:277:ALA:HB1	2.51	0.40
1:B:213:GLU:OE2	1:B:269:HIS:HB2	2.21	0.40
1:C:58:SER:OG	1:C:59:SER:O	2.27	0.40
1:A:252:ASN:HD22	1:A:252:ASN:N	2.18	0.40
1:C:216:ALA:HB2	3:C:503:6Y0:CAL	2.52	0.40
1:A:179:LEU:HD13	1:A:183:ILE:HD12	2.03	0.40
1:B:40:ARG:NH2	1:B:45:GLU:OE1	2.48	0.40
1:D:289:ASN:OD1	1:D:291:PHE:N	2.50	0.40
1:A:149:LYS:CB	1:A:288:VAL:HA	2.51	0.40
1:A:228:ASP:OD1	1:A:256:ARG:NE	2.54	0.40
1:A:262:ILE:O	1:A:266:GLU:HG2	2.21	0.40
1:B:45:GLU:O	1:B:48:PRO:HD2	2.21	0.40
1:B:167:MET:O	1:B:170:ILE:HG22	2.21	0.40
1:B:219:THR:HG21	3:B:503:6Y0:OAB	2.22	0.40
1:D:70:ILE:CD1	1:D:261:VAL:HA	2.51	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	A	262/329 (80%)	237 (90%)	20 (8%)	5 (2%)	8 39
1	B	262/329 (80%)	240 (92%)	20 (8%)	2 (1%)	19 58
1	C	262/329 (80%)	224 (86%)	33 (13%)	5 (2%)	8 39
1	D	262/329 (80%)	228 (87%)	29 (11%)	5 (2%)	8 39
All	All	1048/1316 (80%)	929 (89%)	102 (10%)	17 (2%)	9 43

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	110	ILE
1	A	294	LEU
1	A	117	SER
1	B	285	GLN
1	C	72	ASN
1	C	255	PHE
1	D	113	SER
1	D	255	PHE
1	C	44	LEU
1	D	128	VAL
1	A	120	LEU
1	D	283	ARG
1	D	73	VAL
1	A	293	VAL
1	B	242	VAL
1	C	242	VAL
1	C	110	ILE

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	239/292 (82%)	214 (90%)	25 (10%)	7 28
1	B	239/292 (82%)	213 (89%)	26 (11%)	6 26
1	C	239/292 (82%)	204 (85%)	35 (15%)	3 15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	D	239/292 (82%)	204 (85%)	35 (15%)	3 15
All	All	956/1168 (82%)	835 (87%)	121 (13%)	4 20

All (121) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	GLN
1	A	44	LEU
1	A	45	GLU
1	A	47	VAL
1	A	54	VAL
1	A	86	THR
1	A	96	ARG
1	A	98	LEU
1	A	107	PHE
1	A	146	THR
1	A	154	THR
1	A	156	LEU
1	A	166	LEU
1	A	170	ILE
1	A	179	LEU
1	A	180	ARG
1	A	182	SER
1	A	196	VAL
1	A	225	ARG
1	A	235	THR
1	A	242	VAL
1	A	252	ASN
1	A	263	ARG
1	A	284	LEU
1	A	285	GLN
1	B	44	LEU
1	B	54	VAL
1	B	64	THR
1	B	87	LEU
1	B	91	SER
1	B	96	ARG
1	B	98	LEU
1	B	106	ARG
1	B	107	PHE
1	B	117	SER
1	B	123	GLU

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Mol	Chain	Res	Type
1	B	136	LEU
1	B	156	LEU
1	B	158	GLU
1	B	170	ILE
1	B	179	LEU
1	B	180	ARG
1	B	212	LEU
1	B	225	ARG
1	B	236	LYS
1	B	242	VAL
1	B	245	VAL
1	B	258	LEU
1	B	284	LEU
1	B	285	GLN
1	B	288	VAL
1	C	35	HIS
1	C	42	SER
1	C	47	VAL
1	C	52	LEU
1	C	72	ASN
1	C	81	ASN
1	C	98	LEU
1	C	100	ASP
1	C	106	ARG
1	C	114	LYS
1	C	117	SER
1	C	120	LEU
1	C	122	LEU
1	C	132	VAL
1	C	135	MET
1	C	156	LEU
1	C	166	LEU
1	C	170	ILE
1	C	171	GLU
1	C	179	LEU
1	C	196	VAL
1	C	212	LEU
1	C	221	THR
1	C	225	ARG
1	C	231	ARG
1	C	233	ARG
1	C	242	VAL

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Mol	Chain	Res	Type
1	C	245	VAL
1	C	248	ASN
1	C	263	ARG
1	C	275	THR
1	C	284	LEU
1	C	285	GLN
1	C	294	LEU
1	C	295	LYS
1	D	38	LEU
1	D	42	SER
1	D	52	LEU
1	D	55	SER
1	D	59	SER
1	D	66	SER
1	D	72	ASN
1	D	79	LYS
1	D	81	ASN
1	D	91	SER
1	D	96	ARG
1	D	106	ARG
1	D	117	SER
1	D	118	ARG
1	D	122	LEU
1	D	135	MET
1	D	136	LEU
1	D	140	SER
1	D	146	THR
1	D	156	LEU
1	D	166	LEU
1	D	170	ILE
1	D	179	LEU
1	D	185	ILE
1	D	192	LEU
1	D	212	LEU
1	D	225	ARG
1	D	233	ARG
1	D	242	VAL
1	D	245	VAL
1	D	248	ASN
1	D	273	ASN
1	D	284	LEU
1	D	294	LEU

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Mol	Chain	Res	Type
1	D	295	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	ASN
1	A	81	ASN
1	A	153	ASN
1	A	187	GLN
1	A	252	ASN
1	A	260	ASN
1	A	274	HIS
1	B	187	GLN
1	B	237	ASN
1	B	273	ASN
1	B	274	HIS
1	C	35	HIS
1	C	77	HIS
1	C	81	ASN
1	C	248	ASN
1	C	260	ASN
1	C	269	HIS
1	C	274	HIS
1	C	285	GLN
1	D	35	HIS
1	D	248	ASN
1	D	269	HIS
1	D	274	HIS
1	D	285	GLN
1	D	286	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 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	6Y0	B	503	2	18,18,18	1.65	3 (16%)	25,25,25	2.25	7 (28%)
3	6Y0	A	503	2	18,18,18	1.75	3 (16%)	25,25,25	1.71	6 (24%)
3	6Y0	D	503	2	18,18,18	1.57	3 (16%)	25,25,25	1.97	6 (24%)
3	6Y0	C	503	2	18,18,18	1.56	3 (16%)	25,25,25	1.88	6 (24%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	6Y0	B	503	2	-	0/4/4/4	0/2/2/2
3	6Y0	A	503	2	-	0/4/4/4	0/2/2/2
3	6Y0	D	503	2	-	1/4/4/4	0/2/2/2
3	6Y0	C	503	2	-	1/4/4/4	0/2/2/2

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	503	6Y0	CAJ-CAM	-5.29	1.41	1.50
3	C	503	6Y0	CAJ-CAM	-4.84	1.42	1.50
3	B	503	6Y0	CAJ-CAM	-4.77	1.42	1.50
3	D	503	6Y0	CAJ-CAM	-4.56	1.42	1.50
3	D	503	6Y0	CAG-CAM	2.84	1.41	1.35
3	A	503	6Y0	CAP-CAM	-2.61	1.41	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	503	6Y0	CAG-CAM	2.50	1.40	1.35
3	D	503	6Y0	CAP-CAM	-2.39	1.41	1.46
3	B	503	6Y0	CAG-CAO	-2.30	1.39	1.44
3	B	503	6Y0	CAG-CAM	2.14	1.39	1.35
3	A	503	6Y0	CAG-CAM	2.13	1.39	1.35
3	C	503	6Y0	CAG-CAO	-2.01	1.40	1.44

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	503	6Y0	OAB-CAO-CAG	-5.07	115.50	125.84
3	D	503	6Y0	CAQ-OAK-CAO	-5.03	117.69	121.99
3	B	503	6Y0	OAK-CAO-OAB	4.95	122.75	116.44
3	C	503	6Y0	CAJ-CAM-CAP	4.69	124.06	118.62
3	B	503	6Y0	CAJ-CAM-CAP	4.53	123.89	118.62
3	C	503	6Y0	OAB-CAO-CAG	-4.36	116.93	125.84
3	C	503	6Y0	OAK-CAO-OAB	4.32	121.94	116.44
3	D	503	6Y0	CAJ-CAM-CAP	4.17	123.46	118.62
3	A	503	6Y0	CAJ-CAM-CAP	4.02	123.29	118.62
3	D	503	6Y0	OAB-CAO-CAG	-3.84	117.99	125.84
3	B	503	6Y0	OAK-CAO-CAG	3.55	121.74	117.17
3	D	503	6Y0	OAK-CAO-CAG	3.54	121.72	117.17
3	A	503	6Y0	OAB-CAO-CAG	-3.50	118.69	125.84
3	B	503	6Y0	CAL-CAN-CAQ	3.23	121.65	118.43
3	C	503	6Y0	OAK-CAO-CAG	3.07	121.12	117.17
3	A	503	6Y0	OAK-CAO-OAB	3.02	120.29	116.44
3	D	503	6Y0	OAK-CAO-OAB	3.01	120.28	116.44
3	D	503	6Y0	CAL-CAN-CAQ	3.00	121.42	118.43
3	A	503	6Y0	CAQ-OAK-CAO	-2.99	119.44	121.99
3	A	503	6Y0	OAK-CAO-CAG	2.96	120.98	117.17
3	B	503	6Y0	CAQ-OAK-CAO	-2.67	119.71	121.99
3	A	503	6Y0	CAL-CAN-CAQ	2.56	120.98	118.43
3	B	503	6Y0	CAI-CAJ-CAM	-2.47	108.02	114.06
3	C	503	6Y0	CAQ-OAK-CAO	-2.40	119.94	121.99
3	C	503	6Y0	CAL-CAN-CAQ	2.11	120.53	118.43

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	503	6Y0	CAH-CAI-CAJ-CAM
3	D	503	6Y0	CAH-CAI-CAJ-CAM

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	503	6Y0	3	0
3	D	503	6Y0	2	0
3	C	503	6Y0	2	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	264/329 (80%)	0.20	1 (0%)	92	89	34, 55, 92, 136	0
1	B	264/329 (80%)	0.16	2 (0%)	86	78	31, 55, 88, 139	0
1	C	264/329 (80%)	0.44	12 (4%)	33	21	38, 74, 139, 182	0
1	D	264/329 (80%)	0.46	10 (3%)	40	26	43, 76, 132, 198	0
All	All	1056/1316 (80%)	0.31	25 (2%)	59	44	31, 65, 118, 198	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	109	SER	8.9
1	D	108	GLY	7.7
1	C	105	TYR	7.2
1	D	109	SER	6.8
1	D	110	ILE	6.6
1	D	106	ARG	6.2
1	D	105	TYR	6.2
1	C	235	THR	5.5
1	A	107	PHE	4.5
1	D	112	GLU	4.4
1	C	110	ILE	4.4
1	D	107	PHE	3.8
1	C	108	GLY	3.8
1	D	111	THR	3.8
1	C	234	PRO	3.6
1	C	232	LEU	3.6
1	B	238	ASP	3.4
1	C	119	CYS	3.2
1	C	106	ARG	2.6
1	D	52	LEU	2.5
1	B	106	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	233	ARG	2.3
1	C	116	ILE	2.2
1	C	115	VAL	2.1
1	D	100	ASP	2.1

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

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

6.3 Carbohydrates (i)

There are no 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
2	FE	A	502	1/1	0.96	0.22	54,54,54,54	0
3	6Y0	C	503	17/17	0.97	0.56	65,103,118,124	0
3	6Y0	D	503	17/17	0.97	0.33	62,104,114,116	0
3	6Y0	A	503	17/17	0.98	0.25	38,59,82,102	0
3	6Y0	B	503	17/17	0.98	0.38	46,73,95,111	0
2	FE	D	501	1/1	0.99	0.20	66,66,66,66	0
2	FE	D	502	1/1	0.99	0.20	56,56,56,56	0
2	FE	C	502	1/1	0.99	0.16	55,55,55,55	0
2	FE	C	501	1/1	1.00	0.17	61,61,61,61	0
2	FE	A	501	1/1	1.00	0.20	46,46,46,46	0
2	FE	B	501	1/1	1.00	0.17	44,44,44,44	0
2	FE	B	502	1/1	1.00	0.17	47,47,47,47	0

6.5 Other polymers (i)

There are no such residues in this entry.