



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:45 AM GMT

PDB ID : 2E74
Title : Crystal Structure of the Cytochrome b6f Complex from M.laminosus
Authors : Cramer, W.A.; Yamashita, E.; Zhang, H.
Deposited on : 2007-01-05
Resolution : 3.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

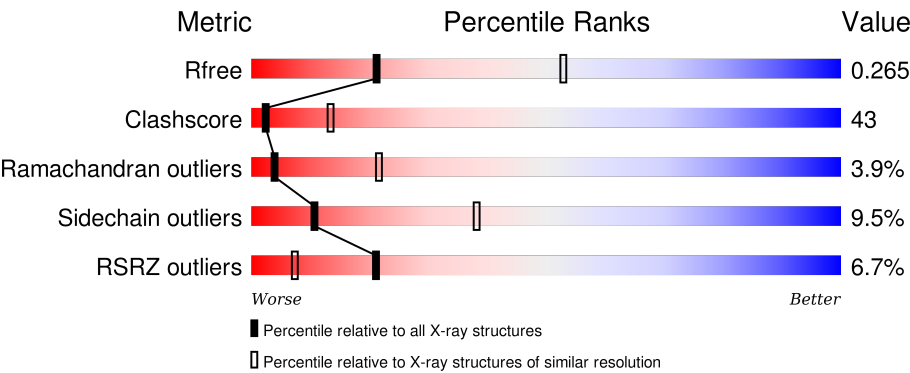
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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.



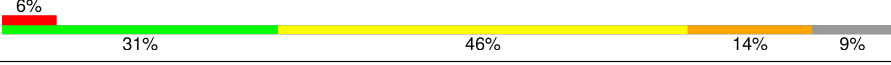


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	91344	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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 <=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	215	<div><div></div><div>60%33%6%</div></div>
2	B	160	<div><div></div><div>42%48%9%</div></div>
3	C	289	<div><div>9%</div><div>43%48%8%</div></div>
4	D	179	<div><div>18%</div><div>38%47%7%7%</div></div>
5	E	32	<div><div>3%</div><div>38%59%</div></div>

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Mol	Chain	Length	Quality of chain
6	F	35	
7	G	37	
8	H	29	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
11	UMQ	A	1101	X	-	-	X
11	UMQ	A	1102	X	-	-	X
11	UMQ	A	1103	X	-	-	-
11	UMQ	A	1104	X	-	-	-
12	CLA	B	201	X	-	-	-
13	OPC	B	202	-	-	-	X
13	OPC	H	1002	-	-	X	-
14	FES	D	200	-	-	X	-
15	SQD	D	201	X	-	-	X
16	BCR	G	101	-	-	-	X

2 Entry composition [i](#)

There are 17 unique types of molecules in this entry. The entry contains 8025 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 Cytochrome b6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	215	Total	C	N	O	S	0	0	0
			1711	1140	272	288	11			

- Molecule 2 is a protein called Cytochrome b6-f complex subunit 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	160	Total	C	N	O	S	0	0	0
			1249	841	193	209	6			

- Molecule 3 is a protein called Apocytochrome f.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	288	Total	C	N	O	S	0	0	0
			2216	1415	369	424	8			

- Molecule 4 is a protein called Cytochrome b6-f complex iron-sulfur subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	166	Total	C	N	O	S	0	0	0
			1260	805	218	230	7			

- Molecule 5 is a protein called Cytochrome b6-f complex subunit 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	32	Total	C	N	O	S	0	0	0
			248	179	34	34	1			

- Molecule 6 is a protein called Cytochrome b6-f complex subunit 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	32	Total	C	N	O	S	0	0	0
			242	165	35	40	2			

- Molecule 7 is a protein called Cytochrome b6-f complex subunit 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	37	Total	C	N	O	S	0	0	0
			283	188	44	50	1			

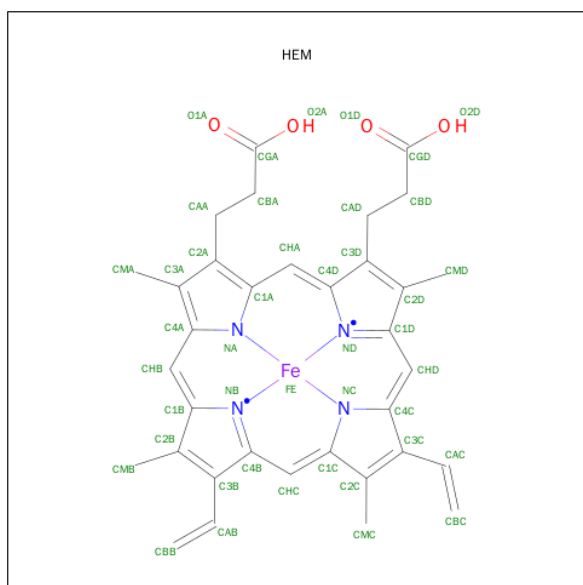
- Molecule 8 is a protein called Cytochrome b6-f complex subunit 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	29	Total	C	N	O	S	0	0	0
			230	156	36	36	2			

- Molecule 9 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	1	Total	Cd	0	0
			1	1		
9	A	1	Total	Cd	0	0
			1	1		

- Molecule 10 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



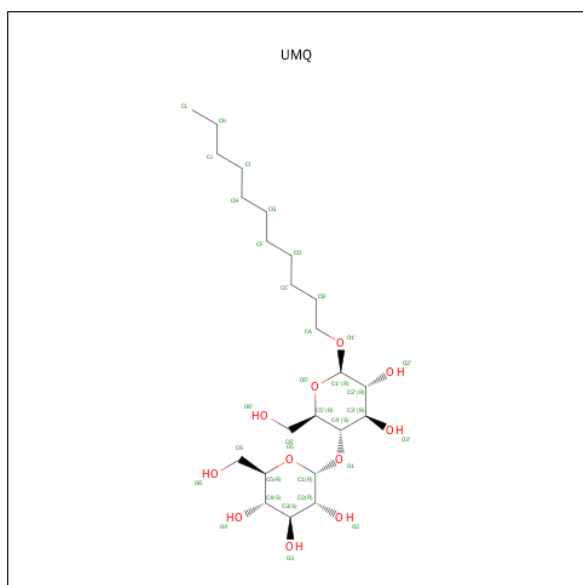
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
10	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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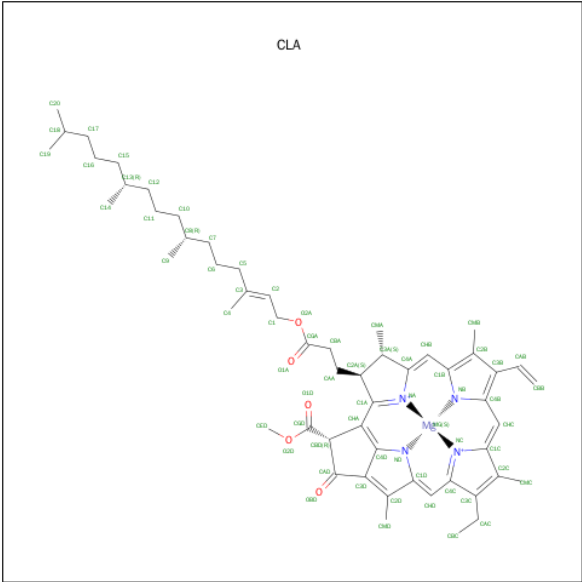
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	A	1	Total	C	Fe	N	O	
			43	34	1	4	4	
10	C	1	Total	C	Fe	N	O	
			43	34	1	4	4	

- Molecule 11 is UNDECYL-MALTOSIDE (three-letter code: UMQ) (formula: $C_{23}H_{44}O_{11}$).



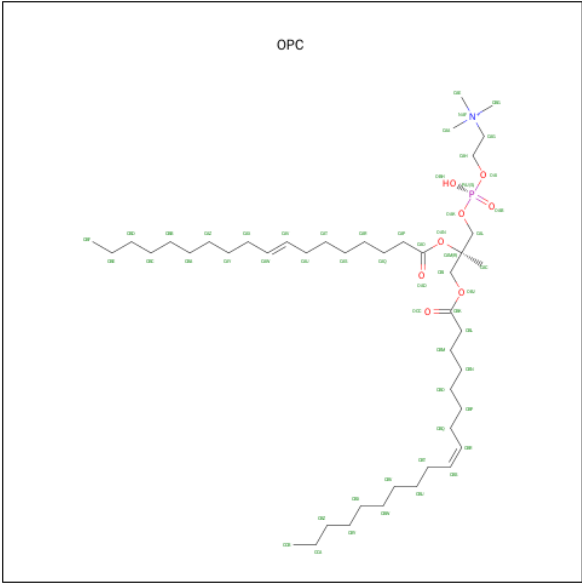
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O		
			34	23	11		
11	A	1	Total	C	O		
			34	23	11		
11	A	1	Total	C	O		
			34	23	11		
11	A	1	Total	C	O		
			34	23	11		

- Molecule 12 is CHLOROPHYLL A (three-letter code: CLA) (formula: $C_{55}H_{72}MgN_4O_5$).



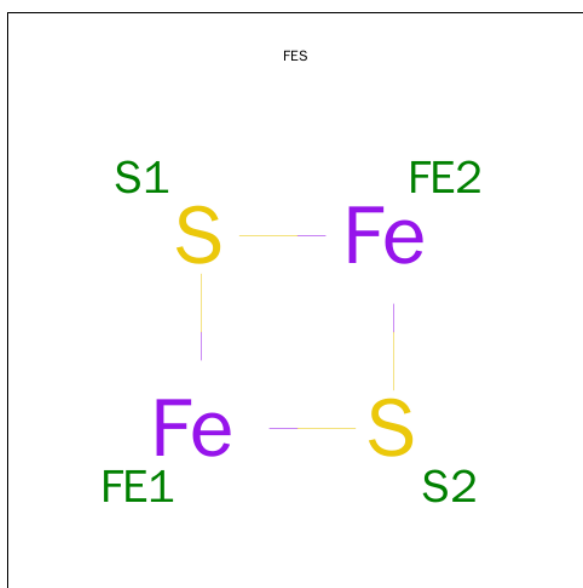
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
12	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		

- Molecule 13 is (7R,17E)-4-HYDROXY-N,N,N,7-TETRAMETHYL-7-[(8E)-OCTADEC-8-ENOYLOXY]-10-OXO-3,5,9-TRIOXA-4-PHOSPHAHEPTACOS-17-EN-1-AMINIUM 4-OXIDE (three-letter code: OPC) (formula: C₄₅H₈₇NO₈P).



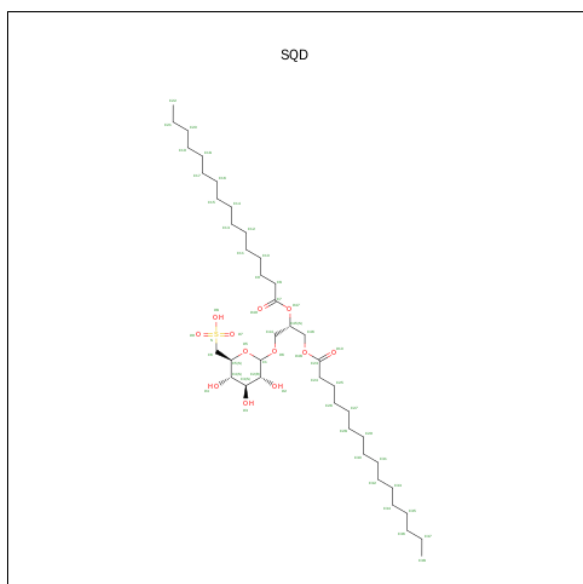
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
13	B	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
13	H	1	Total	C	N	O	P	0	0
			54	44	1	8	1		

- Molecule 14 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).



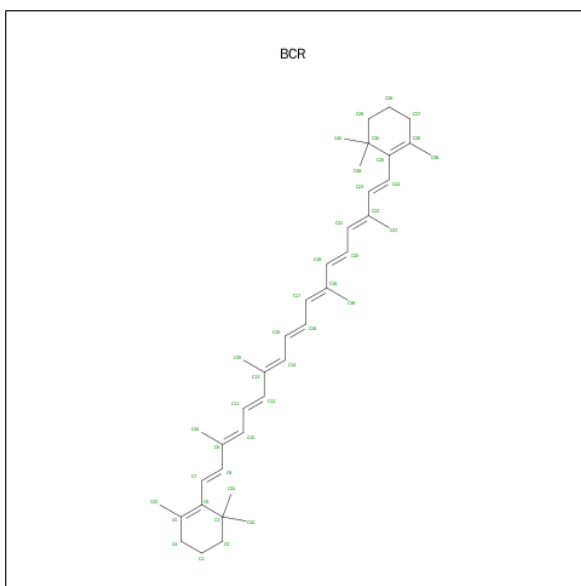
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
14	D	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 15 is 1,2-DI-O-ACYL-3-O-[6-DEOXY-6-SULFO-ALPHA-D-GLUCOPYRANOSYL]-SN-GLYCEROL (three-letter code: SQD) (formula: $\text{C}_{41}\text{H}_{78}\text{O}_{12}\text{S}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
15	D	1	Total	C	O	S	0	0
			54	41	12	1		

- Molecule 16 is BETA-CAROTENE (three-letter code: BCR) (formula: $C_{40}H_{56}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	G	1	Total C 40 40	0	0

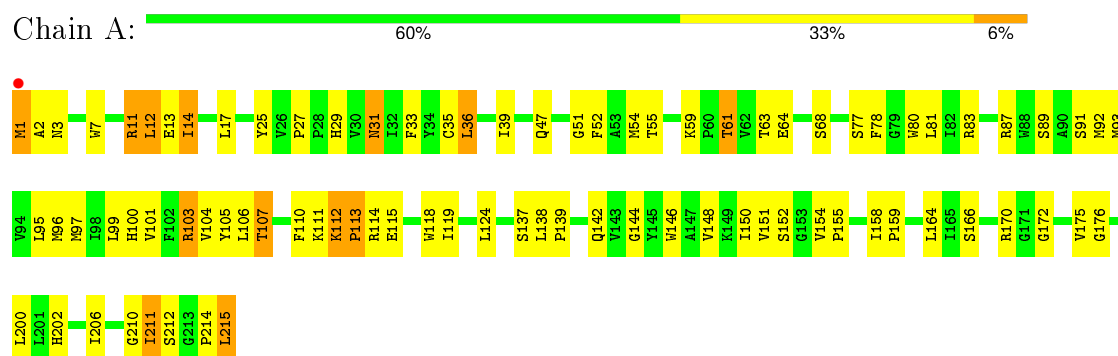
- Molecule 17 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
17	A	2	Total O 2 2	0	0
17	B	2	Total O 2 2	0	0
17	C	1	Total O 1 1	0	0

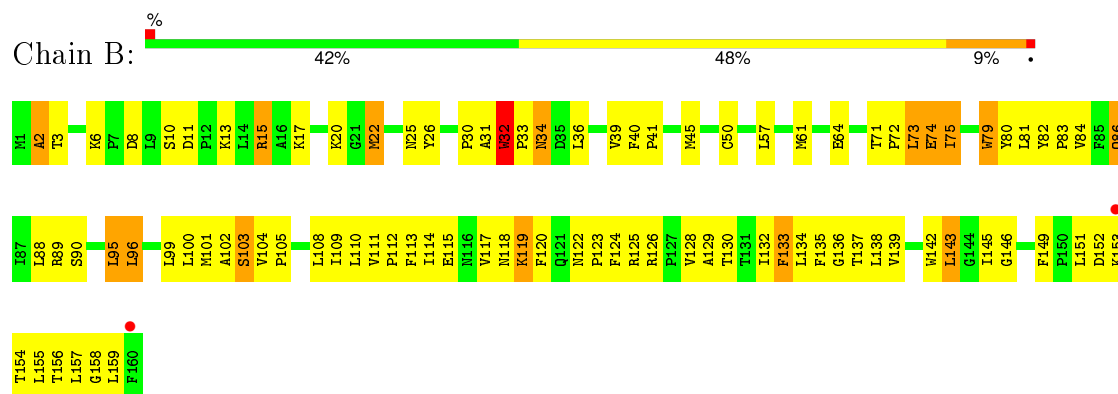
3 Residue-property plots [i](#)

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.

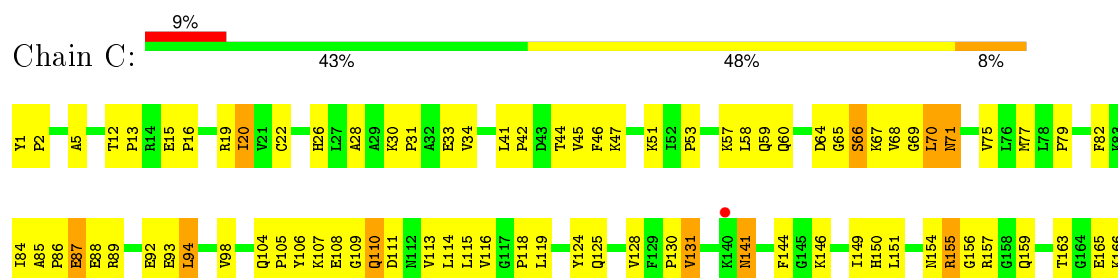
• Molecule 1: Cytochrome b6

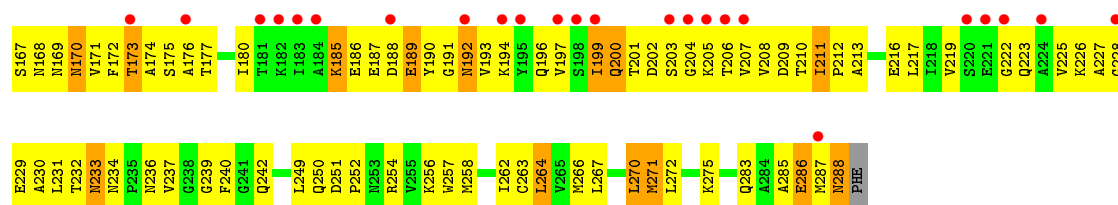


• Molecule 2: Cytochrome b6-f complex subunit 4

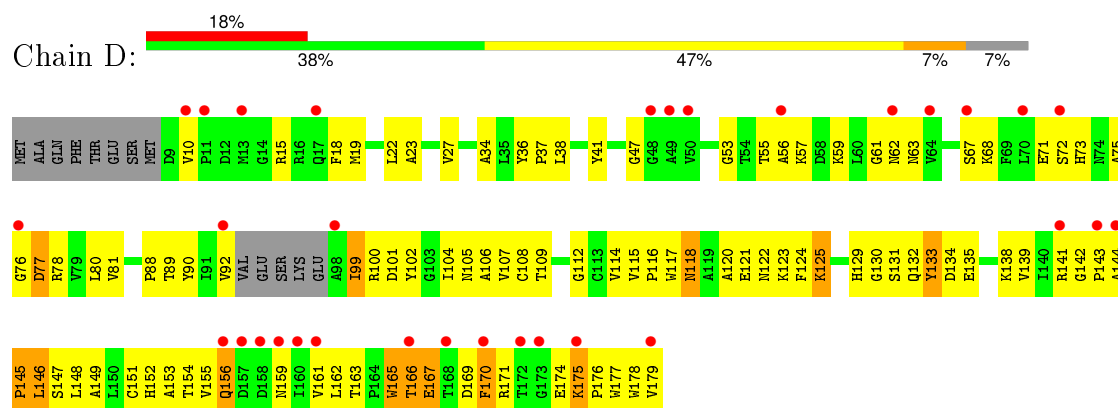


• Molecule 3: Apocytochrome f

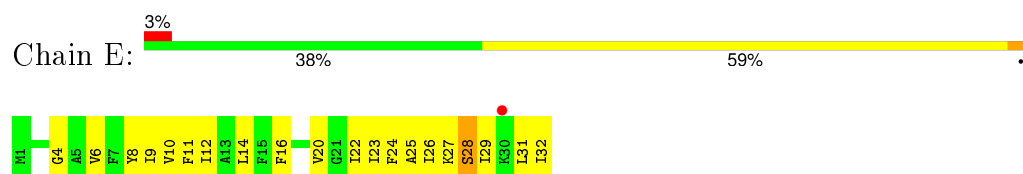




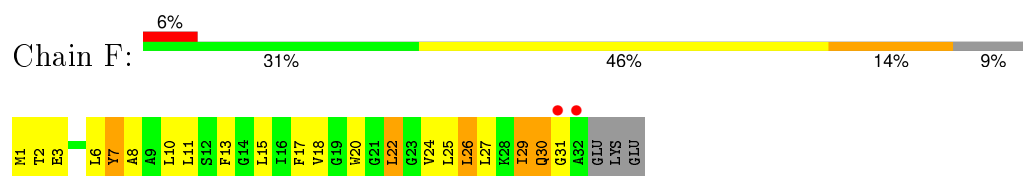
● Molecule 4: Cytochrome b6-f complex iron-sulfur subunit



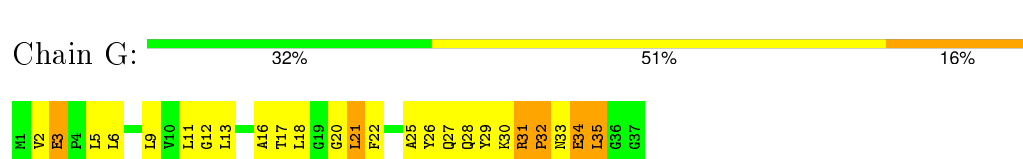
● Molecule 5: Cytochrome b6-f complex subunit 6



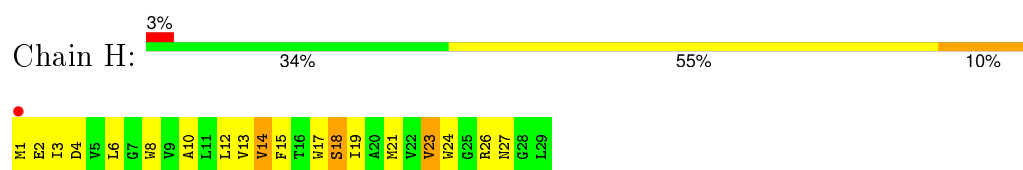
● Molecule 6: Cytochrome b6-f complex subunit 7



● Molecule 7: Cytochrome b6-f complex subunit 5



● Molecule 8: Cytochrome b6-f complex subunit 8



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	158.34Å 158.34Å 361.09Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.30 – 3.00 39.27 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (39.30-3.00) 99.7 (39.27-3.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.71 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.222 , 0.268 0.219 , 0.265	Depositor DCC
R_{free} test set	2740 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	89.0	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 92.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	1 of 54187 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8025	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.80% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: UMQ, CLA, CD, FES, OPC, HEM, BCR, SQD

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	0.78	1/1763 (0.1%)	0.81	1/2405 (0.0%)
2	B	0.75	0/1288	0.87	3/1765 (0.2%)
3	C	0.57	1/2264 (0.0%)	0.66	0/3082
4	D	0.45	0/1292	0.57	0/1760
5	E	0.55	0/253	0.76	0/340
6	F	0.66	0/246	0.74	0/331
7	G	0.67	0/289	0.73	0/391
8	H	0.79	0/236	0.78	0/323
All	All	0.65	2/7631 (0.0%)	0.74	4/10397 (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
2	B	0	1
8	H	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	87	GLU	CG-CD	5.81	1.60	1.51
1	A	113	PRO	CB-CG	5.09	1.75	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	15	ARG	NE-CZ-NH2	-5.49	117.56	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	126	ARG	NE-CZ-NH2	-5.41	117.60	120.30
1	A	113	PRO	CA-N-CD	5.15	118.92	111.70
2	B	126	ARG	NE-CZ-NH1	5.13	122.86	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	32	TRP	Peptide
8	H	27	ASN	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	1711	0	1736	138	1
2	B	1249	0	1308	135	0
3	C	2216	0	2232	199	2
4	D	1260	0	1243	121	0
5	E	248	0	284	27	0
6	F	242	0	260	27	0
7	G	283	0	289	42	1
8	H	230	0	239	21	0
9	A	1	0	0	0	0
9	B	1	0	0	0	0
10	A	129	0	90	24	0
10	C	43	0	30	8	0
11	A	136	0	164	13	0
12	B	65	0	72	4	0
13	B	54	0	83	2	0
13	H	54	0	83	24	0
14	D	4	0	0	2	0
15	D	54	0	57	12	0
16	G	40	0	52	11	0
17	A	2	0	0	0	0
17	B	2	0	0	0	0
17	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8025	0	8222	692	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 43.

The worst 5 of 692 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)
15:D:201:SQD:C4	15:D:201:SQD:C3	1.85	1.54
1:A:113:PRO:CG	1:A:113:PRO:CB	1.75	1.41
15:D:201:SQD:C2	15:D:201:SQD:C4	2.11	1.27
2:B:151:LEU:O	2:B:154:THR:HG22	1.25	1.25
2:B:151:LEU:O	2:B:154:THR:CG2	1.86	1.23

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)
3:C:108:GLU:OE1	7:G:33:ASN:CB[8_565]	1.89	0.31
1:A:112:LYS:CE	3:C:87:GLU:OE1[8_665]	2.14	0.06

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	213/215 (99%)	185 (87%)	26 (12%)	2 (1%)	21	64
2	B	158/160 (99%)	126 (80%)	25 (16%)	7 (4%)	3	18
3	C	286/289 (99%)	244 (85%)	31 (11%)	11 (4%)	4	22
4	D	162/179 (90%)	124 (76%)	28 (17%)	10 (6%)	2	10
5	E	30/32 (94%)	23 (77%)	6 (20%)	1 (3%)	5	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	30/35 (86%)	25 (83%)	5 (17%)	0	100	100
7	G	35/37 (95%)	16 (46%)	14 (40%)	5 (14%)	0	1
8	H	27/29 (93%)	24 (89%)	2 (7%)	1 (4%)	4	23
All	All	941/976 (96%)	767 (82%)	137 (15%)	37 (4%)	4	21

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	112	LYS
2	B	32	TRP
2	B	74	GLU
2	B	125	ARG
3	C	66	SER

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	184/184 (100%)	167 (91%)	17 (9%)	11	40
2	B	137/137 (100%)	123 (90%)	14 (10%)	9	33
3	C	242/243 (100%)	222 (92%)	20 (8%)	14	46
4	D	134/146 (92%)	126 (94%)	8 (6%)	24	62
5	E	25/25 (100%)	23 (92%)	2 (8%)	15	47
6	F	24/27 (89%)	17 (71%)	7 (29%)	0	2
7	G	28/28 (100%)	25 (89%)	3 (11%)	8	31
8	H	24/24 (100%)	19 (79%)	5 (21%)	1	7
All	All	798/814 (98%)	722 (90%)	76 (10%)	11	38

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	94	LEU

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Mol	Chain	Res	Type
3	C	249	LEU
7	G	21	LEU
3	C	131	VAL
3	C	166	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	123	GLN
3	C	192	ASN
4	D	159	ASN
3	C	141	ASN
3	C	196	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 16 ligands modelled in this entry, 2 are monoatomic - leaving 14 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
11	UMQ	A	1101	-	35,35,35	1.44	4 (11%)	46,46,46	2.34	9 (19%)
11	UMQ	A	1102	-	35,35,35	1.58	4 (11%)	46,46,46	2.40	11 (23%)
11	UMQ	A	1103	-	35,35,35	1.47	4 (11%)	46,46,46	2.29	8 (17%)
11	UMQ	A	1104	-	35,35,35	1.38	3 (8%)	46,46,46	2.24	7 (15%)
10	HEM	A	301	1	30,50,50	2.25	6 (20%)	24,82,82	2.80	10 (41%)
10	HEM	A	302	1	30,50,50	2.29	4 (13%)	24,82,82	2.45	9 (37%)
10	HEM	A	303	1	30,50,50	2.27	8 (26%)	24,82,82	2.79	11 (45%)
12	CLA	B	201	-	55,73,73	1.78	12 (21%)	61,113,113	2.33	17 (27%)
13	OPC	B	202	-	53,53,54	1.98	14 (26%)	57,61,64	2.49	12 (21%)
10	HEM	C	301	3	30,50,50	1.82	8 (26%)	24,82,82	2.81	11 (45%)
14	FES	D	200	4	0,4,4	0.00	-	0,4,4	0.00	-
15	SQD	D	201	-	53,54,54	3.41	24 (45%)	61,65,65	4.59	23 (37%)
16	BCR	G	101	-	41,41,41	2.76	13 (31%)	56,56,56	6.74	16 (28%)
13	OPC	H	1002	-	53,53,54	2.06	14 (26%)	57,61,64	2.38	18 (31%)

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
11	UMQ	A	1101	-	2/2/10/10	0/20/60/60	0/2/2/2
11	UMQ	A	1102	-	2/2/10/10	0/20/60/60	0/2/2/2
11	UMQ	A	1103	-	2/2/10/10	0/20/60/60	0/2/2/2
11	UMQ	A	1104	-	2/2/10/10	0/20/60/60	0/2/2/2
10	HEM	A	301	1	-	0/10/54/54	0/0/8/8
10	HEM	A	302	1	-	0/10/54/54	0/0/8/8
10	HEM	A	303	1	-	0/10/54/54	0/0/8/8
12	CLA	B	201	-	4/4/20/25	0/37/135/135	0/0/9/9
13	OPC	B	202	-	-	0/57/57/60	0/0/0/0
10	HEM	C	301	3	-	0/10/54/54	0/0/8/8
14	FES	D	200	4	-	0/0/4/4	0/1/1/1
15	SQD	D	201	-	1/1/9/9	0/49/69/69	0/1/1/1
16	BCR	G	101	-	-	0/29/63/63	0/2/2/2
13	OPC	H	1002	-	-	0/57/57/60	0/0/0/0

The worst 5 of 118 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	D	201	SQD	C6-S	-13.01	1.58	1.77
10	A	302	HEM	C3B-C4B	-9.06	1.43	1.51
16	G	101	BCR	C8-C9	-8.64	1.26	1.45
16	G	101	BCR	C23-C22	-8.23	1.27	1.45
10	A	301	HEM	C3B-C4B	-7.91	1.44	1.51

The worst 5 of 162 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	D	201	SQD	C4-C3-C2	-18.25	76.74	110.79
15	D	201	SQD	O3-C3-C4	-9.99	87.85	110.34
13	B	202	OPC	CAA-NAF-CBG	-9.08	85.62	108.98
13	B	202	OPC	CAA-NAF-CAE	-8.67	86.67	108.98
13	H	1002	OPC	CAA-NAF-CAE	-8.64	86.75	108.98

5 of 13 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
11	A	1103	UMQ	C2'
11	A	1103	UMQ	C1'
11	A	1102	UMQ	C2'
11	A	1102	UMQ	C1'
15	D	201	SQD	C5

There are no torsion outliers.

There are no ring outliers.

14 monomers are involved in 97 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	A	1101	UMQ	6	0
11	A	1102	UMQ	2	0
11	A	1103	UMQ	1	0
11	A	1104	UMQ	4	0
10	A	301	HEM	11	0
10	A	302	HEM	8	0
10	A	303	HEM	5	0
12	B	201	CLA	4	0
13	B	202	OPC	2	0
10	C	301	HEM	8	0
14	D	200	FES	2	0
15	D	201	SQD	12	0
16	G	101	BCR	11	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	H	1002	OPC	24	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 ⓘ

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	215/215 (100%)	-0.52	1 (0%) 91 76	21, 41, 72, 160	0
2	B	160/160 (100%)	-0.40	2 (1%) 79 53	32, 57, 103, 135	0
3	C	288/289 (99%)	0.45	25 (8%) 13 4	20, 54, 114, 130	1 (0%)
4	D	166/179 (92%)	0.87	32 (19%) 2 1	38, 91, 125, 171	0
5	E	32/32 (100%)	-0.27	1 (3%) 52 24	60, 75, 106, 122	0
6	F	32/35 (91%)	-0.37	2 (6%) 23 9	47, 69, 124, 139	0
7	G	37/37 (100%)	-0.25	0 100 100	42, 57, 123, 131	0
8	H	29/29 (100%)	-0.32	1 (3%) 49 21	40, 52, 76, 118	0
All	All	959/976 (98%)	0.06	64 (6%) 21 7	20, 57, 115, 171	1 (0%)

The worst 5 of 64 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	220	SER	7.7
3	C	184	ALA	6.5
4	D	159	ASN	6.2
3	C	206	THR	6.0
4	D	50	VAL	5.8

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

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(Å ²)	Q<0.9
16	BCR	G	101	40/40	0.68	0.43	4.38	33,70,131,136	0
11	UMQ	A	1102	34/34	0.81	0.37	4.05	62,119,148,149	0
11	UMQ	A	1101	34/34	0.77	0.40	3.98	35,109,146,149	0
15	SQD	D	201	54/54	0.86	0.57	2.44	67,164,194,196	0
13	OPC	B	202	54/55	0.92	0.27	2.03	48,82,157,162	0
11	UMQ	A	1103	34/34	0.87	0.34	1.22	76,112,134,135	0
13	OPC	H	1002	54/55	0.83	0.26	1.18	41,93,187,196	0
10	HEM	A	302	43/43	0.98	0.21	0.32	9,34,57,74	0
11	UMQ	A	1104	34/34	0.83	0.32	0.28	86,134,171,175	0
12	CLA	B	201	65/65	0.96	0.18	0.24	41,60,91,99	0
10	HEM	A	301	43/43	0.98	0.18	0.22	9,32,51,75	0
10	HEM	A	303	43/43	0.97	0.19	-0.18	26,59,68,76	0
9	CD	B	161	1/1	0.92	0.20	-0.23	166,166,166,166	0
10	HEM	C	301	43/43	0.97	0.21	-0.45	29,54,89,97	0
14	FES	D	200	4/4	0.96	0.08	-1.93	96,101,102,113	0
9	CD	A	1001	1/1	0.97	0.14	-	65,65,65,65	0

6.5 Other polymers

There are no such residues in this entry.