Full wwPDB X-ray Structure Validation Report (i)

Feb 3, 2024 – 09:37 PM EST

PDB ID	:	1NF4
Title	:	X-Ray Structure of the Desulfovibrio desulfuricans bacterioferritin: the diiron site in different states (reduced structure)
Authors	:	Macedo, S.; Romao, C.V.; Mitchell, E.; Matias, P.M.; Liu, M.Y.; Xavier, A.V.; LeGall, J.; Teixeira, M.; Lindley, P.; Carrondo, M.A.
Deposited on	:	2002-12-13
Resolution	:	2.05 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:

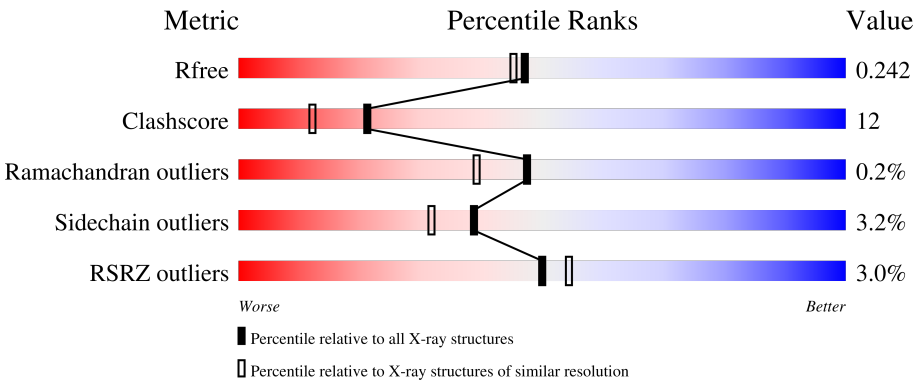
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 2.05 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	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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	179	3% 79% 13% • 6%
1	B	179	2% 77% 17% • 6%
1	C	179	4% 77% 17% • 6%
1	D	179	2% 77% 15% • 6%

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Mol	Chain	Length	Quality of chain
1	E	179	3% 75% 18% 6%
1	F	179	3% 77% 17% 6%
1	G	179	3% 73% 20% 6%
1	H	179	4% 77% 17% 5%
1	I	179	2% 80% 13% 5%
1	J	179	3% 78% 14% 6%
1	K	179	2% 76% 17% 6%
1	L	179	4% 78% 15% 5%
1	M	179	3% 79% 16% 5%
1	N	179	2% 79% 14% 6%
1	O	179	2% 69% 25% 6%
1	P	179	2% 77% 16% 5%

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
3	SO4	A	1006	-	-	X	-
3	SO4	B	1005	-	-	X	-
3	SO4	B	1104	-	-	X	-
3	SO4	C	1206	-	-	X	-
3	SO4	D	1301	-	-	X	-
3	SO4	E	1403	-	-	X	-
3	SO4	H	1702	-	-	-	X
3	SO4	I	1704	-	-	X	-
3	SO4	I	1802	-	-	X	-
3	SO4	L	2102	-	-	X	-
3	SO4	L	2104	-	-	X	-
3	SO4	M	2202	-	-	-	X
3	SO4	O	2406	-	-	X	-
3	SO4	P	1504	-	-	X	-
4	FEC	C	1207[B]	-	-	X	-
4	FEC	I	1805[B]	-	-	X	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 23945 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.

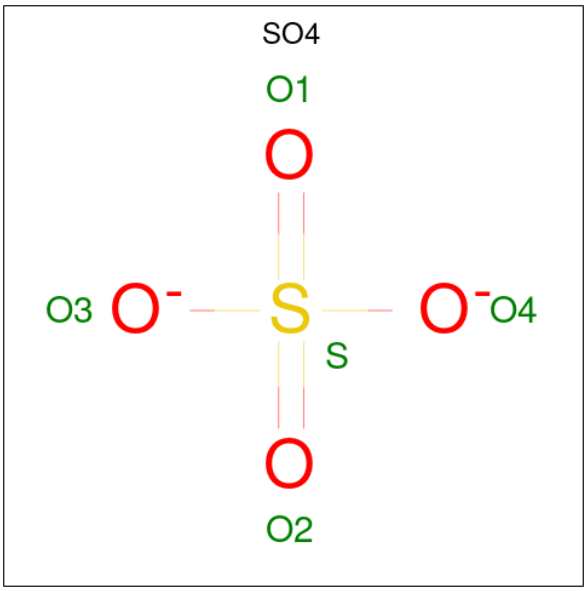
- Molecule 1 is a protein called bacterioferritin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	169	1328	828	229	265	6	0	0	0
1	B	169	1321	823	227	265	6	0	0	0
1	C	169	1318	821	227	264	6	0	0	0
1	D	169	1328	828	228	266	6	0	1	0
1	E	169	1322	824	228	264	6	0	0	0
1	F	169	1324	825	227	266	6	0	0	0
1	G	169	1321	823	226	266	6	0	0	0
1	H	170	1324	824	228	266	6	0	0	0
1	I	170	1328	827	229	266	6	0	0	0
1	J	169	1311	818	224	263	6	0	1	0
1	K	169	1322	824	228	264	6	0	0	0
1	L	170	1336	832	231	267	6	0	1	0
1	M	170	1338	832	232	268	6	0	2	0
1	N	169	1326	826	228	266	6	0	0	0
1	O	169	1315	819	225	265	6	0	0	0
1	P	170	1328	827	229	266	6	0	0	0

- Molecule 2 is FE (II) ION (three-letter code: FE2) (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
2	E	2	2	2	0	0
2	F	2	2	2	0	0
2	G	2	2	2	0	0
2	H	2	2	2	0	0
2	I	2	2	2	0	0
2	J	2	2	2	0	0
2	K	2	2	2	0	0
2	L	2	2	2	0	0
2	M	2	2	2	0	0
2	N	2	2	2	0	0
2	O	2	2	2	0	0
2	P	2	2	2	0	0

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



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
3	D	1	5	4	1	0	0
3	E	1	5	4	1	0	0
3	E	1	5	4	1	0	0
3	E	1	5	4	1	0	0
3	F	1	5	4	1	0	0
3	F	1	5	4	1	0	0
3	F	1	5	4	1	0	0
3	G	1	5	4	1	0	0
3	G	1	5	4	1	0	0
3	G	1	5	4	1	0	0
3	H	1	5	4	1	0	0
3	H	1	5	4	1	0	0
3	H	1	5	4	1	0	0
3	H	1	5	4	1	0	0
3	I	1	5	4	1	0	0
3	I	1	5	4	1	0	0
3	I	1	5	4	1	0	0
3	I	1	5	4	1	0	0
3	I	1	5	4	1	0	0
3	J	1	5	4	1	0	0
3	J	1	5	4	1	0	0

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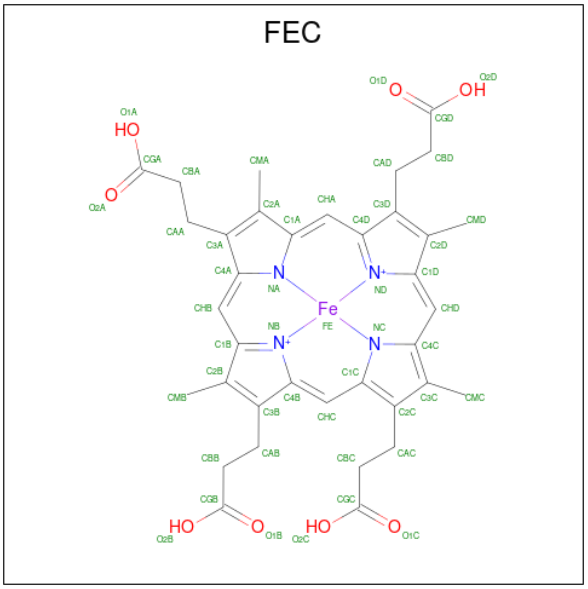
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	J	1	Total O S 5 4 1	0	0
3	K	1	Total O S 5 4 1	0	0
3	K	1	Total O S 5 4 1	0	0
3	K	1	Total O S 5 4 1	0	0
3	L	1	Total O S 5 4 1	0	0
3	L	1	Total O S 5 4 1	0	0
3	L	1	Total O S 5 4 1	0	0
3	L	1	Total O S 5 4 1	0	0
3	M	1	Total O S 5 4 1	0	0
3	M	1	Total O S 5 4 1	0	0
3	M	1	Total O S 5 4 1	0	0
3	M	1	Total O S 5 4 1	0	0
3	N	1	Total O S 5 4 1	0	0
3	N	1	Total O S 5 4 1	0	0
3	N	1	Total O S 5 4 1	0	0
3	O	1	Total O S 5 4 1	0	0
3	O	1	Total O S 5 4 1	0	0
3	P	1	Total O S 5 4 1	0	0
3	P	1	Total O S 5 4 1	0	0
3	P	1	Total O S 5 4 1	0	0
3	P	1	Total O S 5 4 1	0	0

- Molecule 4 is 1,3,5,8-TETRAMETHYL-PORPHINE-2,4,6,7-TETRAPROPIONIC ACID FERROUS COMPLEX (three-letter code: FEC) (formula: $C_{36}H_{36}FeN_4O_8$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Fe	N	O		
4	A	1	98	72	2	8	16	0	1
4	C	1	98	72	2	8	16	0	1
4	E	1	98	72	2	8	16	0	1
4	G	1	98	72	2	8	16	0	1
4	I	1	98	72	2	8	16	0	1
4	L	1	98	72	2	8	16	0	1
4	M	1	98	72	2	8	16	0	1
4	P	1	98	72	2	8	16	0	1

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	123	123	123	0	0
5	B	114	114	114	0	0

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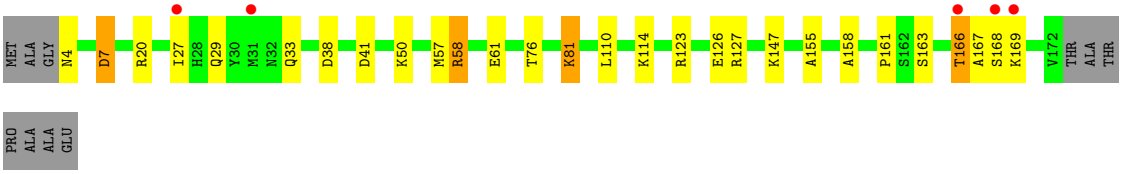
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	99	Total O 99 99	0	0
5	D	103	Total O 103 103	0	0
5	E	86	Total O 86 86	0	0
5	F	89	Total O 89 89	0	0
5	G	104	Total O 104 104	0	0
5	H	93	Total O 93 93	0	0
5	I	121	Total O 121 121	0	0
5	J	91	Total O 91 91	0	0
5	K	105	Total O 105 105	0	0
5	L	129	Total O 129 129	0	0
5	M	124	Total O 124 124	0	0
5	N	108	Total O 108 108	0	0
5	O	74	Total O 74 74	0	0
5	P	96	Total O 96 96	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.

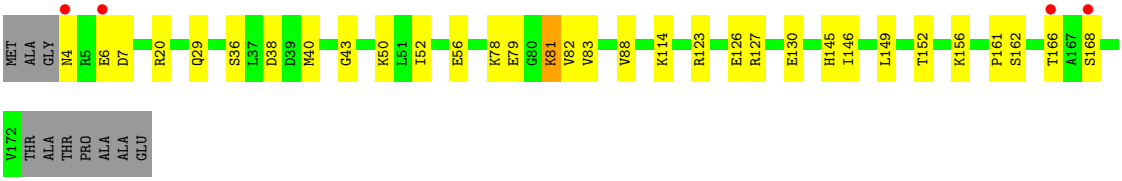
• Molecule 1: bacterioferritin

Chain A: 3% 79% 13% • 6%



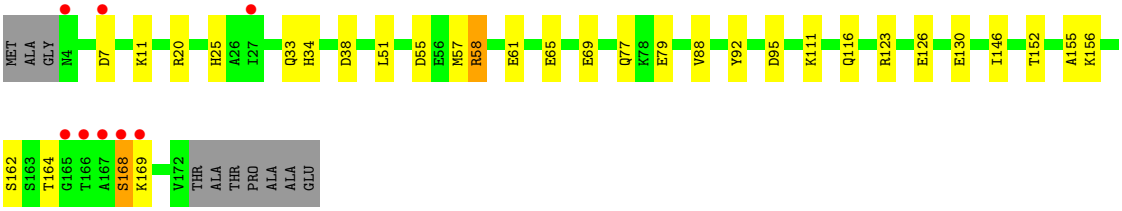
• Molecule 1: bacterioferritin

Chain B: 2% 77% 17% • 6%



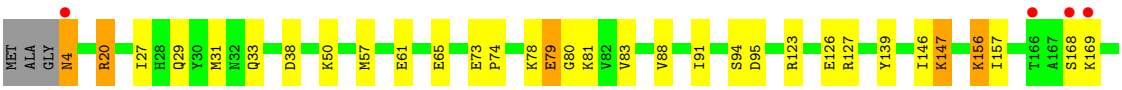
• Molecule 1: bacterioferritin

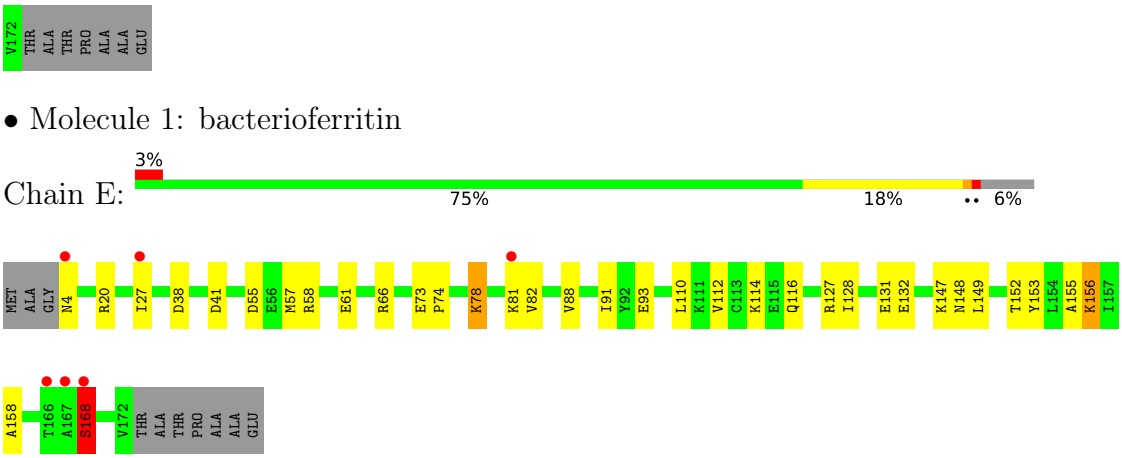
Chain C: 4% 77% 17% • 6%

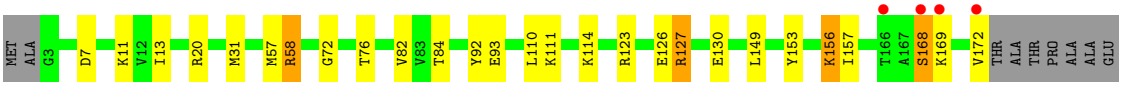


• Molecule 1: bacterioferritin

Chain D: 2% 77% 15% • 6%

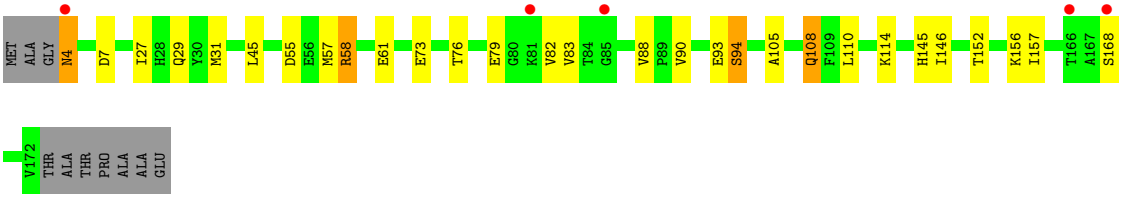



V172 THR ALA THR PRO ALA ALA GLU
• Molecule 1: bacterioferritin
Chain E:
3%
75%
18%
6%
MET ALA GLY N4 R20 I27 D38 D41 D55 E56 M57 R58 E61 R66 E73 P74 K78 K81 V82 V88 I91 Y92 E93 L110 K111 V112 C113 K114 E115 Q116 R127 I128 E131 E132 K147 N148 L149 T152 Y153 L154 A155 K156 I157
A158 T166 A167 S168 V172 THR ALA THR PRO ALA ALA GLU
• Molecule 1: bacterioferritin
Chain F:
3%
77%
17%
6%
MET ALA GLY N4 R5 E6 D7 R8 E14 K18 A19 R20 Q29 Q33 S36 L37 D38 D39 M40 M57 R58 E61 E65 E79 V83 V88 P89 V90 D95 K114 R127 T137 H145 L149 K156 S163 T166 A167 S168 K169
V172 THR ALA THR PRO ALA ALA GLU
• Molecule 1: bacterioferritin
Chain G:
3%
73%
20%
6%
MET ALA GLY N4 R5 R8 E14 K18 A19 R20 I27 M31 N32 Q33 H34 Y35 D38 G43 A53 M57 R58 E61 K68 V88 P89 Y92 D95 K114 E115 Q116 R123 E126 R127 I128 E132 H145 L149 G150 D151 T152
A155 A158 S162 S163 T164 G165 T166 A167 S168 K169 V172 THR ALA THR PRO ALA ALA GLU
• Molecule 1: bacterioferritin
Chain H:
4%
77%
17%
5%
MET ALA G3 N4 D7 E14 K18 I27 H28 Q29 D41 K50 M57 R58 E61 E65 E69 Q77 K81 V82 V83 Y92 L110 K111 K114 E115 R123 E126 R127 I128 E132 L136 E140 H145 T152 A155 K156
G165 T166 A167 S168 K169 V172 THR ALA THR PRO ALA ALA GLU
• Molecule 1: bacterioferritin
Chain I:
2%
80%
13%
5%



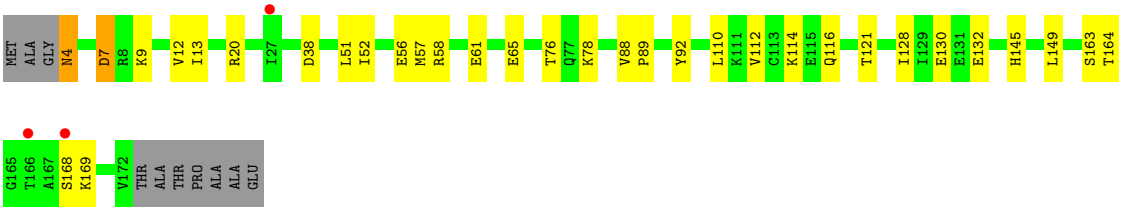
• Molecule 1: bacterioferritin

Chain J:



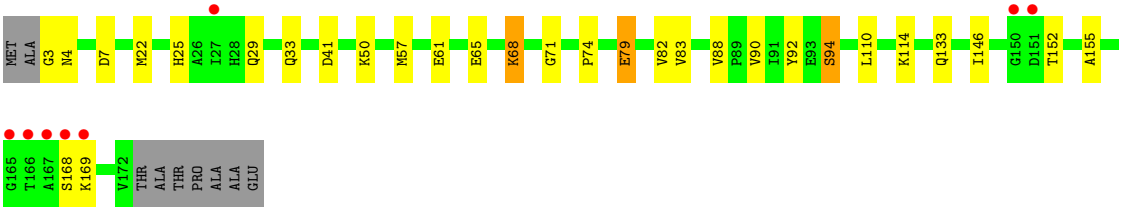
• Molecule 1: bacterioferritin

Chain K:



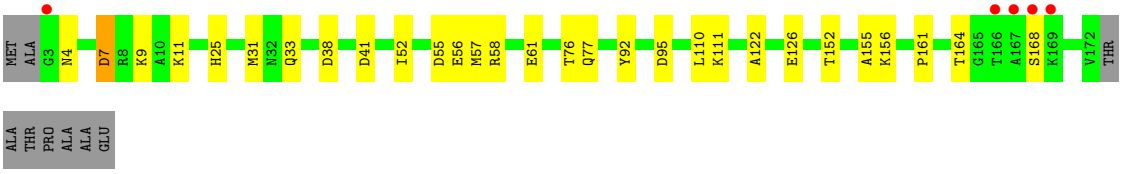
• Molecule 1: bacterioferritin

Chain L:



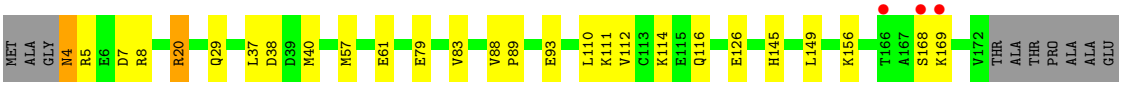
• Molecule 1: bacterioferritin

Chain M:

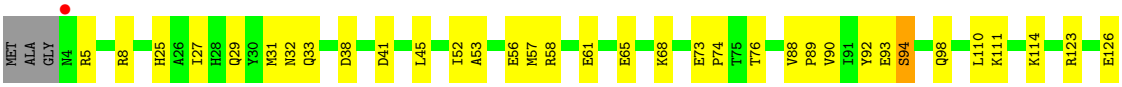


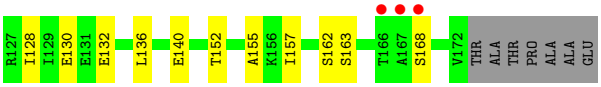
• Molecule 1: bacterioferritin

Chain N:

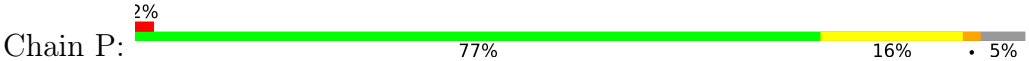


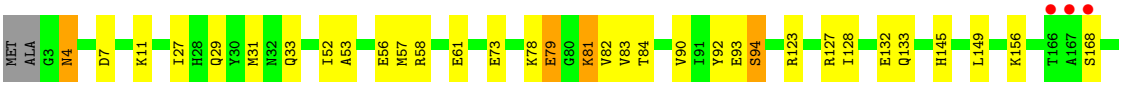
• Molecule 1: bacterioferritin





• Molecule 1: bacterioferritin





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α, β, γ	225.68Å 225.68Å 225.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.05 29.63 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.0 (30.00-2.05) 98.8 (29.63-2.05)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.90 (at 2.04Å)	Xtriage
Refinement program	SHELXL-97, CNS	Depositor
R, R_{free}	0.231 , 0.270 0.196 , 0.242	Depositor DCC
R_{free} test set	4891 reflections (2.08%)	wwPDB-VP
Wilson B-factor (Å^2)	28.5	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 60.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	0.012 for l,-k,h	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	23945	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.46% 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, FE2, FEC

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	0.31	0/1348	0.85	5/1816 (0.3%)
1	B	0.35	0/1341	0.78	1/1809 (0.1%)
1	C	0.29	0/1338	0.83	3/1805 (0.2%)
1	D	0.31	0/1353	0.83	1/1823 (0.1%)
1	E	0.31	0/1342	0.84	2/1809 (0.1%)
1	F	0.37	1/1344 (0.1%)	0.79	0/1812
1	G	0.29	0/1341	0.85	5/1809 (0.3%)
1	H	0.30	0/1344	0.80	2/1813 (0.1%)
1	I	0.30	0/1348	0.80	3/1817 (0.2%)
1	J	0.37	2/1336 (0.1%)	0.76	0/1804
1	K	0.30	0/1342	0.82	1/1809 (0.1%)
1	L	0.32	0/1361	0.78	1/1833 (0.1%)
1	M	0.30	0/1368	0.79	1/1843 (0.1%)
1	N	0.31	0/1346	0.78	3/1814 (0.2%)
1	O	0.30	0/1335	0.83	2/1802 (0.1%)
1	P	0.31	0/1348	0.80	1/1817 (0.1%)
All	All	0.32	3/21535 (0.0%)	0.81	31/29035 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	6	GLU	CD-OE2	6.04	1.32	1.25
1	J	108[A]	GLN	CD-OE1	5.15	1.35	1.24
1	J	108[B]	GLN	CD-OE1	5.15	1.35	1.24

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	58	ARG	NE-CZ-NH1	8.53	124.57	120.30
1	E	127	ARG	NE-CZ-NH1	7.79	124.19	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	N	20	ARG	NE-CZ-NH1	7.66	124.13	120.30
1	A	20	ARG	NE-CZ-NH2	-7.02	116.79	120.30
1	G	127	ARG	NE-CZ-NH2	-6.57	117.02	120.30
1	C	58	ARG	NE-CZ-NH2	-6.34	117.13	120.30
1	E	66	ARG	NE-CZ-NH2	-6.27	117.17	120.30
1	G	92	TYR	CA-CB-CG	-6.12	101.77	113.40
1	A	127	ARG	CD-NE-CZ	5.93	131.90	123.60
1	A	20	ARG	NE-CZ-NH1	5.83	123.22	120.30
1	L	92	TYR	CA-CB-CG	-5.81	102.37	113.40
1	A	58	ARG	NE-CZ-NH2	-5.74	117.43	120.30
1	H	58	ARG	NE-CZ-NH1	5.70	123.15	120.30
1	D	20	ARG	NE-CZ-NH2	-5.69	117.45	120.30
1	G	127	ARG	NE-CZ-NH1	5.67	123.13	120.30
1	A	127	ARG	NE-CZ-NH2	-5.64	117.48	120.30
1	G	35	TYR	CB-CG-CD2	-5.60	117.64	121.00
1	O	58	ARG	NE-CZ-NH2	-5.49	117.56	120.30
1	K	92	TYR	CA-CB-CG	-5.43	103.09	113.40
1	H	92	TYR	CA-CB-CG	-5.34	103.26	113.40
1	N	20	ARG	NE-CZ-NH2	-5.29	117.65	120.30
1	C	92	TYR	CA-CB-CG	-5.29	103.36	113.40
1	N	20	ARG	CD-NE-CZ	5.28	130.99	123.60
1	I	92	TYR	CA-CB-CG	-5.27	103.39	113.40
1	I	58	ARG	NE-CZ-NH1	-5.22	117.69	120.30
1	M	92	TYR	CA-CB-CG	-5.13	103.64	113.40
1	O	92	TYR	CA-CB-CG	-5.11	103.69	113.40
1	P	92	TYR	CA-CB-CG	-5.08	103.74	113.40
1	I	127	ARG	NE-CZ-NH2	-5.07	117.77	120.30
1	G	58	ARG	NE-CZ-NH2	-5.05	117.78	120.30
1	B	127	ARG	NE-CZ-NH1	5.01	122.81	120.30

There are no chirality outliers.

There are no planarity outliers.

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	1328	0	1296	31	0
1	B	1321	0	1276	29	0
1	C	1318	0	1269	24	0
1	D	1328	0	1292	30	0
1	E	1322	0	1280	29	0
1	F	1324	0	1283	24	0
1	G	1321	0	1274	31	0
1	H	1324	0	1277	37	0
1	I	1328	0	1288	45	0
1	J	1311	0	1259	30	0
1	K	1322	0	1280	27	0
1	L	1336	0	1303	41	5
1	M	1338	0	1299	24	0
1	N	1326	0	1284	29	0
1	O	1315	0	1258	36	0
1	P	1328	0	1288	38	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
2	E	2	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
2	I	2	0	0	0	0
2	J	2	0	0	0	0
2	K	2	0	0	0	0
2	L	2	0	0	0	0
2	M	2	0	0	0	0
2	N	2	0	0	0	0
2	O	2	0	0	0	0
2	P	2	0	0	0	0
3	A	15	0	0	2	0
3	B	25	0	0	8	0
3	C	20	0	0	2	0
3	D	15	0	0	3	0
3	E	15	0	0	4	0
3	F	15	0	0	0	0
3	G	15	0	0	1	0
3	H	20	0	0	0	0
3	I	25	0	0	5	14
3	J	15	0	0	0	0
3	K	15	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	L	20	0	0	5	19
3	M	20	0	0	2	0
3	N	15	0	0	1	0
3	O	10	0	0	2	0
3	P	20	0	0	4	0
4	A	98	0	64	21	0
4	C	98	0	64	29	0
4	E	98	0	64	21	0
4	G	98	0	64	24	0
4	I	98	0	64	37	0
4	L	98	0	64	29	0
4	M	98	0	64	19	0
4	P	98	0	64	30	0
5	A	123	0	0	3	0
5	B	114	0	0	10	0
5	C	99	0	0	2	0
5	D	103	0	0	7	0
5	E	86	0	0	1	0
5	F	89	0	0	3	0
5	G	104	0	0	1	0
5	H	93	0	0	5	0
5	I	121	0	0	4	0
5	J	91	0	0	4	0
5	K	105	0	0	3	0
5	L	129	0	0	6	0
5	M	124	0	0	5	0
5	N	108	0	0	2	0
5	O	74	0	0	2	0
5	P	96	0	0	4	0
All	All	23945	0	21018	522	19

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 12.

All (522) 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)
4:L:2107[B]:FEC:NA	4:L:2107[B]:FEC:C4A	1.75	1.45
4:P:2507[B]:FEC:C4A	4:P:2507[B]:FEC:NA	1.80	1.44
4:C:1207[B]:FEC:FE	4:C:1207[B]:FEC:NC	0.70	1.43
4:E:1407[B]:FEC:C4B	4:E:1407[B]:FEC:NB	1.68	1.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1007[B]:FEC:NA	4:A:1007[B]:FEC:C1A	1.72	1.34
4:C:1207[B]:FEC:C4B	4:C:1207[B]:FEC:NB	1.84	1.34
4:I:1805[B]:FEC:C1D	4:I:1805[B]:FEC:ND	1.84	1.33
4:G:1607[B]:FEC:ND	4:G:1607[B]:FEC:C1D	1.76	1.32
4:A:1007[B]:FEC:ND	4:A:1007[B]:FEC:C1D	1.90	1.26
4:I:1805[B]:FEC:FE	4:I:1805[B]:FEC:NC	0.99	1.26
1:E:147:LYS:HE2	3:E:1403:SO4:O4	1.28	1.26
4:L:2107[B]:FEC:NA	4:L:2107[B]:FEC:C1A	1.97	1.25
1:P:168:SER:HA	4:P:2507[A]:FEC:O2C	1.21	1.24
4:G:1607[A]:FEC:O2C	1:H:168:SER:HA	1.28	1.24
1:A:168:SER:HA	4:A:1007[B]:FEC:O2C	1.38	1.23
4:P:2507[B]:FEC:NA	4:P:2507[B]:FEC:NB	1.87	1.22
1:C:168:SER:HA	4:C:1207[B]:FEC:O2C	1.12	1.21
1:I:168:SER:CA	4:I:1805[B]:FEC:O2C	1.88	1.20
4:C:1207[B]:FEC:NC	4:C:1207[B]:FEC:NB	1.89	1.19
1:I:168:SER:HA	4:I:1805[B]:FEC:O2C	0.98	1.13
4:C:1207[B]:FEC:NC	1:D:57:MET:SD	2.21	1.13
1:O:57:MET:SD	4:P:2507[B]:FEC:NA	2.23	1.12
1:P:168:SER:CA	4:P:2507[A]:FEC:O2C	1.98	1.11
1:L:114:LYS:CD	3:L:2104:SO4:O4	1.99	1.11
4:I:1805[B]:FEC:NC	4:I:1805[B]:FEC:C1C	2.13	1.10
1:A:168:SER:CA	4:A:1007[B]:FEC:O2C	2.00	1.09
1:L:114:LYS:NZ	3:L:2104:SO4:O4	1.87	1.07
1:C:168:SER:CA	4:C:1207[B]:FEC:O2C	2.02	1.07
4:I:1805[B]:FEC:NC	4:I:1805[B]:FEC:C4C	2.16	1.07
1:L:114:LYS:CE	3:L:2104:SO4:O4	2.04	1.04
1:L:168:SER:CB	4:L:2107[A]:FEC:O2C	2.06	1.04
4:P:2507[B]:FEC:NA	4:P:2507[B]:FEC:C1A	2.22	1.02
1:L:114:LYS:HD2	3:L:2104:SO4:O4	1.60	1.02
4:E:1407[B]:FEC:NC	4:E:1407[B]:FEC:C4C	2.25	0.99
4:I:1805[B]:FEC:ND	4:I:1805[B]:FEC:NC	2.11	0.97
1:L:168:SER:HA	4:L:2107[A]:FEC:O2C	1.63	0.96
1:L:168:SER:CA	4:L:2107[A]:FEC:O2C	2.14	0.95
1:N:29:GLN:HE22	1:N:83:VAL:H	1.08	0.94
4:G:1607[A]:FEC:O2C	1:H:168:SER:CA	2.15	0.93
3:B:1005:SO4:O2	5:B:1216:HOH:O	1.87	0.92
4:L:2107[B]:FEC:NA	4:L:2107[B]:FEC:FE	1.37	0.92
3:N:2301:SO4:O2	5:N:2413:HOH:O	1.86	0.92
1:L:29:GLN:HE22	1:L:83:VAL:H	1.12	0.91
1:D:29:GLN:HE22	1:D:83:VAL:H	1.20	0.90
1:I:168:SER:HB3	4:I:1805[B]:FEC:CGB	2.03	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:SER:CB	4:A:1007[B]:FEC:O2C	2.21	0.88
1:M:110:LEU:HD11	1:M:126[B]:GLU:HG2	1.54	0.88
4:C:1207[B]:FEC:NC	4:C:1207[B]:FEC:C1C	2.36	0.88
1:I:168:SER:HB3	4:I:1805[B]:FEC:HBB2	1.56	0.87
1:J:29:GLN:HE22	1:J:83:VAL:H	1.24	0.85
4:P:2507[B]:FEC:NA	4:P:2507[B]:FEC:CHB	2.39	0.85
1:E:147:LYS:CE	3:E:1403:SO4:O4	2.20	0.85
1:A:168:SER:HA	4:A:1007[B]:FEC:CGC	2.06	0.85
4:I:1805[B]:FEC:NC	1:J:57:MET:SD	2.51	0.84
1:L:168:SER:HA	4:L:2107[A]:FEC:CGC	2.07	0.84
3:C:1206:SO4:O3	5:C:9486:HOH:O	1.95	0.83
1:B:29:GLN:HE22	1:B:83:VAL:H	1.27	0.83
1:H:29:GLN:HE22	1:H:83:VAL:H	1.22	0.82
1:B:81:LYS:HE2	3:B:1005:SO4:O1	1.79	0.82
4:L:2107[B]:FEC:NA	4:L:2107[B]:FEC:NB	2.28	0.82
1:I:57:MET:SD	4:I:1805[B]:FEC:NC	2.52	0.81
1:A:168:SER:HB3	4:A:1007[B]:FEC:HBB2	1.63	0.80
1:F:114:LYS:NZ	3:P:1504:SO4:O3	2.15	0.80
4:P:2507[B]:FEC:NA	4:P:2507[B]:FEC:FE	1.48	0.80
1:P:93:GLU:HG3	5:P:9559:HOH:O	1.81	0.79
1:I:168:SER:HB3	4:I:1805[B]:FEC:CBB	2.11	0.79
4:L:2107[B]:FEC:NA	4:L:2107[B]:FEC:CHB	2.46	0.78
3:B:1005:SO4:S	5:B:1216:HOH:O	2.38	0.78
1:C:155:ALA:O	1:E:156:LYS:HE3	1.83	0.78
1:E:168:SER:HA	4:E:1407[B]:FEC:O2C	1.83	0.77
1:P:29:GLN:HE22	1:P:83:VAL:H	1.30	0.77
4:I:1805[B]:FEC:NC	4:I:1805[B]:FEC:NB	2.33	0.77
4:G:1607[A]:FEC:HBC2	4:G:1607[A]:FEC:HHC	1.66	0.77
1:H:156:LYS:HE2	5:H:9565:HOH:O	1.83	0.77
4:A:1007[B]:FEC:HBC2	4:A:1007[B]:FEC:HHC	1.65	0.77
3:B:1104:SO4:O4	1:G:114:LYS:NZ	2.16	0.77
1:M:122:ALA:O	1:M:126[B]:GLU:HG3	1.84	0.77
1:I:168:SER:HA	4:I:1805[B]:FEC:CGC	2.08	0.77
4:G:1607[A]:FEC:HBB2	1:H:168:SER:HB3	1.66	0.77
1:I:31:MET:HG3	4:I:1805[A]:FEC:HBD1	1.66	0.76
1:E:148:ASN:ND2	3:E:1403:SO4:O1	2.15	0.76
1:B:123:ARG:HD3	1:N:126:GLU:OE1	1.87	0.75
1:L:168:SER:HB2	4:L:2107[A]:FEC:O2C	1.84	0.75
1:P:4:ASN:ND2	1:P:7:ASP:H	1.84	0.74
1:P:168:SER:HB3	4:P:2507[A]:FEC:HBB2	1.67	0.74
1:K:114:LYS:HE2	3:P:1504:SO4:O1	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:169:LYS:HB3	5:D:9513:HOH:O	1.87	0.74
1:H:114:LYS:NZ	3:I:1704:SO4:O2	2.18	0.73
1:M:168:SER:HA	4:M:2207[B]:FEC:O2C	1.88	0.73
1:P:168:SER:HA	4:P:2507[A]:FEC:CGC	2.16	0.72
4:P:2507[B]:FEC:NA	4:P:2507[B]:FEC:C1B	2.53	0.72
1:F:29:GLN:HE22	1:F:83:VAL:H	1.36	0.72
1:C:57:MET:SD	4:C:1207[B]:FEC:NC	2.62	0.72
1:E:168:SER:OG	1:F:58:ARG:HD3	1.90	0.72
1:J:79:GLU:HG2	5:J:9508:HOH:O	1.88	0.72
1:P:78:LYS:HE2	1:P:81:LYS:NZ	2.05	0.72
1:C:155:ALA:HA	1:E:149:LEU:HD13	1.71	0.72
1:O:57:MET:CE	4:P:2507[B]:FEC:NA	2.52	0.72
1:C:7:ASP:O	1:C:11:LYS:HG3	1.91	0.71
1:F:4:ASN:ND2	1:F:7:ASP:H	1.87	0.71
1:A:168:SER:HB3	4:A:1007[B]:FEC:O2C	1.90	0.70
1:N:4:ASN:ND2	1:N:7:ASP:H	1.89	0.70
1:I:114:LYS:NZ	3:I:1704:SO4:O4	2.22	0.70
4:P:2507[A]:FEC:HBC2	4:P:2507[A]:FEC:HHC	1.73	0.70
3:D:1301:SO4:O1	5:D:9670:HOH:O	0.72	0.70
1:I:168:SER:HB3	4:I:1805[B]:FEC:O2B	1.91	0.70
4:M:2207[A]:FEC:HBB2	1:N:168:SER:HB3	1.73	0.70
4:C:1207[B]:FEC:NC	4:C:1207[B]:FEC:C4C	2.55	0.69
1:I:168:SER:CB	4:I:1805[B]:FEC:O2B	2.40	0.69
4:E:1407[A]:FEC:HBC2	1:F:168:SER:HB2	1.74	0.69
1:L:57:MET:SD	4:L:2107[B]:FEC:NA	2.66	0.69
1:O:31:MET:HG3	4:P:2507[A]:FEC:HBD1	1.74	0.69
1:B:4:ASN:HD22	1:B:7:ASP:H	1.39	0.68
1:E:147:LYS:HE2	3:E:1403:SO4:S	2.32	0.68
1:I:93:GLU:HG3	5:I:9455:HOH:O	1.92	0.68
1:N:110:LEU:HD23	1:N:114:LYS:HE2	1.76	0.68
1:B:4:ASN:ND2	1:B:7:ASP:H	1.89	0.68
3:D:1306:SO4:O4	5:D:9704:HOH:O	2.11	0.68
1:P:78:LYS:HE2	1:P:81:LYS:HZ1	1.58	0.68
4:L:2107[A]:FEC:HBC2	4:L:2107[A]:FEC:HHC	1.76	0.67
3:B:1005:SO4:O4	5:B:1216:HOH:O	2.12	0.67
4:C:1207[B]:FEC:HBC2	4:C:1207[B]:FEC:HHC	1.76	0.67
1:B:161:PRO:HA	5:B:1207:HOH:O	1.94	0.67
1:H:123:ARG:HG3	1:H:127:ARG:NH2	2.10	0.66
1:J:156:LYS:HE2	5:J:841:HOH:O	1.96	0.66
1:O:152:THR:HG22	5:O:9706:HOH:O	1.94	0.66
1:I:76:THR:HG21	1:J:82:VAL:HG11	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:4:ASN:ND2	1:J:7:ASP:H	1.93	0.66
1:G:155:ALA:HA	1:I:149:LEU:HD13	1.78	0.66
1:E:41:ASP:OD2	1:P:145:HIS:HE1	1.79	0.66
1:P:81:LYS:HD3	1:P:82:VAL:H	1.60	0.66
1:P:168:SER:CB	4:P:2507[A]:FEC:O2C	2.44	0.65
1:E:110:LEU:HD23	1:E:114:LYS:HD2	1.78	0.65
1:O:168:SER:OG	1:P:58:ARG:HD3	1.96	0.65
1:I:172:VAL:HG23	1:J:55:ASP:OD2	1.97	0.65
1:L:4:ASN:HD22	1:L:7:ASP:H	1.45	0.65
1:L:168:SER:HB3	4:L:2107[A]:FEC:HBB2	1.79	0.65
1:I:58:ARG:HD3	1:J:168:SER:OG	1.97	0.65
4:I:1805[B]:FEC:ND	1:J:57:MET:CE	2.60	0.64
1:F:61:GLU:O	1:F:65:GLU:HG3	1.97	0.64
1:E:155:ALA:HA	1:P:149:LEU:HD13	1.79	0.64
1:H:29:GLN:NE2	1:H:83:VAL:H	1.95	0.64
4:L:2107[B]:FEC:HBC2	4:L:2107[B]:FEC:HHC	1.78	0.64
1:G:149:LEU:HD13	1:M:155:ALA:HA	1.79	0.64
1:H:65:GLU:O	1:H:69:GLU:HG3	1.98	0.64
1:K:168:SER:HA	4:L:2107[B]:FEC:O2C	1.98	0.63
1:G:168:SER:HB3	4:G:1607[B]:FEC:HBB2	1.79	0.63
1:H:114:LYS:HD2	3:I:1704:SO4:O2	1.98	0.63
4:I:1805[A]:FEC:O2C	1:J:168:SER:HA	1.99	0.62
4:A:1007[A]:FEC:O2C	1:B:168:SER:HA	2.00	0.62
1:M:31:MET:HG3	4:M:2207[A]:FEC:HBD1	1.81	0.61
1:O:136:LEU:O	1:O:140:GLU:HG3	2.00	0.61
1:D:80:GLY:O	1:D:81:LYS:HE2	2.00	0.61
4:I:1805[A]:FEC:HBC2	4:I:1805[A]:FEC:HHC	1.81	0.61
1:N:29:GLN:NE2	1:N:83:VAL:H	1.90	0.61
1:O:168:SER:HA	4:P:2507[B]:FEC:O2C	2.00	0.61
1:A:155:ALA:HA	1:N:149:LEU:HD13	1.83	0.60
1:A:169:LYS:HB3	5:B:1211:HOH:O	2.00	0.60
1:C:57:MET:HB3	4:C:1207[B]:FEC:C1D	2.32	0.60
1:I:126:GLU:HG2	5:I:9732:HOH:O	2.00	0.60
4:I:1805[A]:FEC:C1D	1:J:57:MET:HB3	2.32	0.60
4:I:1805[A]:FEC:HMD2	1:J:61:GLU:HB2	1.83	0.60
1:M:76:THR:HG22	5:M:8936:HOH:O	2.01	0.60
1:P:128:ILE:O	1:P:132:GLU:HG2	2.02	0.60
1:I:168:SER:OG	1:J:58:ARG:HD3	2.01	0.60
1:K:58:ARG:HB2	5:L:9682:HOH:O	2.02	0.59
1:B:82:VAL:HB	5:B:1216:HOH:O	2.02	0.59
1:G:57:MET:HB3	4:G:1607[B]:FEC:C1D	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:4:ASN:HD22	1:P:7:ASP:H	1.50	0.59
1:B:152:THR:HG21	1:H:152:THR:HG23	1.84	0.59
1:B:156:LYS:HD3	5:H:9690:HOH:O	2.03	0.59
1:H:123:ARG:NH1	1:H:126:GLU:OE1	2.36	0.59
1:M:4:ASN:OD1	1:M:7:ASP:HB2	2.02	0.59
4:C:1207[A]:FEC:HBB2	1:D:168:SER:HB3	1.83	0.59
1:C:152:THR:HA	1:E:152:THR:HG21	1.85	0.59
1:L:22:MET:HA	1:L:79:GLU:OE1	2.02	0.59
1:N:29:GLN:HE22	1:N:83:VAL:N	1.89	0.59
1:D:4:ASN:N	1:D:4:ASN:HD22	2.00	0.59
4:E:1407[B]:FEC:NC	4:E:1407[B]:FEC:CHD	2.65	0.59
1:B:126:GLU:O	1:B:130:GLU:HG3	2.03	0.58
1:J:110:LEU:CD2	1:J:114:LYS:HE2	2.33	0.58
1:O:5:ARG:HD2	1:O:8:ARG:NH1	2.18	0.58
1:E:20:ARG:HH22	4:E:1407[A]:FEC:CGA	2.17	0.58
1:E:61:GLU:HB2	4:E:1407[B]:FEC:CMD	2.33	0.58
1:I:168:SER:CB	4:I:1805[B]:FEC:HBB2	2.32	0.58
1:L:68:LYS:HD3	1:L:74:PRO:HD3	1.86	0.58
4:L:2107[B]:FEC:NA	4:L:2107[B]:FEC:C1B	2.66	0.58
4:M:2207[A]:FEC:CMD	1:N:61:GLU:HB2	2.34	0.58
4:I:1805[B]:FEC:HHC	4:I:1805[B]:FEC:HBC1	1.86	0.58
4:M:2207[A]:FEC:C1D	1:N:57:MET:HB3	2.33	0.58
1:M:25:HIS:HD2	5:M:9724:HOH:O	1.86	0.58
4:C:1207[B]:FEC:NC	4:C:1207[B]:FEC:C4B	2.66	0.57
1:J:29:GLN:NE2	1:J:83:VAL:H	1.98	0.57
1:O:61:GLU:HB2	4:P:2507[B]:FEC:HMD2	1.84	0.57
1:P:57:MET:HB3	4:P:2507[A]:FEC:C1D	2.34	0.57
1:H:169:LYS:HB2	5:H:9507:HOH:O	2.05	0.57
1:C:20:ARG:HH22	4:C:1207[B]:FEC:CGD	2.17	0.57
1:G:128:ILE:O	1:G:132:GLU:HG2	2.04	0.57
1:L:57:MET:HB3	4:L:2107[A]:FEC:C1D	2.35	0.57
1:K:110:LEU:HD23	1:K:114:LYS:HD2	1.87	0.56
1:K:114:LYS:CE	3:P:1504:SO4:O1	2.53	0.56
1:L:168:SER:HB3	4:L:2107[A]:FEC:O2C	2.03	0.56
1:B:81:LYS:HE2	5:B:1202:HOH:O	2.05	0.56
1:K:149:LEU:HD13	1:O:155:ALA:HA	1.86	0.56
1:P:31:MET:HG3	4:P:2507[B]:FEC:HBD1	1.88	0.56
4:A:1007[A]:FEC:HBC2	4:A:1007[A]:FEC:HHC	1.87	0.56
4:E:1407[A]:FEC:O2C	1:F:168:SER:HA	2.06	0.56
1:C:126:GLU:O	1:C:130:GLU:HG3	2.06	0.56
1:L:114:LYS:NZ	3:L:2104:SO4:S	2.65	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:152:THR:HG21	1:M:152:THR:HG23	1.86	0.56
1:I:110:LEU:HD23	1:I:114:LYS:HD2	1.86	0.56
4:E:1407[B]:FEC:NC	4:E:1407[B]:FEC:C1C	2.69	0.55
4:M:2207[B]:FEC:HHC	4:M:2207[B]:FEC:HBC2	1.87	0.55
1:L:61:GLU:O	1:L:65:GLU:HG3	2.06	0.55
1:M:9:LYS:HE2	5:M:9323:HOH:O	2.06	0.55
1:A:169:LYS:HB2	5:A:1118:HOH:O	2.05	0.55
1:K:114:LYS:HE2	3:P:1504:SO4:S	2.47	0.55
1:B:50:LYS:HD3	5:B:1219:HOH:O	2.05	0.55
1:E:78:LYS:HE2	5:E:490:HOH:O	2.05	0.55
1:K:145:HIS:CE1	1:O:41:ASP:HB3	2.42	0.55
1:C:168:SER:HB3	4:C:1207[B]:FEC:HBB2	1.88	0.54
1:J:27:ILE:HD11	1:J:57:MET:HA	1.90	0.54
1:O:57:MET:HE2	4:P:2507[B]:FEC:NA	2.22	0.54
1:P:53:ALA:O	1:P:57:MET:HG3	2.07	0.54
1:N:4:ASN:HD21	1:N:7:ASP:H	1.56	0.54
1:I:57:MET:HB3	4:I:1805[A]:FEC:C1B	2.37	0.54
4:E:1407[B]:FEC:NC	4:E:1407[B]:FEC:C1D	2.49	0.54
1:H:145:HIS:HD2	5:H:9052:HOH:O	1.90	0.54
1:O:57:MET:HB3	4:P:2507[B]:FEC:C1D	2.38	0.54
1:F:145:HIS:HE1	1:L:41:ASP:OD2	1.90	0.54
1:A:81:LYS:HE2	5:A:1076:HOH:O	2.08	0.54
1:I:57:MET:HB3	4:I:1805[B]:FEC:C1D	2.37	0.54
1:P:27:ILE:HD11	1:P:57:MET:HA	1.90	0.54
1:F:5:ARG:HD2	1:F:8:ARG:NH1	2.24	0.53
1:H:123:ARG:HE	1:H:127:ARG:HE	1.55	0.53
1:O:88:VAL:HB	1:O:89:PRO:HD3	1.90	0.53
1:L:168:SER:HB3	4:L:2107[A]:FEC:CGB	2.38	0.53
4:E:1407[B]:FEC:HAC2	1:F:168:SER:HB2	1.89	0.53
1:A:58:ARG:HB2	5:B:1220:HOH:O	2.09	0.53
1:A:166:THR:HG22	1:A:167:ALA:O	2.09	0.53
1:J:145:HIS:HD2	5:J:786:HOH:O	1.91	0.52
4:M:2207[A]:FEC:CGC	1:N:168:SER:HA	2.39	0.52
1:K:12:VAL:CG1	1:K:121:THR:HG21	2.40	0.52
1:G:61:GLU:HB2	4:G:1607[B]:FEC:HMD2	1.92	0.52
1:H:110:LEU:CD2	1:H:114:LYS:HE2	2.40	0.52
1:D:27:ILE:HD11	1:D:57:MET:HA	1.92	0.52
1:K:57:MET:HB3	4:L:2107[A]:FEC:C1B	2.39	0.52
1:L:88:VAL:HG12	1:L:146:ILE:HD13	1.92	0.52
4:E:1407[A]:FEC:HBC2	1:F:168:SER:CB	2.39	0.52
1:L:110:LEU:CD2	1:L:114:LYS:HE3	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:145:HIS:HE1	1:H:41:ASP:OD2	1.93	0.51
1:J:156:LYS:HD3	5:J:9480:HOH:O	2.10	0.51
1:K:164:THR:O	1:L:169:LYS:HD3	2.10	0.51
1:C:55:ASP:OD1	1:C:58:ARG:NH2	2.43	0.51
1:C:61:GLU:HB2	4:C:1207[B]:FEC:HMD2	1.93	0.51
1:C:162:SER:N	3:C:1206:SO4:O3	2.32	0.51
1:G:61:GLU:HB2	4:G:1607[B]:FEC:CMD	2.41	0.51
4:G:1607[A]:FEC:CBB	1:H:168:SER:HB3	2.40	0.51
1:H:136:LEU:HD11	1:H:140:GLU:OE2	2.10	0.51
1:H:156:LYS:HD3	5:H:9520:HOH:O	2.11	0.51
1:I:84:THR:HB	1:J:73:GLU:OE2	2.11	0.51
1:O:53:ALA:O	1:O:57:MET:HG3	2.11	0.51
1:A:161:PRO:HB3	3:A:1006:SO4:O2	2.11	0.51
1:M:57:MET:HB3	4:M:2207[A]:FEC:C1B	2.41	0.51
1:O:61:GLU:HB2	4:P:2507[B]:FEC:CMD	2.40	0.51
1:D:81:LYS:HD3	5:D:296:HOH:O	2.10	0.50
1:I:114:LYS:CE	3:I:1704:SO4:O4	2.58	0.50
1:P:90:VAL:O	1:P:94:SER:OG	2.28	0.50
1:B:88:VAL:HG12	1:B:146:ILE:HD13	1.93	0.50
4:I:1805[A]:FEC:HBB2	1:J:168:SER:HB3	1.94	0.50
1:N:37:LEU:HA	1:N:40:MET:HE3	1.94	0.50
1:N:111:LYS:HA	1:N:114:LYS:CE	2.41	0.50
1:P:52:ILE:O	1:P:56:GLU:HG2	2.12	0.50
1:I:168:SER:OG	4:I:1805[B]:FEC:O2B	2.28	0.50
1:A:168:SER:HB3	4:A:1007[B]:FEC:CBB	2.40	0.49
1:J:88:VAL:HG12	1:J:146:ILE:HD13	1.94	0.49
1:N:88:VAL:HB	1:N:89:PRO:HD3	1.94	0.49
1:I:82:VAL:HG11	1:J:76:THR:HG21	1.93	0.49
1:O:29:GLN:O	1:O:33:GLN:HG3	2.12	0.49
1:H:110:LEU:HD22	1:H:114:LYS:HE2	1.94	0.49
1:K:130:GLU:OE1	1:P:123:ARG:HG2	2.12	0.49
1:E:128:ILE:O	1:E:132:GLU:HG2	2.12	0.49
1:L:168:SER:HB3	4:L:2107[A]:FEC:O2B	2.13	0.49
1:E:158:ALA:HB1	1:P:145:HIS:CD2	2.48	0.49
1:H:114:LYS:CD	3:I:1704:SO4:O2	2.60	0.49
1:L:168:SER:HA	4:L:2107[A]:FEC:O1C	2.13	0.49
1:O:32:ASN:OD1	1:P:73:GLU:OE2	2.29	0.49
1:B:78:LYS:HE2	3:B:1005:SO4:O2	2.13	0.48
1:B:114:LYS:NZ	3:B:1104:SO4:O3	2.39	0.48
4:E:1407[A]:FEC:CGD	1:F:20:ARG:HH22	2.26	0.48
1:L:61:GLU:HB2	4:L:2107[A]:FEC:HMD2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:ALA:O	1:N:156:LYS:NZ	2.46	0.48
4:G:1607[A]:FEC:C1D	1:H:57:MET:HB3	2.43	0.48
1:K:88:VAL:HB	1:K:89:PRO:HD3	1.95	0.48
1:A:169:LYS:NZ	1:B:166:THR:HG22	2.29	0.48
4:G:1607[B]:FEC:ND	1:H:57:MET:CE	2.76	0.48
1:K:20:ARG:HH22	4:L:2107[B]:FEC:CGD	2.26	0.48
1:K:52:ILE:O	1:K:56:GLU:HG2	2.13	0.48
1:L:29:GLN:O	1:L:33:GLN:HG3	2.13	0.48
1:A:50:LYS:HE3	4:A:1007[B]:FEC:HAB2	1.94	0.48
1:K:61:GLU:O	1:K:65:GLU:HG3	2.13	0.48
1:O:128:ILE:O	1:O:132:GLU:HG2	2.12	0.48
1:A:29:GLN:O	1:A:33:GLN:HG3	2.13	0.48
1:G:145:HIS:CE1	1:M:41:ASP:HB3	2.49	0.48
1:I:57:MET:HB3	4:I:1805[A]:FEC:CHB	2.43	0.48
4:C:1207[A]:FEC:O2C	1:D:168:SER:HB3	2.14	0.48
1:D:156:LYS:HG2	1:D:157:ILE:HD13	1.95	0.48
4:E:1407[B]:FEC:HBC1	4:E:1407[B]:FEC:HHC	1.96	0.48
1:G:88:VAL:HB	1:G:89:PRO:HD3	1.94	0.48
4:M:2207[A]:FEC:HMD2	1:N:61:GLU:HB2	1.95	0.48
1:P:133:GLN:NE2	5:P:517:HOH:O	2.46	0.48
1:A:41:ASP:OD2	1:N:145:HIS:HE1	1.97	0.48
4:C:1207[A]:FEC:CGD	1:D:20:ARG:HH22	2.26	0.48
1:I:58:ARG:HG2	5:I:9611:HOH:O	2.13	0.48
1:A:163:SER:HB2	3:A:1006:SO4:O4	2.14	0.48
1:L:61:GLU:HB2	4:L:2107[A]:FEC:CMD	2.44	0.48
1:E:20:ARG:HH22	4:E:1407[B]:FEC:CGD	2.25	0.48
1:G:5:ARG:HG2	5:G:9341:HOH:O	2.14	0.48
1:B:36:SER:C	1:B:40:MET:HE3	2.34	0.47
1:B:130:GLU:OE2	1:G:127:ARG:NH2	2.47	0.47
3:D:1301:SO4:S	5:D:9670:HOH:O	1.98	0.47
1:B:149:LEU:HD13	1:H:155:ALA:HA	1.95	0.47
1:D:123:ARG:NH1	1:D:126:GLU:OE1	2.47	0.47
1:E:78:LYS:HE3	1:E:82:VAL:HG23	1.96	0.47
1:H:14:GLU:O	1:H:18:LYS:HG3	2.14	0.47
1:I:169:LYS:N	4:I:1805[B]:FEC:O2C	2.47	0.47
1:O:57:MET:CE	4:P:2507[B]:FEC:NB	2.77	0.47
1:L:168:SER:HB3	4:L:2107[A]:FEC:CBB	2.43	0.47
1:N:111:LYS:HA	1:N:114:LYS:HE3	1.96	0.47
1:B:123:ARG:NH1	1:B:126:GLU:OE1	2.48	0.47
1:I:58:ARG:HD3	1:J:168:SER:HG	1.79	0.47
1:L:3:GLY:HA3	5:L:9493:HOH:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:168:SER:HB3	4:P:2507[A]:FEC:CBB	2.40	0.47
1:C:65:GLU:O	1:C:69:GLU:HG3	2.14	0.47
1:G:14:GLU:O	1:G:18:LYS:HG3	2.13	0.47
4:I:1805[B]:FEC:NC	4:I:1805[B]:FEC:C4B	2.77	0.47
1:O:123:ARG:NH1	1:O:126:GLU:OE1	2.47	0.47
1:C:51:LEU:HD21	1:C:164:THR:HB	1.96	0.47
1:F:5:ARG:HD2	1:F:8:ARG:HH11	1.80	0.47
1:O:25:HIS:HE1	1:O:98:GLN:OE1	1.98	0.47
1:A:76:THR:OG1	5:B:1216:HOH:O	2.20	0.47
1:O:8:ARG:NH1	5:O:9358:HOH:O	2.48	0.47
1:J:90:VAL:O	1:J:94:SER:OG	2.33	0.47
4:E:1407[A]:FEC:C1D	1:F:57:MET:HB3	2.45	0.46
4:G:1607[A]:FEC:O2B	1:H:168:SER:HB3	2.15	0.46
4:I:1805[B]:FEC:HBD1	1:J:31:MET:HG3	1.97	0.46
1:O:110:LEU:CD2	1:O:114:LYS:HE3	2.45	0.46
1:A:110:LEU:HD23	1:A:114:LYS:HD2	1.97	0.46
1:I:123:ARG:NH1	5:I:9732:HOH:O	2.47	0.46
1:A:123:ARG:NH1	1:A:126:GLU:OE1	2.48	0.46
1:I:123:ARG:NH1	1:I:127:ARG:HG3	2.30	0.46
1:C:123:ARG:NH1	1:C:126:GLU:OE1	2.49	0.46
1:M:55:ASP:OD1	1:M:58:ARG:NH2	2.48	0.46
1:P:57:MET:CE	4:P:2507[B]:FEC:ND	2.78	0.46
1:F:127:ARG:NH2	5:F:9540:HOH:O	2.49	0.46
1:O:76:THR:O	1:P:78:LYS:HE3	2.15	0.46
1:P:79:GLU:HB2	5:P:9131:HOH:O	2.15	0.46
1:P:168:SER:HB3	4:P:2507[A]:FEC:O2B	2.15	0.46
1:D:147:LYS:HE3	1:D:147:LYS:HB2	1.74	0.46
1:K:112:VAL:O	1:K:116:GLN:HG2	2.14	0.46
1:K:128:ILE:O	1:K:132:GLU:HG2	2.16	0.46
1:P:29:GLN:O	1:P:33:GLN:HG3	2.15	0.46
4:C:1207[B]:FEC:HBA2	4:C:1207[B]:FEC:HHB	1.97	0.46
1:G:158:ALA:O	1:I:156:LYS:NZ	2.48	0.46
1:K:57:MET:HB3	4:L:2107[A]:FEC:CHB	2.46	0.46
4:G:1607[A]:FEC:HMD2	1:H:61:GLU:HB2	1.96	0.46
1:A:169:LYS:HZ2	1:B:166:THR:HG22	1.81	0.46
1:D:61:GLU:O	1:D:65:GLU:HG3	2.16	0.46
4:E:1407[A]:FEC:HMD2	1:F:61:GLU:HB2	1.97	0.46
1:G:53:ALA:O	1:G:57:MET:HG3	2.16	0.46
4:I:1805[B]:FEC:NC	4:I:1805[B]:FEC:CHC	2.74	0.46
1:M:57:MET:HB3	4:M:2207[B]:FEC:C1D	2.45	0.46
4:M:2207[A]:FEC:O1C	1:N:168:SER:HA	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:157:ILE:HD13	1:J:157:ILE:N	2.30	0.45
4:M:2207[B]:FEC:C1B	1:N:57:MET:HB3	2.45	0.45
1:G:31:MET:HG3	4:G:1607[A]:FEC:HBD1	1.99	0.45
1:G:123:ARG:NH1	1:G:126:GLU:OE1	2.49	0.45
5:K:9231:HOH:O	1:P:127:ARG:NH2	2.49	0.45
1:G:27:ILE:HD11	1:G:57:MET:HA	1.99	0.45
1:H:111:LYS:O	1:H:115:GLU:HG3	2.17	0.45
4:M:2207[A]:FEC:NB	1:N:57:MET:CE	2.79	0.45
1:G:68:LYS:HA	1:G:68:LYS:HD2	1.81	0.45
4:G:1607[B]:FEC:C1B	1:H:57:MET:HB3	2.46	0.45
1:L:50:LYS:HE3	4:L:2107[B]:FEC:HMC2	1.99	0.45
1:L:133:GLN:NE2	5:L:9208:HOH:O	2.48	0.45
1:M:7:ASP:OD2	1:M:11:LYS:NZ	2.49	0.45
1:M:164:THR:N	5:M:9457:HOH:O	2.47	0.45
1:F:149:LEU:HD13	1:L:155:ALA:HA	1.99	0.45
1:E:55:ASP:OD1	1:E:58:ARG:NH2	2.49	0.45
4:C:1207[B]:FEC:C1B	1:D:57:MET:HB3	2.47	0.45
1:G:43:GLY:HA2	1:G:162:SER:HB3	1.98	0.45
4:G:1607[A]:FEC:CMD	1:H:61:GLU:HB2	2.47	0.45
1:L:25:HIS:HD2	5:L:9609:HOH:O	1.99	0.45
1:P:61:GLU:HB2	4:P:2507[A]:FEC:HMD2	1.99	0.45
1:C:33:GLN:NE2	1:C:95:ASP:OD2	2.48	0.45
1:D:127:ARG:NH2	5:D:410:HOH:O	2.49	0.45
1:L:90:VAL:O	1:L:94:SER:OG	2.28	0.45
1:A:61:GLU:HB2	4:A:1007[B]:FEC:CMD	2.47	0.44
4:A:1007[B]:FEC:CGA	1:B:20:ARG:HH22	2.30	0.44
1:C:11:LYS:HD2	1:C:116:GLN:NE2	2.32	0.44
1:E:27:ILE:HD11	1:E:57:MET:HA	1.98	0.44
1:E:88:VAL:HA	1:E:91:ILE:HD12	1.99	0.44
4:C:1207[A]:FEC:HBA2	1:D:31:MET:HG3	2.00	0.44
1:D:79:GLU:OE1	1:D:79:GLU:O	2.35	0.44
1:H:128:ILE:O	1:H:132:GLU:HG2	2.18	0.44
1:M:4:ASN:HB2	3:M:2202:SO4:O1	2.17	0.44
1:D:88:VAL:HG12	1:D:146:ILE:HD13	1.99	0.44
1:G:20:ARG:HH22	4:G:1607[B]:FEC:CGD	2.29	0.44
4:A:1007[A]:FEC:CGD	1:B:20:ARG:HH22	2.30	0.44
1:K:58:ARG:HG3	5:K:9548:HOH:O	2.18	0.44
1:O:61:GLU:O	1:O:65:GLU:HG3	2.17	0.44
1:G:163:SER:HA	3:G:1601:SO4:O4	2.18	0.44
1:I:123:ARG:NH1	1:I:126:GLU:OE1	2.51	0.44
1:K:78:LYS:NZ	5:K:924:HOH:O	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:M:2207[B]:FEC:CGA	1:N:20:ARG:HH22	2.31	0.44
1:O:163:SER:N	3:O:2406:SO4:O3	2.46	0.44
1:A:57:MET:HB3	4:A:1007[A]:FEC:C1B	2.47	0.44
4:C:1207[A]:FEC:CGC	1:D:168:SER:HA	2.47	0.44
1:K:51:LEU:HD21	1:K:164:THR:HB	1.99	0.44
1:M:61:GLU:HB2	4:M:2207[B]:FEC:HMD2	2.00	0.44
1:D:95:ASP:HB3	1:D:139:TYR:CE1	2.53	0.43
1:I:20:ARG:HH22	4:I:1805[B]:FEC:CGD	2.30	0.43
1:M:161:PRO:HB3	3:M:2206:SO4:O2	2.18	0.43
1:O:45:LEU:HG	1:O:157:ILE:HG21	2.00	0.43
1:A:57:MET:HB3	4:A:1007[B]:FEC:C1D	2.48	0.43
4:A:1007[A]:FEC:CGB	1:B:168:SER:HB3	2.47	0.43
1:C:57:MET:CE	4:C:1207[B]:FEC:NB	2.81	0.43
1:K:110:LEU:CD2	1:K:114:LYS:HD2	2.48	0.43
4:C:1207[B]:FEC:HMC2	1:D:50:LYS:CE	2.48	0.43
1:E:58:ARG:NH1	1:E:131:GLU:OE1	2.51	0.43
4:G:1607[B]:FEC:HMC2	1:H:50:LYS:HE3	2.01	0.43
1:L:68:LYS:HD2	1:L:68:LYS:HA	1.74	0.43
1:O:73:GLU:OE2	1:P:84:THR:HB	2.18	0.43
1:D:33:GLN:OE1	1:D:95:ASP:OD2	2.36	0.43
1:G:168:SER:HB3	4:G:1607[B]:FEC:O2C	2.18	0.43
1:N:5:ARG:HD2	1:N:8:ARG:NH1	2.33	0.43
1:O:90:VAL:O	1:O:94:SER:OG	2.37	0.43
1:B:78:LYS:CE	3:B:1005:SO4:O2	2.66	0.43
1:K:57:MET:HB3	4:L:2107[B]:FEC:C1D	2.49	0.43
1:L:29:GLN:NE2	1:L:83:VAL:H	1.96	0.43
4:C:1207[B]:FEC:NC	4:C:1207[B]:FEC:CHC	2.82	0.43
1:F:137:THR:HG23	5:F:999:HOH:O	2.19	0.43
1:I:7:ASP:OD2	1:I:11:LYS:NZ	2.38	0.43
5:A:1068:HOH:O	1:N:145:HIS:HD2	2.02	0.43
4:P:2507[A]:FEC:HBC2	4:P:2507[A]:FEC:CHC	2.47	0.43
1:B:52:ILE:O	1:B:56:GLU:HG2	2.19	0.43
4:C:1207[A]:FEC:HMD2	1:D:61:GLU:HB2	2.01	0.43
1:I:153:TYR:O	1:I:156:LYS:HB3	2.19	0.43
1:I:168:SER:C	4:I:1805[B]:FEC:O2C	2.52	0.43
1:D:95:ASP:HB3	1:D:139:TYR:CD1	2.53	0.42
4:E:1407[B]:FEC:CGA	1:F:20:ARG:HH22	2.30	0.42
1:I:156:LYS:HD3	1:I:157:ILE:HD13	2.00	0.42
1:D:127:ARG:NE	5:D:9572:HOH:O	2.49	0.42
4:M:2207[A]:FEC:O2C	1:N:168:SER:HA	2.19	0.42
1:O:52:ILE:O	1:O:56:GLU:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:25:HIS:HB2	1:C:79:GLU:O	2.19	0.42
1:E:112:VAL:O	1:E:116:GLN:HG2	2.19	0.42
1:G:168:SER:HA	4:G:1607[B]:FEC:O2C	2.20	0.42
1:M:168:SER:HB3	4:M:2207[B]:FEC:HBB2	2.00	0.42
1:G:168:SER:HA	4:G:1607[B]:FEC:CGC	2.49	0.42
1:H:27:ILE:HD11	1:H:57:MET:HA	2.02	0.42
1:E:61:GLU:HB2	4:E:1407[B]:FEC:HMD2	2.00	0.42
1:G:8:ARG:HG2	1:G:116:GLN:OE1	2.20	0.42
1:J:45:LEU:HG	1:J:157:ILE:HG21	2.01	0.42
1:P:11:LYS:NZ	5:P:9174:HOH:O	2.48	0.42
1:D:88:VAL:HA	1:D:91:ILE:HD12	2.01	0.42
1:H:123:ARG:HE	1:H:127:ARG:NE	2.16	0.42
4:I:1805[A]:FEC:CMD	1:J:61:GLU:HB2	2.50	0.42
1:O:27:ILE:HD11	1:O:57:MET:HA	2.02	0.42
1:B:43:GLY:HA2	1:B:162:SER:HB3	2.00	0.42
1:D:73:GLU:HA	1:D:74:PRO:HD3	1.88	0.42
4:I:1805[A]:FEC:O2B	1:J:168:SER:HB3	2.20	0.42
1:C:88:VAL:HG12	1:C:146:ILE:HD13	2.02	0.42
1:O:162:SER:N	3:O:2406:SO4:O3	2.53	0.42
1:F:33:GLN:OE1	1:F:95:ASP:OD2	2.37	0.42
1:K:76:THR:HG21	1:L:82:VAL:HG11	2.02	0.42
1:F:36:SER:HB3	1:F:40:MET:HE2	2.02	0.41
4:G:1607[B]:FEC:HHC	4:G:1607[B]:FEC:HBC2	2.01	0.41
1:K:9:LYS:O	1:K:13:ILE:HG13	2.20	0.41
1:A:27:ILE:HD11	1:A:57:MET:HA	2.03	0.41
1:C:77:GLN:NE2	1:D:78:LYS:NZ	2.68	0.41
1:E:158:ALA:O	1:P:156:LYS:NZ	2.48	0.41
1:F:14:GLU:O	1:F:18:LYS:HG3	2.20	0.41
1:F:88:VAL:HB	1:F:89:PRO:HD3	2.02	0.41
1:F:90:VAL:HG21	5:F:9309:HOH:O	2.19	0.41
1:G:155:ALA:CA	1:I:149:LEU:HD13	2.48	0.41
1:K:4:ASN:OD1	1:K:7:ASP:HB2	2.20	0.41
1:M:61:GLU:HB2	4:M:2207[B]:FEC:CMD	2.50	0.41
1:E:153:TYR:O	1:E:156:LYS:HB3	2.21	0.41
1:J:105:ALA:HA	1:J:108[A]:GLN:NE2	2.35	0.41
1:L:4:ASN:HB3	5:L:9356:HOH:O	2.21	0.41
1:G:57:MET:HB3	4:G:1607[A]:FEC:C1B	2.50	0.41
1:M:52:ILE:O	1:M:56:GLU:HG2	2.19	0.41
4:M:2207[B]:FEC:CHB	1:N:57:MET:HB3	2.51	0.41
1:N:169:LYS:HB3	5:N:2404:HOH:O	2.20	0.41
1:A:50:LYS:CE	4:A:1007[B]:FEC:HAB2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:57:MET:HB3	4:E:1407[A]:FEC:C1B	2.51	0.41
1:H:123:ARG:HG3	1:H:127:ARG:HH21	1.85	0.41
1:C:34:HIS:HE1	5:C:371:HOH:O	2.03	0.41
4:C:1207[B]:FEC:NC	4:C:1207[B]:FEC:ND	2.68	0.41
1:G:155:ALA:O	1:I:156:LYS:NZ	2.44	0.41
1:I:110:LEU:CD2	1:I:114:LYS:HD2	2.51	0.41
1:N:112:VAL:O	1:N:116:GLN:HG2	2.21	0.41
1:H:110:LEU:O	1:H:114:LYS:HG3	2.21	0.41
1:L:71:GLY:HA2	5:L:956:HOH:O	2.21	0.41
1:O:5:ARG:HA	1:O:8:ARG:HH11	1.86	0.41
4:P:2507[B]:FEC:HBC2	4:P:2507[B]:FEC:HHC	2.02	0.41
1:I:13:ILE:HD13	1:I:72:GLY:HA3	2.02	0.40
1:O:73:GLU:HA	1:O:74:PRO:HD3	1.90	0.40
4:C:1207[A]:FEC:HBC2	4:C:1207[A]:FEC:HHC	2.03	0.40
1:M:77:GLN:NE2	5:M:8918:HOH:O	2.54	0.40
1:O:68:LYS:HA	1:O:68:LYS:HD2	1.95	0.40
4:C:1207[A]:FEC:C1D	1:D:57:MET:HB3	2.51	0.40
4:E:1407[B]:FEC:HHB	4:E:1407[B]:FEC:HBA2	2.04	0.40
1:I:58:ARG:HH11	1:I:58:ARG:HD2	1.67	0.40
1:M:33:GLN:NE2	1:M:95:ASP:OD2	2.49	0.40
1:A:4:ASN:HB3	1:A:7:ASP:HB2	2.04	0.40
1:E:73:GLU:HA	1:E:74:PRO:HD3	1.83	0.40
1:I:126:GLU:O	1:I:130:GLU:HG3	2.21	0.40
1:A:57:MET:HB3	4:A:1007[A]:FEC:CHB	2.51	0.40
1:G:33:GLN:NE2	1:G:95:ASP:OD2	2.53	0.40
1:P:57:MET:CE	4:P:2507[A]:FEC:NB	2.84	0.40

All (19) 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:I:1802:SO4:O3	3:L:2102:SO4:O1[9_465]	0.18	2.02
3:I:1802:SO4:O2	3:L:2102:SO4:O4[9_465]	0.28	1.92
3:I:1802:SO4:O1	3:L:2102:SO4:O3[9_465]	0.31	1.89
3:I:1802:SO4:O4	3:L:2102:SO4:O2[9_465]	0.50	1.70
3:I:1802:SO4:S	3:L:2102:SO4:S[9_465]	0.56	1.64
3:I:1802:SO4:O1	3:L:2102:SO4:S[9_465]	1.22	0.98
3:I:1802:SO4:S	3:L:2102:SO4:O1[9_465]	1.23	0.97
3:I:1802:SO4:O2	3:L:2102:SO4:S[9_465]	1.38	0.82
3:I:1802:SO4:S	3:L:2102:SO4:O2[9_465]	1.44	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:1802:SO4:S	3:L:2102:SO4:O4[9_465]	1.63	0.57
3:I:1802:SO4:O4	3:L:2102:SO4:S[9_465]	1.65	0.55
3:I:1802:SO4:O3	3:L:2102:SO4:S[9_465]	1.76	0.44
1:L:114:LYS:NZ	3:L:2104:SO4:O2[12_554]	1.80	0.40
3:I:1802:SO4:S	3:L:2102:SO4:O3[9_465]	1.81	0.39
1:L:114:LYS:CE	3:L:2104:SO4:O2[12_554]	2.09	0.11
1:L:114:LYS:NZ	3:L:2104:SO4:O1[6_555]	2.15	0.05
3:I:1802:SO4:O1	3:L:2102:SO4:O2[9_465]	2.16	0.04
1:L:114:LYS:CD	3:L:2104:SO4:O1[6_555]	2.16	0.04
1:L:114:LYS:CE	3:L:2104:SO4:O1[6_555]	2.19	0.01

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	167/179 (93%)	163 (98%)	4 (2%)	0	100	100
1	B	167/179 (93%)	164 (98%)	3 (2%)	0	100	100
1	C	167/179 (93%)	165 (99%)	1 (1%)	1 (1%)	25	15
1	D	168/179 (94%)	166 (99%)	2 (1%)	0	100	100
1	E	167/179 (93%)	163 (98%)	3 (2%)	1 (1%)	25	15
1	F	167/179 (93%)	165 (99%)	2 (1%)	0	100	100
1	G	167/179 (93%)	163 (98%)	3 (2%)	1 (1%)	25	15
1	H	168/179 (94%)	165 (98%)	2 (1%)	1 (1%)	25	15
1	I	168/179 (94%)	164 (98%)	3 (2%)	1 (1%)	25	15
1	J	168/179 (94%)	165 (98%)	3 (2%)	0	100	100
1	K	167/179 (93%)	165 (99%)	2 (1%)	0	100	100
1	L	169/179 (94%)	166 (98%)	3 (2%)	0	100	100
1	M	170/179 (95%)	166 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	N	167/179 (93%)	164 (98%)	3 (2%)	0	100	100
1	O	167/179 (93%)	165 (99%)	2 (1%)	0	100	100
1	P	168/179 (94%)	163 (97%)	5 (3%)	0	100	100
All	All	2682/2864 (94%)	2632 (98%)	45 (2%)	5 (0%)	47	39

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	168	SER
1	I	168	SER
1	C	168	SER
1	E	168	SER
1	G	151	ASP

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	139/145 (96%)	134 (96%)	5 (4%)	35	28
1	B	137/145 (94%)	133 (97%)	4 (3%)	42	35
1	C	136/145 (94%)	132 (97%)	4 (3%)	42	35
1	D	139/145 (96%)	133 (96%)	6 (4%)	29	22
1	E	137/145 (94%)	130 (95%)	7 (5%)	24	15
1	F	138/145 (95%)	133 (96%)	5 (4%)	35	28
1	G	137/145 (94%)	133 (97%)	4 (3%)	42	35
1	H	137/145 (94%)	134 (98%)	3 (2%)	52	46
1	I	138/145 (95%)	136 (99%)	2 (1%)	67	65
1	J	135/145 (93%)	130 (96%)	5 (4%)	34	27
1	K	137/145 (94%)	132 (96%)	5 (4%)	35	28
1	L	140/145 (97%)	136 (97%)	4 (3%)	42	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	140/145 (97%)	136 (97%)	4 (3%)	42	35
1	N	138/145 (95%)	134 (97%)	4 (3%)	42	35
1	O	135/145 (93%)	130 (96%)	5 (4%)	34	27
1	P	138/145 (95%)	134 (97%)	4 (3%)	42	35
All	All	2201/2320 (95%)	2130 (97%)	71 (3%)	39	32

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	ASP
1	A	38	ASP
1	A	81	LYS
1	A	147	LYS
1	A	166	THR
1	B	6	GLU
1	B	38	ASP
1	B	79	GLU
1	B	81	LYS
1	C	38	ASP
1	C	111	LYS
1	C	156	LYS
1	C	169	LYS
1	D	4	ASN
1	D	38	ASP
1	D	79	GLU
1	D	94	SER
1	D	147	LYS
1	D	156	LYS
1	E	4	ASN
1	E	38	ASP
1	E	78	LYS
1	E	81	LYS
1	E	93	GLU
1	E	156	LYS
1	E	168	SER
1	F	4	ASN
1	F	38	ASP
1	F	79	GLU
1	F	156	LYS
1	F	163	SER
1	G	38	ASP

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Mol	Chain	Res	Type
1	G	152	THR
1	G	166	THR
1	G	169	LYS
1	H	77	GLN
1	H	81	LYS
1	H	156	LYS
1	I	111	LYS
1	I	156	LYS
1	J	4	ASN
1	J	58	ARG
1	J	93	GLU
1	J	94	SER
1	J	152	THR
1	K	4	ASN
1	K	7	ASP
1	K	38	ASP
1	K	163	SER
1	K	169	LYS
1	L	68	LYS
1	L	79	GLU
1	L	94	SER
1	L	152	THR
1	M	7	ASP
1	M	38	ASP
1	M	111	LYS
1	M	156	LYS
1	N	4	ASN
1	N	38	ASP
1	N	79	GLU
1	N	93	GLU
1	O	38	ASP
1	O	93	GLU
1	O	94	SER
1	O	111	LYS
1	O	130	GLU
1	P	4	ASN
1	P	79	GLU
1	P	81	LYS
1	P	94	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (60) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	ASN
1	A	33	GLN
1	B	4	ASN
1	B	29	GLN
1	B	62	ASN
1	B	133	GLN
1	B	145	HIS
1	C	25	HIS
1	C	32	ASN
1	C	33	GLN
1	C	77	GLN
1	C	108	GLN
1	D	29	GLN
1	D	98	GLN
1	D	133	GLN
1	E	4	ASN
1	E	32	ASN
1	F	4	ASN
1	F	29	GLN
1	F	133	GLN
1	F	145	HIS
1	G	32	ASN
1	G	33	GLN
1	H	25	HIS
1	H	29	GLN
1	H	133	GLN
1	H	145	HIS
1	I	32	ASN
1	I	33	GLN
1	J	4	ASN
1	J	25	HIS
1	J	29	GLN
1	J	98	GLN
1	J	145	HIS
1	J	148	ASN
1	K	32	ASN
1	K	33	GLN
1	K	108	GLN
1	L	4	ASN
1	L	25	HIS
1	L	29	GLN
1	L	133	GLN
1	M	32	ASN

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Mol	Chain	Res	Type
1	M	33	GLN
1	M	77	GLN
1	M	108	GLN
1	N	4	ASN
1	N	29	GLN
1	N	133	GLN
1	N	145	HIS
1	O	25	HIS
1	O	32	ASN
1	O	33	GLN
1	O	77	GLN
1	P	4	ASN
1	P	25	HIS
1	P	29	GLN
1	P	98	GLN
1	P	133	GLN
1	P	145	HIS

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 104 ligands modelled in this entry, 32 are monoatomic - leaving 72 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	G	1606	-	4,4,4	0.24	0	6,6,6	0.71	0
3	SO4	L	2102	-	4,4,4	1.95	1 (25%)	6,6,6	0.87	0
3	SO4	I	1801	-	4,4,4	1.93	1 (25%)	6,6,6	0.92	0
4	FEC	L	2107[A]	1	40,56,56	1.75	6 (15%)	42,90,90	1.79	10 (23%)
3	SO4	C	1203	-	4,4,4	0.41	0	6,6,6	0.98	0
3	SO4	H	1706	-	4,4,4	0.46	0	6,6,6	0.87	0
4	FEC	L	2107[B]	1	40,56,56	3.52	7 (17%)	42,90,90	2.35	9 (21%)
3	SO4	C	1201	-	4,4,4	1.92	1 (25%)	6,6,6	0.93	0
3	SO4	N	2306	-	4,4,4	0.18	0	6,6,6	0.76	0
4	FEC	C	1207[A]	1	40,56,56	2.11	5 (12%)	42,90,90	1.75	10 (23%)
3	SO4	B	1005	-	4,4,4	0.52	0	6,6,6	2.46	2 (33%)
3	SO4	M	2206	-	4,4,4	0.23	0	6,6,6	0.40	0
3	SO4	I	1704	-	4,4,4	1.95	2 (50%)	6,6,6	0.80	0
3	SO4	F	1501	-	4,4,4	2.02	1 (25%)	6,6,6	0.83	0
3	SO4	P	2501	-	4,4,4	1.90	1 (25%)	6,6,6	0.90	0
4	FEC	C	1207[B]	1	40,56,56	4.70	8 (20%)	42,90,90	2.58	14 (33%)
4	FEC	G	1607[A]	1	40,56,56	2.04	5 (12%)	42,90,90	1.92	14 (33%)
3	SO4	K	2001	-	4,4,4	1.92	1 (25%)	6,6,6	0.94	0
3	SO4	L	2104	-	4,4,4	1.95	1 (25%)	6,6,6	0.87	0
3	SO4	B	1106	-	4,4,4	0.13	0	6,6,6	1.50	0
3	SO4	F	1502	-	4,4,4	1.91	1 (25%)	6,6,6	0.92	0
4	FEC	G	1607[B]	1	40,56,56	4.32	7 (17%)	42,90,90	1.77	12 (28%)
3	SO4	J	1904	-	4,4,4	1.93	1 (25%)	6,6,6	0.92	0
3	SO4	C	1204	-	4,4,4	1.99	1 (25%)	6,6,6	0.88	0
3	SO4	H	1702	-	4,4,4	1.94	1 (25%)	6,6,6	0.87	0
3	SO4	D	1306	-	4,4,4	0.37	0	6,6,6	0.70	0
3	SO4	A	1003	-	4,4,4	2.00	1 (25%)	6,6,6	0.84	0
3	SO4	D	1303	-	4,4,4	0.17	0	6,6,6	0.60	0
3	SO4	M	2203	-	4,4,4	1.94	1 (25%)	6,6,6	0.81	0
3	SO4	O	2406	-	4,4,4	0.30	0	6,6,6	1.07	0
3	SO4	P	2506	-	4,4,4	0.46	0	6,6,6	0.56	0
3	SO4	J	1901	-	4,4,4	1.89	1 (25%)	6,6,6	0.84	0
3	SO4	L	2106	-	4,4,4	0.19	0	6,6,6	1.21	1 (16%)
4	FEC	A	1007[A]	1	40,56,56	2.23	4 (10%)	42,90,90	1.72	11 (26%)
3	SO4	D	1301	-	4,4,4	1.99	1 (25%)	6,6,6	0.88	0
3	SO4	H	1701	-	4,4,4	1.83	1 (25%)	6,6,6	0.84	0
3	SO4	E	1406	-	4,4,4	0.29	0	6,6,6	1.22	1 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	SO4	H	1703	-	4,4,4	0.28	0	6,6,6	0.58	0
3	SO4	I	1802	-	4,4,4	1.96	2 (50%)	6,6,6	0.80	0
3	SO4	K	2006	-	4,4,4	0.17	0	6,6,6	0.67	0
4	FEC	A	1007[B]	1	40,56,56	5.47	8 (20%)	42,90,90	2.31	12 (28%)
4	FEC	M	2207[A]	1	40,56,56	2.83	6 (15%)	42,90,90	1.61	8 (19%)
4	FEC	M	2207[B]	1	40,56,56	3.03	7 (17%)	42,90,90	1.79	8 (19%)
3	SO4	P	1504	-	4,4,4	1.94	1 (25%)	6,6,6	0.86	0
3	SO4	B	1104	-	4,4,4	2.02	1 (25%)	6,6,6	0.89	0
4	FEC	I	1805[A]	1	40,56,56	2.00	5 (12%)	42,90,90	1.64	10 (23%)
4	FEC	I	1805[B]	1	40,56,56	4.85	7 (17%)	42,90,90	2.15	12 (28%)
3	SO4	F	1506	-	4,4,4	0.26	0	6,6,6	1.31	1 (16%)
3	SO4	I	1804	-	4,4,4	0.39	0	6,6,6	0.60	0
3	SO4	P	2503	-	4,4,4	0.20	0	6,6,6	0.92	0
3	SO4	E	1304	-	4,4,4	1.93	1 (25%)	6,6,6	0.93	0
3	SO4	M	2202	-	4,4,4	2.00	1 (25%)	6,6,6	0.85	0
3	SO4	B	1103	-	4,4,4	0.24	0	6,6,6	0.33	0
3	SO4	E	1403	-	4,4,4	0.36	0	6,6,6	1.21	1 (16%)
3	SO4	G	1601	-	4,4,4	2.18	1 (25%)	6,6,6	0.78	0
3	SO4	K	2003	-	4,4,4	1.91	1 (25%)	6,6,6	0.92	0
3	SO4	N	2303	-	4,4,4	0.18	0	6,6,6	0.81	0
4	FEC	P	2507[A]	1	40,56,56	2.70	6 (15%)	42,90,90	1.92	9 (21%)
4	FEC	P	2507[B]	1	40,56,56	3.44	8 (20%)	42,90,90	1.73	10 (23%)
3	SO4	C	1206	-	4,4,4	0.34	0	6,6,6	0.63	0
3	SO4	G	1603	-	4,4,4	2.02	1 (25%)	6,6,6	0.89	0
3	SO4	A	1006	-	4,4,4	0.24	0	6,6,6	1.10	0
3	SO4	A	1001	-	4,4,4	1.81	1 (25%)	6,6,6	0.95	0
3	SO4	M	2201	-	4,4,4	1.89	1 (25%)	6,6,6	0.93	0
3	SO4	O	2403	-	4,4,4	0.38	0	6,6,6	0.44	0
3	SO4	B	1101	-	4,4,4	1.88	1 (25%)	6,6,6	0.92	0
4	FEC	E	1407[B]	1	40,56,56	3.61	8 (20%)	42,90,90	1.77	12 (28%)
3	SO4	J	1906	-	4,4,4	0.16	0	6,6,6	0.95	0
3	SO4	N	2301	-	4,4,4	1.94	1 (25%)	6,6,6	0.82	0
3	SO4	L	2101	-	4,4,4	1.91	1 (25%)	6,6,6	0.92	0
4	FEC	E	1407[A]	1	40,56,56	2.08	5 (12%)	42,90,90	1.88	10 (23%)
3	SO4	I	1803	-	4,4,4	0.34	0	6,6,6	0.49	0

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
4	FEC	G	1607[A]	1	-	6/20/120/120	-
4	FEC	A	1007[B]	1	-	10/20/120/120	-
4	FEC	G	1607[B]	1	-	10/20/120/120	-
4	FEC	L	2107[A]	1	-	8/20/120/120	-
4	FEC	L	2107[B]	1	-	9/20/120/120	-
4	FEC	M	2207[B]	1	-	9/20/120/120	-
4	FEC	I	1805[A]	1	-	11/20/120/120	-
4	FEC	I	1805[B]	1	-	6/20/120/120	-
4	FEC	E	1407[B]	1	-	5/20/120/120	-
4	FEC	C	1207[B]	1	-	11/20/120/120	-
4	FEC	P	2507[B]	1	-	13/20/120/120	-
4	FEC	C	1207[A]	1	-	10/20/120/120	-
4	FEC	E	1407[A]	1	-	9/20/120/120	-
4	FEC	A	1007[A]	1	-	10/20/120/120	-
4	FEC	P	2507[A]	1	-	9/20/120/120	-
4	FEC	M	2207[A]	1	-	10/20/120/120	-

All (134) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1007[B]	FEC	C1D-ND	28.25	1.90	1.36
4	C	1207[B]	FEC	C4B-NB	25.52	1.84	1.36
4	I	1805[B]	FEC	C1D-ND	25.16	1.84	1.36
4	G	1607[B]	FEC	C1D-ND	20.88	1.76	1.36
4	L	2107[B]	FEC	C4D-ND	-19.13	1.00	1.36
4	E	1407[B]	FEC	C4B-NB	16.62	1.68	1.36
4	M	2207[B]	FEC	C4D-ND	15.23	1.65	1.36
4	A	1007[B]	FEC	C4B-NB	14.33	1.63	1.36
4	G	1607[B]	FEC	C4B-NB	14.21	1.63	1.36
4	M	2207[A]	FEC	C1B-NB	13.67	1.62	1.36
4	P	2507[B]	FEC	C4B-NB	13.47	1.62	1.36
4	P	2507[A]	FEC	C1B-NB	13.09	1.61	1.36
4	E	1407[B]	FEC	C1D-ND	12.29	1.59	1.36
4	C	1207[B]	FEC	C1D-ND	-11.87	1.14	1.36
4	I	1805[B]	FEC	C4D-ND	11.82	1.59	1.36
4	A	1007[A]	FEC	C1B-NB	11.56	1.58	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	P	2507[B]	FEC	C1B-NB	11.13	1.57	1.36
4	P	2507[B]	FEC	C1D-ND	10.15	1.55	1.36
4	G	1607[A]	FEC	C1B-NB	10.15	1.55	1.36
4	I	1805[A]	FEC	C1B-NB	9.34	1.54	1.36
4	A	1007[B]	FEC	C4D-ND	9.11	1.53	1.36
4	E	1407[A]	FEC	C1B-NB	8.85	1.53	1.36
4	M	2207[A]	FEC	C4B-NB	8.40	1.52	1.36
4	I	1805[B]	FEC	C1B-NB	-7.81	1.22	1.36
4	C	1207[A]	FEC	C1B-NB	7.76	1.51	1.36
4	C	1207[A]	FEC	C1D-ND	7.72	1.51	1.36
4	L	2107[B]	FEC	C1B-NB	7.56	1.51	1.36
4	P	2507[A]	FEC	C4B-NB	7.45	1.50	1.36
4	I	1805[B]	FEC	C4B-NB	7.20	1.50	1.36
4	G	1607[B]	FEC	C4D-ND	7.17	1.50	1.36
4	L	2107[A]	FEC	C1B-NB	6.88	1.49	1.36
4	A	1007[B]	FEC	C1B-NB	-6.87	1.23	1.36
4	M	2207[B]	FEC	C4B-NB	-6.79	1.23	1.36
4	E	1407[A]	FEC	C1D-ND	6.26	1.48	1.36
4	M	2207[B]	FEC	C1B-NB	5.79	1.47	1.36
4	E	1407[B]	FEC	C4D-ND	5.26	1.46	1.36
4	C	1207[B]	FEC	C1B-NB	4.93	1.46	1.36
4	L	2107[A]	FEC	C1D-ND	4.12	1.44	1.36
4	I	1805[A]	FEC	C1D-ND	3.99	1.44	1.36
3	G	1601	SO4	O1-S	3.99	1.67	1.46
3	A	1003	SO4	O1-S	3.64	1.65	1.46
3	G	1603	SO4	O1-S	3.64	1.65	1.46
3	M	2202	SO4	O1-S	3.64	1.65	1.46
3	B	1104	SO4	O1-S	3.64	1.65	1.46
3	F	1501	SO4	O1-S	3.56	1.65	1.46
3	D	1301	SO4	O1-S	3.52	1.65	1.46
3	C	1204	SO4	O1-S	3.51	1.65	1.46
3	H	1702	SO4	O1-S	3.50	1.65	1.46
3	L	2104	SO4	O1-S	3.48	1.64	1.46
3	L	2102	SO4	O1-S	3.48	1.64	1.46
3	P	1504	SO4	O1-S	3.48	1.64	1.46
3	E	1304	SO4	O1-S	3.46	1.64	1.46
3	N	2301	SO4	O1-S	3.45	1.64	1.46
3	M	2203	SO4	O1-S	3.45	1.64	1.46
3	C	1201	SO4	O1-S	3.45	1.64	1.46
3	F	1502	SO4	O1-S	3.39	1.64	1.46
3	K	2003	SO4	O1-S	3.38	1.64	1.46
3	I	1801	SO4	O1-S	3.38	1.64	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	J	1901	SO4	O1-S	3.37	1.64	1.46
3	K	2001	SO4	O1-S	3.37	1.64	1.46
3	P	2501	SO4	O1-S	3.37	1.64	1.46
3	J	1904	SO4	O1-S	3.37	1.64	1.46
3	L	2101	SO4	O1-S	3.36	1.64	1.46
3	B	1101	SO4	O1-S	3.36	1.64	1.46
3	M	2201	SO4	O1-S	3.30	1.63	1.46
3	I	1802	SO4	O1-S	3.30	1.63	1.46
3	I	1704	SO4	O1-S	3.28	1.63	1.46
3	H	1701	SO4	O1-S	3.20	1.63	1.46
3	A	1001	SO4	O1-S	3.08	1.62	1.46
4	E	1407[B]	FEC	C1B-NB	-3.05	1.31	1.36
4	C	1207[B]	FEC	C4D-ND	3.03	1.42	1.36
4	L	2107[B]	FEC	CMB-C2B	3.01	1.55	1.50
4	C	1207[B]	FEC	CMB-C2B	2.96	1.55	1.50
4	A	1007[A]	FEC	CMD-C2D	2.88	1.55	1.50
4	P	2507[B]	FEC	C4D-ND	2.87	1.42	1.36
4	L	2107[A]	FEC	CMB-C2B	2.85	1.55	1.50
4	L	2107[B]	FEC	CMD-C2D	2.83	1.55	1.50
4	C	1207[B]	FEC	CMD-C2D	2.78	1.55	1.50
4	A	1007[B]	FEC	CMB-C2B	2.77	1.55	1.50
4	A	1007[A]	FEC	CMB-C2B	2.75	1.55	1.50
4	P	2507[B]	FEC	CMB-C2B	2.74	1.55	1.50
4	L	2107[B]	FEC	C1D-ND	-2.74	1.31	1.36
4	I	1805[B]	FEC	CMD-C2D	2.73	1.55	1.50
4	P	2507[A]	FEC	CMB-C2B	2.72	1.55	1.50
4	M	2207[A]	FEC	C1D-ND	2.69	1.41	1.36
4	G	1607[B]	FEC	CMD-C2D	2.69	1.55	1.50
4	P	2507[A]	FEC	C1D-ND	2.69	1.41	1.36
4	E	1407[B]	FEC	CMB-C2B	2.68	1.55	1.50
4	G	1607[A]	FEC	CMD-C2D	2.68	1.55	1.50
4	M	2207[A]	FEC	CMD-C2D	2.68	1.54	1.50
4	M	2207[A]	FEC	CMB-C2B	2.67	1.54	1.50
4	E	1407[A]	FEC	CMB-C2B	2.65	1.54	1.50
4	L	2107[A]	FEC	CMD-C2D	2.64	1.54	1.50
4	I	1805[A]	FEC	CMB-C2B	2.64	1.54	1.50
4	E	1407[B]	FEC	CMD-C2D	2.63	1.54	1.50
4	G	1607[A]	FEC	CMB-C2B	2.62	1.54	1.50
4	P	2507[B]	FEC	CMD-C2D	2.62	1.54	1.50
4	C	1207[A]	FEC	CMB-C2B	2.60	1.54	1.50
4	I	1805[B]	FEC	CMB-C2B	2.57	1.54	1.50
4	P	2507[A]	FEC	CMD-C2D	2.57	1.54	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1207[A]	FEC	CMD-C2D	2.57	1.54	1.50
4	E	1407[A]	FEC	CAB-C3B	2.54	1.55	1.51
4	M	2207[B]	FEC	CMD-C2D	2.53	1.54	1.50
4	M	2207[B]	FEC	CMB-C2B	2.52	1.54	1.50
4	C	1207[B]	FEC	CAB-C3B	2.50	1.55	1.51
4	A	1007[B]	FEC	CMD-C2D	2.47	1.54	1.50
4	A	1007[B]	FEC	CAD-C3D	2.45	1.55	1.51
4	A	1007[B]	FEC	CAB-C3B	2.44	1.55	1.51
4	I	1805[A]	FEC	CMD-C2D	2.44	1.54	1.50
4	A	1007[A]	FEC	CAD-C3D	2.43	1.55	1.51
4	G	1607[B]	FEC	CMB-C2B	2.42	1.54	1.50
4	E	1407[A]	FEC	CMD-C2D	2.42	1.54	1.50
4	G	1607[A]	FEC	CAB-C3B	2.42	1.55	1.51
4	G	1607[A]	FEC	CAD-C3D	2.40	1.55	1.51
4	M	2207[B]	FEC	CAB-C3B	2.38	1.55	1.51
4	E	1407[B]	FEC	CAD-C3D	2.30	1.55	1.51
4	G	1607[B]	FEC	CAD-C3D	2.30	1.55	1.51
4	E	1407[B]	FEC	CAB-C3B	2.30	1.55	1.51
4	P	2507[B]	FEC	CAD-C3D	2.29	1.55	1.51
4	L	2107[B]	FEC	CAB-C3B	2.24	1.55	1.51
4	L	2107[A]	FEC	CAB-C3B	2.23	1.55	1.51
4	L	2107[A]	FEC	CAD-C3D	2.19	1.54	1.51
4	I	1805[A]	FEC	CAB-C3B	2.18	1.54	1.51
4	M	2207[A]	FEC	CAD-C3D	2.15	1.54	1.51
4	M	2207[B]	FEC	CAD-C3D	2.14	1.54	1.51
4	C	1207[A]	FEC	CAD-C3D	2.12	1.54	1.51
4	I	1805[B]	FEC	CAD-C3D	2.07	1.54	1.51
4	L	2107[B]	FEC	CAD-C3D	2.06	1.54	1.51
4	C	1207[B]	FEC	CAD-C3D	2.05	1.54	1.51
4	P	2507[A]	FEC	CAB-C3B	2.04	1.54	1.51
4	P	2507[B]	FEC	CAB-C3B	2.03	1.54	1.51
3	I	1802	SO4	O3-S	-2.03	1.31	1.47
3	I	1704	SO4	O3-S	-2.03	1.31	1.47
4	G	1607[B]	FEC	CAA-C3A	2.02	1.55	1.52

All (177) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	C	1207[B]	FEC	C3D-C4D-ND	-11.53	90.10	114.98
4	L	2107[B]	FEC	C3D-C4D-ND	-10.16	93.07	114.98
4	A	1007[B]	FEC	CBC-CAC-C2C	7.66	125.51	112.60
4	P	2507[A]	FEC	CBC-CAC-C2C	7.31	124.93	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	E	1407[A]	FEC	CBC-CAC-C2C	6.73	123.95	112.60
4	M	2207[B]	FEC	CBC-CAC-C2C	6.46	123.49	112.60
4	I	1805[B]	FEC	CBC-CAC-C2C	6.26	123.16	112.60
4	A	1007[B]	FEC	C3D-C4D-ND	6.10	128.15	114.98
4	C	1207[B]	FEC	CBC-CAC-C2C	5.83	122.43	112.60
4	L	2107[A]	FEC	CBC-CAC-C2C	5.34	121.61	112.60
4	I	1805[B]	FEC	C3B-C4B-NB	-5.34	103.45	114.98
4	A	1007[A]	FEC	CBC-CAC-C2C	5.28	121.50	112.60
4	L	2107[B]	FEC	CBC-CAC-C2C	5.27	121.49	112.60
4	G	1607[A]	FEC	CBC-CAC-C2C	5.17	121.31	112.60
4	E	1407[B]	FEC	CBC-CAC-C2C	4.98	120.99	112.60
4	G	1607[A]	FEC	C4B-CHC-C1C	4.93	132.01	118.67
4	C	1207[A]	FEC	CBC-CAC-C2C	4.92	120.89	112.60
4	I	1805[B]	FEC	C3D-C4D-ND	4.54	124.77	114.98
4	I	1805[A]	FEC	CBC-CAC-C2C	4.45	120.10	112.60
4	G	1607[B]	FEC	CBC-CAC-C2C	4.40	120.02	112.60
3	B	1005	SO4	O4-S-O1	4.25	131.49	109.31
4	P	2507[B]	FEC	CBC-CAC-C2C	4.01	119.36	112.60
4	A	1007[B]	FEC	C3B-C4B-NB	-3.95	106.46	114.98
4	M	2207[A]	FEC	CBC-CAC-C2C	3.74	118.91	112.60
4	A	1007[B]	FEC	C4B-CHC-C1C	3.65	128.54	118.67
4	P	2507[A]	FEC	C4B-CHC-C1C	3.58	128.35	118.67
4	L	2107[B]	FEC	CBA-CAA-C3A	3.54	118.58	112.60
4	E	1407[A]	FEC	C4B-CHC-C1C	3.54	128.24	118.67
4	C	1207[A]	FEC	C4B-CHC-C1C	3.52	128.18	118.67
4	P	2507[B]	FEC	C4B-CHC-C1C	3.49	128.11	118.67
4	C	1207[B]	FEC	CBA-CAA-C3A	3.48	118.46	112.60
3	B	1005	SO4	O4-S-O3	-3.36	94.70	109.06
4	L	2107[B]	FEC	C4B-CHC-C1C	3.34	127.70	118.67
4	I	1805[B]	FEC	CMC-C3C-C2C	3.29	131.15	124.94
4	E	1407[B]	FEC	CBA-CAA-C3A	3.28	118.13	112.60
4	A	1007[B]	FEC	C1B-CHB-C4A	3.25	127.47	118.67
4	E	1407[B]	FEC	C4B-CHC-C1C	3.21	127.35	118.67
4	G	1607[B]	FEC	C3D-C4D-ND	3.19	121.86	114.98
4	I	1805[B]	FEC	CBB-CAB-C3B	3.18	121.39	112.62
4	E	1407[B]	FEC	C3B-C4B-NB	-3.13	108.22	114.98
4	M	2207[A]	FEC	C4B-CHC-C1C	3.12	127.10	118.67
4	L	2107[A]	FEC	C4B-CHC-C1C	3.09	127.03	118.67
4	A	1007[B]	FEC	CBA-CAA-C3A	3.09	117.81	112.60
4	I	1805[A]	FEC	C4B-CHC-C1C	3.07	126.97	118.67
4	G	1607[B]	FEC	C4B-CHC-C1C	3.06	126.94	118.67
4	P	2507[B]	FEC	CMA-C2A-C3A	3.03	130.66	124.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	G	1607[A]	FEC	C3D-C4D-ND	-3.03	108.45	114.98
4	I	1805[B]	FEC	C4B-CHC-C1C	2.94	126.61	118.67
4	C	1207[A]	FEC	CBB-CAB-C3B	2.88	120.55	112.62
4	A	1007[A]	FEC	C4B-CHC-C1C	2.87	126.43	118.67
4	G	1607[B]	FEC	C1B-CHB-C4A	2.87	126.42	118.67
4	A	1007[A]	FEC	C3D-C4D-ND	-2.83	108.87	114.98
4	E	1407[A]	FEC	C4D-CHA-C1A	2.81	126.28	118.67
4	P	2507[B]	FEC	CBB-CAB-C3B	2.80	120.33	112.62
4	L	2107[B]	FEC	C1B-CHB-C4A	2.76	126.14	118.67
4	A	1007[B]	FEC	CAB-CBB-CGB	2.75	119.52	113.60
4	M	2207[A]	FEC	CBB-CAB-C3B	2.74	120.18	112.62
4	E	1407[A]	FEC	CAB-CBB-CGB	2.74	119.49	113.60
4	G	1607[A]	FEC	O1C-CGC-CBC	-2.73	114.30	123.08
4	C	1207[B]	FEC	C3B-C4B-NB	-2.72	109.10	114.98
4	L	2107[A]	FEC	C1B-CHB-C4A	2.72	126.03	118.67
3	F	1506	SO4	O4-S-O1	2.66	123.20	109.31
4	I	1805[B]	FEC	C1D-CHD-C4C	2.66	125.86	118.67
4	I	1805[A]	FEC	CMA-C2A-C3A	2.65	129.95	124.94
4	E	1407[A]	FEC	CBD-CAD-C3D	2.63	119.88	112.62
4	L	2107[A]	FEC	CMA-C2A-C3A	2.63	129.90	124.94
4	P	2507[B]	FEC	CMC-C3C-C2C	2.62	129.88	124.94
4	G	1607[B]	FEC	CBB-CAB-C3B	2.62	119.83	112.62
4	C	1207[B]	FEC	C4B-CHC-C1C	2.62	125.75	118.67
4	C	1207[B]	FEC	C1B-CHB-C4A	2.60	125.71	118.67
4	A	1007[B]	FEC	CMA-C2A-C3A	2.60	129.85	124.94
4	L	2107[A]	FEC	CBA-CAA-C3A	2.60	116.99	112.60
4	I	1805[B]	FEC	CBA-CAA-C3A	2.57	116.93	112.60
4	P	2507[A]	FEC	C1B-CHB-C4A	2.55	125.58	118.67
4	P	2507[A]	FEC	CMA-C2A-C3A	2.55	129.76	124.94
4	G	1607[B]	FEC	O1D-CGD-CBD	-2.54	114.92	123.08
4	G	1607[A]	FEC	CMC-C3C-C2C	2.54	129.73	124.94
4	I	1805[A]	FEC	CBD-CAD-C3D	2.53	119.60	112.62
4	G	1607[A]	FEC	CBA-CAA-C3A	2.52	116.86	112.60
4	C	1207[B]	FEC	CAB-CBB-CGB	2.52	119.03	113.60
4	M	2207[B]	FEC	C4B-CHC-C1C	2.50	125.44	118.67
4	P	2507[A]	FEC	C1D-CHD-C4C	2.50	125.44	118.67
4	C	1207[A]	FEC	C4D-CHA-C1A	2.49	125.40	118.67
4	P	2507[B]	FEC	O2C-CGC-O1C	2.49	129.50	123.30
4	I	1805[B]	FEC	C4D-CHA-C1A	2.48	125.38	118.67
4	P	2507[B]	FEC	C1D-C2D-C3D	-2.48	106.55	108.61
4	G	1607[A]	FEC	C1B-CHB-C4A	2.47	125.34	118.67
4	I	1805[A]	FEC	C4D-CHA-C1A	2.47	125.34	118.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	1007[B]	FEC	CMC-C3C-C2C	2.47	129.59	124.94
4	C	1207[A]	FEC	C1D-CHD-C4C	2.46	125.32	118.67
4	G	1607[B]	FEC	C4D-CHA-C1A	2.46	125.32	118.67
4	I	1805[A]	FEC	C3D-C4D-ND	-2.45	109.69	114.98
4	E	1407[A]	FEC	C3D-C4D-ND	-2.45	109.70	114.98
4	A	1007[A]	FEC	C1B-CHB-C4A	2.45	125.29	118.67
4	L	2107[A]	FEC	C1D-CHD-C4C	2.45	125.29	118.67
4	I	1805[A]	FEC	C1B-CHB-C4A	2.44	125.27	118.67
4	P	2507[A]	FEC	CMC-C3C-C2C	2.44	129.54	124.94
4	L	2107[A]	FEC	CMC-C3C-C2C	2.44	129.54	124.94
4	L	2107[A]	FEC	C4D-CHA-C1A	2.44	125.26	118.67
4	M	2207[B]	FEC	O2A-CGA-CBA	-2.43	115.27	123.08
4	E	1407[A]	FEC	C1D-CHD-C4C	2.43	125.25	118.67
4	P	2507[B]	FEC	CBA-CAA-C3A	2.43	116.70	112.60
4	M	2207[B]	FEC	C1D-CHD-C4C	2.43	125.24	118.67
4	P	2507[A]	FEC	CBD-CAD-C3D	2.43	119.30	112.62
4	A	1007[A]	FEC	CMA-C2A-C3A	2.42	129.50	124.94
4	A	1007[A]	FEC	CBB-CAB-C3B	2.42	119.28	112.62
3	E	1406	SO4	O3-S-O1	-2.41	96.71	109.31
4	P	2507[A]	FEC	C4D-CHA-C1A	2.41	125.19	118.67
4	C	1207[B]	FEC	CMC-C3C-C2C	2.40	129.47	124.94
4	G	1607[A]	FEC	CAB-CBB-CGB	2.39	118.75	113.60
4	A	1007[A]	FEC	C1D-CHD-C4C	2.38	125.11	118.67
4	A	1007[B]	FEC	C4D-CHA-C1A	2.38	125.10	118.67
4	L	2107[A]	FEC	C3D-C4D-ND	-2.38	109.85	114.98
4	M	2207[A]	FEC	CMC-C3C-C2C	2.38	129.42	124.94
4	I	1805[B]	FEC	O2A-CGA-CBA	-2.35	115.52	123.08
4	M	2207[A]	FEC	C4D-CHA-C1A	2.33	124.96	118.67
4	M	2207[B]	FEC	CAB-CBB-CGB	2.31	118.58	113.60
4	C	1207[A]	FEC	O2A-CGA-CBA	-2.31	115.67	123.08
4	I	1805[B]	FEC	CMA-C2A-C3A	2.28	129.24	124.94
4	A	1007[A]	FEC	O1D-CGD-CBD	-2.28	115.76	123.08
4	C	1207[A]	FEC	O1D-CGD-CBD	-2.26	115.81	123.08
4	M	2207[A]	FEC	CMA-C2A-C3A	2.26	129.21	124.94
4	A	1007[A]	FEC	CMC-C3C-C2C	2.25	129.18	124.94
4	E	1407[B]	FEC	O1D-CGD-CBD	-2.24	115.88	123.08
4	C	1207[B]	FEC	C1D-CHD-C4C	2.24	124.73	118.67
4	L	2107[B]	FEC	CMA-C2A-C3A	2.23	129.15	124.94
4	P	2507[B]	FEC	O1D-CGD-CBD	-2.21	115.97	123.08
4	I	1805[A]	FEC	O2A-CGA-CBA	-2.20	116.01	123.08
4	M	2207[A]	FEC	C1B-CHB-C4A	2.20	124.61	118.67
4	I	1805[B]	FEC	C1B-CHB-C4A	2.19	124.60	118.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	E	1407[B]	FEC	O2A-CGA-CBA	-2.19	116.04	123.08
4	L	2107[B]	FEC	O1D-CGD-CBD	-2.19	116.05	123.08
4	E	1407[A]	FEC	O1C-CGC-CBC	-2.19	116.06	123.08
4	E	1407[B]	FEC	CMA-C2A-C3A	2.18	129.06	124.94
4	G	1607[A]	FEC	O2A-CGA-CBA	-2.18	116.08	123.08
4	G	1607[B]	FEC	C1D-CHD-C4C	2.17	124.54	118.67
4	G	1607[A]	FEC	C1D-CHD-C4C	2.17	124.54	118.67
4	P	2507[B]	FEC	O1C-CGC-CBC	-2.17	116.12	123.08
4	G	1607[A]	FEC	CMA-C2A-C3A	2.16	129.01	124.94
4	M	2207[B]	FEC	C1B-CHB-C4A	2.15	124.49	118.67
4	C	1207[A]	FEC	CBD-CAD-C3D	2.15	118.55	112.62
4	A	1007[B]	FEC	O1D-CGD-CBD	-2.15	116.17	123.08
4	E	1407[B]	FEC	CMC-C3C-C2C	2.14	128.98	124.94
4	M	2207[B]	FEC	C3D-C4D-ND	-2.14	110.36	114.98
4	E	1407[A]	FEC	CMC-C3C-C2C	2.14	128.98	124.94
4	C	1207[B]	FEC	O1C-CGC-CBC	-2.14	116.20	123.08
4	L	2107[A]	FEC	O1C-CGC-CBC	-2.14	116.21	123.08
4	M	2207[B]	FEC	CMC-C3C-C2C	2.14	128.97	124.94
4	I	1805[A]	FEC	C1D-CHD-C4C	2.13	124.44	118.67
4	P	2507[A]	FEC	CBB-CAB-C3B	2.13	118.49	112.62
4	M	2207[A]	FEC	CBD-CAD-C3D	2.13	118.48	112.62
4	G	1607[B]	FEC	O2A-CGA-CBA	-2.12	116.26	123.08
4	E	1407[B]	FEC	O1C-CGC-CBC	-2.12	116.26	123.08
4	A	1007[B]	FEC	O2A-CGA-CBA	-2.12	116.27	123.08
4	C	1207[A]	FEC	C1B-CHB-C4A	2.12	124.39	118.67
4	C	1207[B]	FEC	C4D-CHA-C1A	2.11	124.39	118.67
4	C	1207[B]	FEC	CMA-C2A-C3A	2.11	128.91	124.94
4	L	2107[B]	FEC	O1C-CGC-CBC	-2.11	116.32	123.08
4	C	1207[B]	FEC	O1D-CGD-CBD	-2.10	116.32	123.08
4	I	1805[A]	FEC	CBB-CAB-C3B	2.10	118.41	112.62
4	G	1607[A]	FEC	CBB-CAB-C3B	2.09	118.39	112.62
4	G	1607[A]	FEC	C4D-CHA-C1A	2.09	124.33	118.67
3	E	1403	SO4	O3-S-O2	2.09	120.23	109.31
3	L	2106	SO4	O4-S-O2	-2.09	98.40	109.31
4	C	1207[A]	FEC	O1C-CGC-CBC	-2.08	116.40	123.08
4	C	1207[B]	FEC	C1D-C2D-C3D	-2.08	106.88	108.61
4	L	2107[B]	FEC	C4D-CHA-C1A	2.07	124.26	118.67
4	A	1007[A]	FEC	O2A-CGA-CBA	-2.06	116.48	123.08
4	E	1407[B]	FEC	C1B-CHB-C4A	2.05	124.22	118.67
4	G	1607[B]	FEC	CMC-C3C-C2C	2.05	128.81	124.94
4	G	1607[A]	FEC	O1D-CGD-CBD	-2.05	116.50	123.08
4	E	1407[B]	FEC	C4D-CHA-C1A	2.04	124.19	118.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	E	1407[B]	FEC	O2C-CGC-O1C	2.04	128.38	123.30
4	G	1607[B]	FEC	O1C-CGC-CBC	-2.04	116.53	123.08
4	E	1407[A]	FEC	C1B-CHB-C4A	2.03	124.15	118.67
4	A	1007[A]	FEC	C4D-CHA-C1A	2.02	124.13	118.67
4	G	1607[B]	FEC	C1D-C2D-C3D	-2.00	106.94	108.61

There are no chirality outliers.

All (146) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1007[A]	FEC	C3C-C2C-CAC-CBC
4	A	1007[A]	FEC	C1C-C2C-CAC-CBC
4	A	1007[A]	FEC	C4B-C3B-CAB-CBB
4	A	1007[B]	FEC	C3C-C2C-CAC-CBC
4	A	1007[B]	FEC	C1C-C2C-CAC-CBC
4	A	1007[B]	FEC	C2C-CAC-CBC-CGC
4	C	1207[A]	FEC	C3C-C2C-CAC-CBC
4	C	1207[A]	FEC	C1C-C2C-CAC-CBC
4	C	1207[A]	FEC	C2C-CAC-CBC-CGC
4	C	1207[B]	FEC	C2A-C3A-CAA-CBA
4	C	1207[B]	FEC	C4A-C3A-CAA-CBA
4	C	1207[B]	FEC	C3C-C2C-CAC-CBC
4	C	1207[B]	FEC	C1C-C2C-CAC-CBC
4	E	1407[A]	FEC	C3C-C2C-CAC-CBC
4	E	1407[A]	FEC	C1C-C2C-CAC-CBC
4	E	1407[B]	FEC	C3C-C2C-CAC-CBC
4	E	1407[B]	FEC	C1C-C2C-CAC-CBC
4	G	1607[A]	FEC	C3C-C2C-CAC-CBC
4	G	1607[A]	FEC	C1C-C2C-CAC-CBC
4	G	1607[B]	FEC	C3C-C2C-CAC-CBC
4	G	1607[B]	FEC	C1C-C2C-CAC-CBC
4	I	1805[A]	FEC	C3C-C2C-CAC-CBC
4	I	1805[A]	FEC	C1C-C2C-CAC-CBC
4	I	1805[B]	FEC	C3C-C2C-CAC-CBC
4	I	1805[B]	FEC	C1C-C2C-CAC-CBC
4	L	2107[A]	FEC	C3C-C2C-CAC-CBC
4	L	2107[A]	FEC	C1C-C2C-CAC-CBC
4	L	2107[B]	FEC	C3C-C2C-CAC-CBC
4	L	2107[B]	FEC	C1C-C2C-CAC-CBC
4	M	2207[A]	FEC	C3C-C2C-CAC-CBC
4	M	2207[A]	FEC	C1C-C2C-CAC-CBC
4	M	2207[B]	FEC	C3C-C2C-CAC-CBC

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Mol	Chain	Res	Type	Atoms
4	M	2207[B]	FEC	C1C-C2C-CAC-CBC
4	P	2507[A]	FEC	C3C-C2C-CAC-CBC
4	P	2507[A]	FEC	C1C-C2C-CAC-CBC
4	P	2507[B]	FEC	C3C-C2C-CAC-CBC
4	P	2507[B]	FEC	C1C-C2C-CAC-CBC
4	P	2507[B]	FEC	C4B-C3B-CAB-CBB
4	E	1407[B]	FEC	C3D-CAD-CBD-CGD
4	G	1607[B]	FEC	C2C-CAC-CBC-CGC
4	L	2107[A]	FEC	C2C-CAC-CBC-CGC
4	M	2207[A]	FEC	C2C-CAC-CBC-CGC
4	P	2507[A]	FEC	C2C-CAC-CBC-CGC
4	P	2507[B]	FEC	C2C-CAC-CBC-CGC
4	A	1007[A]	FEC	C3D-CAD-CBD-CGD
4	L	2107[B]	FEC	C2C-CAC-CBC-CGC
4	P	2507[B]	FEC	C2B-C3B-CAB-CBB
4	E	1407[A]	FEC	C3D-CAD-CBD-CGD
4	I	1805[B]	FEC	C3D-CAD-CBD-CGD
4	A	1007[A]	FEC	C2B-C3B-CAB-CBB
4	L	2107[B]	FEC	C3D-CAD-CBD-CGD
4	M	2207[B]	FEC	CAC-CBC-CGC-O1C
4	A	1007[B]	FEC	C3D-CAD-CBD-CGD
4	L	2107[A]	FEC	C3D-CAD-CBD-CGD
4	M	2207[A]	FEC	C3D-CAD-CBD-CGD
4	M	2207[B]	FEC	C3D-CAD-CBD-CGD
4	G	1607[B]	FEC	CAD-CBD-CGD-O1D
4	M	2207[A]	FEC	CAD-CBD-CGD-O1D
4	L	2107[A]	FEC	CAA-CBA-CGA-O2A
4	C	1207[A]	FEC	CAA-CBA-CGA-O2A
4	E	1407[A]	FEC	CAA-CBA-CGA-O2A
4	I	1805[A]	FEC	CAA-CBA-CGA-O2A
4	I	1805[A]	FEC	CAD-CBD-CGD-O1D
4	P	2507[B]	FEC	CAD-CBD-CGD-O1D
4	C	1207[A]	FEC	C3D-CAD-CBD-CGD
4	A	1007[A]	FEC	CAA-CBA-CGA-O2A
4	E	1407[A]	FEC	CAA-CBA-CGA-O1A
4	E	1407[A]	FEC	CAD-CBD-CGD-O1D
4	L	2107[A]	FEC	CAA-CBA-CGA-O1A
4	G	1607[A]	FEC	CAA-CBA-CGA-O2A
4	M	2207[A]	FEC	CAA-CBA-CGA-O2A
4	P	2507[A]	FEC	CAD-CBD-CGD-O1D
4	C	1207[B]	FEC	CAD-CBD-CGD-O1D
4	M	2207[B]	FEC	CAC-CBC-CGC-O2C

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Mol	Chain	Res	Type	Atoms
4	P	2507[A]	FEC	CAA-CBA-CGA-O2A
4	A	1007[A]	FEC	CAA-CBA-CGA-O1A
4	C	1207[A]	FEC	CAC-CBC-CGC-O1C
4	M	2207[A]	FEC	CAC-CBC-CGC-O1C
4	I	1805[A]	FEC	CAA-CBA-CGA-O1A
4	I	1805[B]	FEC	CAA-CBA-CGA-O2A
4	P	2507[A]	FEC	CAD-CBD-CGD-O2D
4	A	1007[A]	FEC	CAC-CBC-CGC-O1C
4	P	2507[B]	FEC	CAC-CBC-CGC-O2C
4	P	2507[B]	FEC	CAD-CBD-CGD-O2D
4	G	1607[B]	FEC	CAA-CBA-CGA-O2A
4	M	2207[A]	FEC	CAA-CBA-CGA-O1A
4	P	2507[A]	FEC	CAC-CBC-CGC-O2C
4	C	1207[A]	FEC	CAA-CBA-CGA-O1A
4	C	1207[B]	FEC	CAC-CBC-CGC-O1C
4	G	1607[A]	FEC	CAC-CBC-CGC-O2C
4	G	1607[B]	FEC	CAA-CBA-CGA-O1A
4	A	1007[B]	FEC	CAA-CBA-CGA-O2A
4	C	1207[B]	FEC	CAC-CBC-CGC-O2C
4	M	2207[A]	FEC	CAD-CBD-CGD-O2D
4	P	2507[A]	FEC	CAC-CBC-CGC-O1C
4	P	2507[B]	FEC	CAC-CBC-CGC-O1C
4	A	1007[B]	FEC	CAA-CBA-CGA-O1A
4	P	2507[A]	FEC	CAA-CBA-CGA-O1A
4	A	1007[A]	FEC	CAC-CBC-CGC-O2C
4	I	1805[A]	FEC	CAC-CBC-CGC-O1C
4	M	2207[A]	FEC	CAC-CBC-CGC-O2C
4	G	1607[A]	FEC	CAC-CBC-CGC-O1C
4	G	1607[B]	FEC	CAD-CBD-CGD-O2D
4	I	1805[A]	FEC	CAD-CBD-CGD-O2D
4	C	1207[A]	FEC	CAC-CBC-CGC-O2C
4	I	1805[A]	FEC	CAC-CBC-CGC-O2C
4	G	1607[B]	FEC	C3D-CAD-CBD-CGD
4	I	1805[B]	FEC	CAA-CBA-CGA-O1A
4	L	2107[B]	FEC	CAA-CBA-CGA-O1A
4	E	1407[A]	FEC	CAC-CBC-CGC-O2C
4	L	2107[A]	FEC	CAC-CBC-CGC-O2C
4	M	2207[B]	FEC	CAA-CBA-CGA-O1A
4	P	2507[B]	FEC	CAA-CBA-CGA-O1A
4	L	2107[A]	FEC	CAC-CBC-CGC-O1C
4	E	1407[A]	FEC	CAC-CBC-CGC-O1C
4	M	2207[B]	FEC	CAD-CBD-CGD-O1D

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Mol	Chain	Res	Type	Atoms
4	A	1007[B]	FEC	CAC-CBC-CGC-O2C
4	C	1207[B]	FEC	C3D-CAD-CBD-CGD
4	E	1407[A]	FEC	CAD-CBD-CGD-O2D
4	G	1607[A]	FEC	CAA-CBA-CGA-O1A
4	L	2107[B]	FEC	CAC-CBC-CGC-O2C
4	A	1007[B]	FEC	CAD-CBD-CGD-O1D
4	L	2107[B]	FEC	CAA-CBA-CGA-O2A
4	P	2507[B]	FEC	CAA-CBA-CGA-O2A
4	E	1407[B]	FEC	CAA-CBA-CGA-O1A
4	E	1407[B]	FEC	CAA-CBA-CGA-O2A
4	P	2507[B]	FEC	CAB-CBB-CGB-O2B
4	C	1207[B]	FEC	CAA-CBA-CGA-O1A
4	G	1607[B]	FEC	CAC-CBC-CGC-O2C
4	L	2107[B]	FEC	CAC-CBC-CGC-O1C
4	C	1207[A]	FEC	CAD-CBD-CGD-O1D
4	M	2207[B]	FEC	CAA-CBA-CGA-O2A
4	P	2507[B]	FEC	CAB-CBB-CGB-O1B
4	G	1607[B]	FEC	CAC-CBC-CGC-O1C
4	A	1007[B]	FEC	CAD-CBD-CGD-O2D
4	C	1207[B]	FEC	CAD-CBD-CGD-O2D
4	C	1207[B]	FEC	CAA-CBA-CGA-O2A
4	I	1805[A]	FEC	CAB-CBB-CGB-O2B
4	A	1007[B]	FEC	CAC-CBC-CGC-O1C
4	I	1805[A]	FEC	C2C-CAC-CBC-CGC
4	M	2207[B]	FEC	CAD-CBD-CGD-O2D
4	C	1207[A]	FEC	CAD-CBD-CGD-O2D
4	L	2107[B]	FEC	CAD-CBD-CGD-O2D
4	I	1805[A]	FEC	CAB-CBB-CGB-O1B
4	A	1007[A]	FEC	CAD-CBD-CGD-O1D
4	I	1805[B]	FEC	CAD-CBD-CGD-O1D

There are no ring outliers.

33 monomers are involved in 268 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L	2102	SO4	0	14
4	L	2107[A]	FEC	17	0
4	L	2107[B]	FEC	12	0
4	C	1207[A]	FEC	8	0
3	B	1005	SO4	6	0
3	M	2206	SO4	1	0
3	I	1704	SO4	5	0

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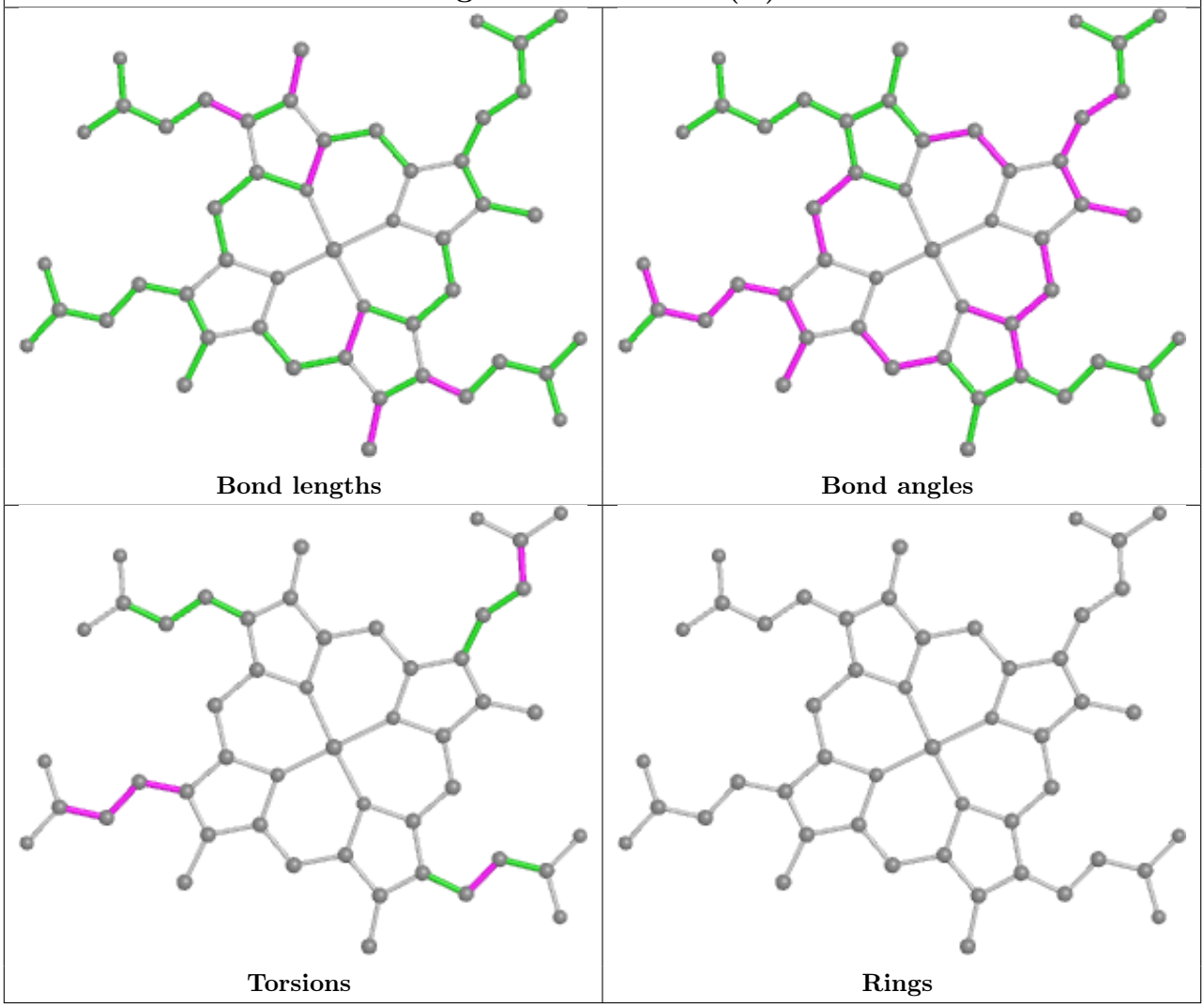
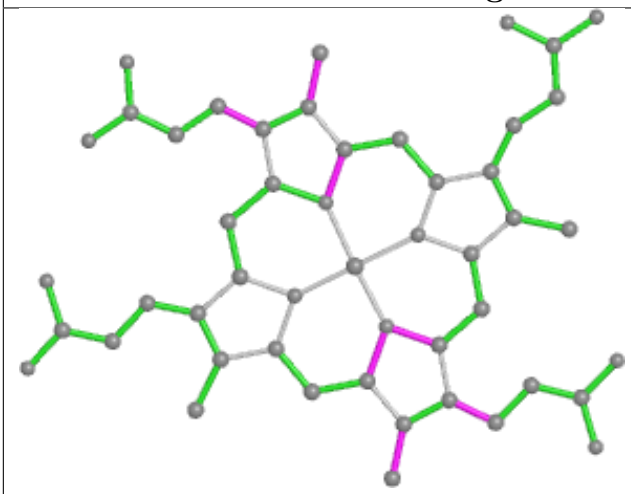
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	1207[B]	FEC	21	0
4	G	1607[A]	FEC	11	0
3	L	2104	SO4	5	5
4	G	1607[B]	FEC	13	0
3	D	1306	SO4	1	0
3	O	2406	SO4	2	0
4	A	1007[A]	FEC	6	0
3	D	1301	SO4	2	0
3	I	1802	SO4	0	14
4	A	1007[B]	FEC	15	0
4	M	2207[A]	FEC	10	0
4	M	2207[B]	FEC	9	0
3	P	1504	SO4	4	0
3	B	1104	SO4	2	0
4	I	1805[A]	FEC	10	0
4	I	1805[B]	FEC	27	0
3	M	2202	SO4	1	0
3	E	1403	SO4	4	0
3	G	1601	SO4	1	0
4	P	2507[A]	FEC	13	0
4	P	2507[B]	FEC	17	0
3	C	1206	SO4	2	0
3	A	1006	SO4	2	0
4	E	1407[B]	FEC	13	0
3	N	2301	SO4	1	0
4	E	1407[A]	FEC	8	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

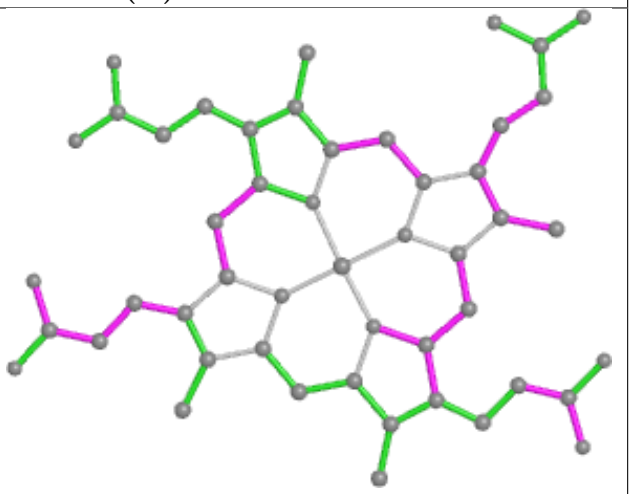
Ligand FEC L 2107 (A)



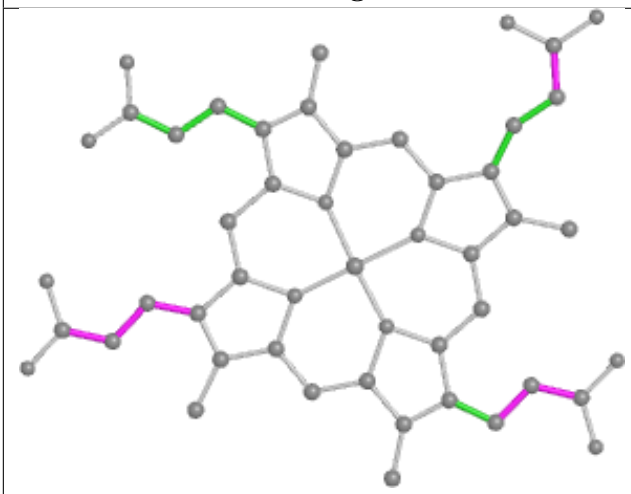
Ligand FEC L 2107 (B)



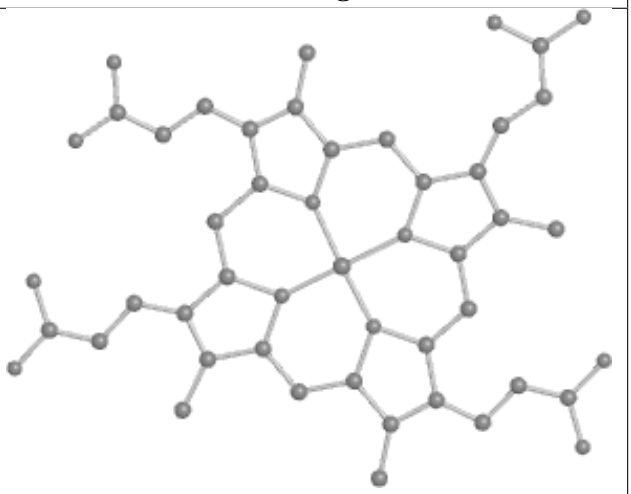
Bond lengths



Bond angles

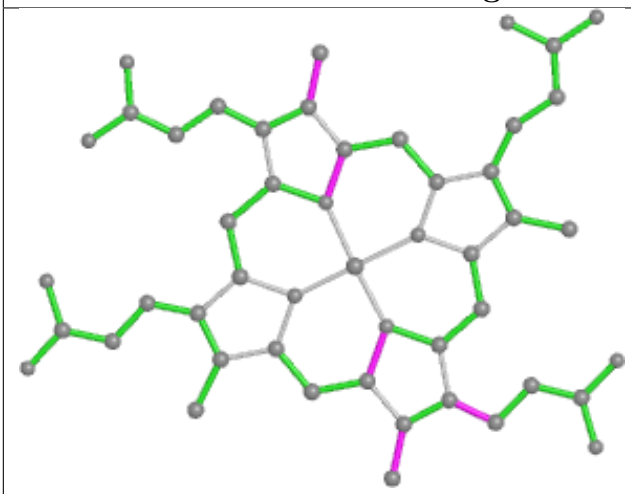


Torsions

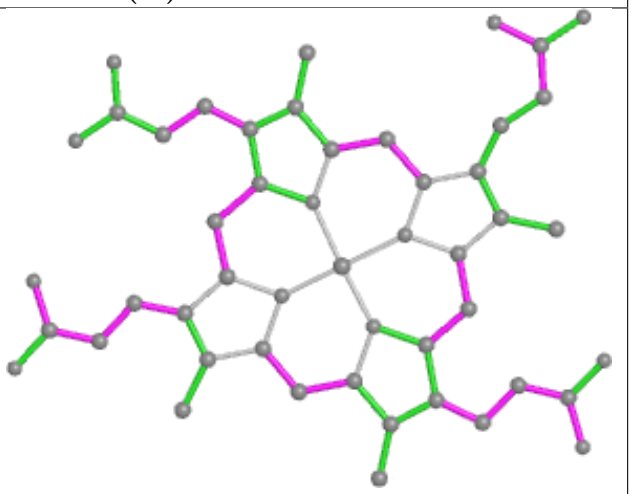


Rings

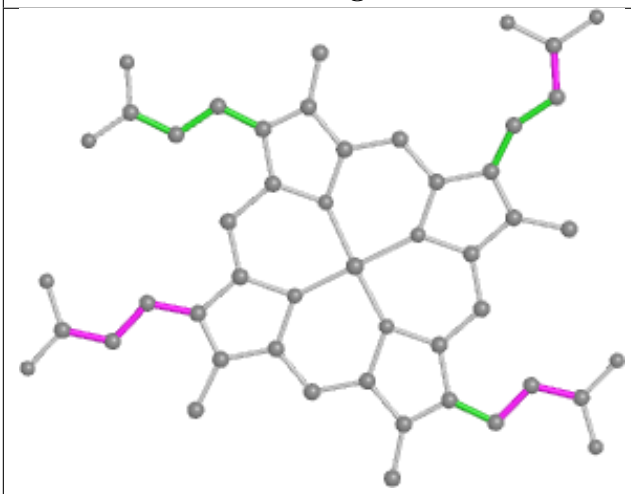
Ligand FEC C 1207 (A)



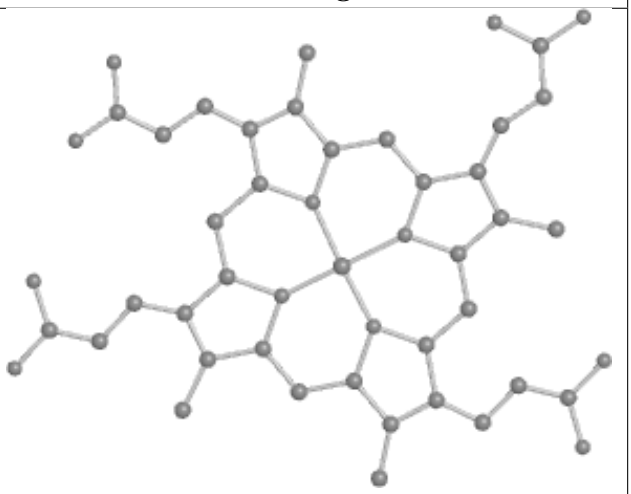
Bond lengths



Bond angles

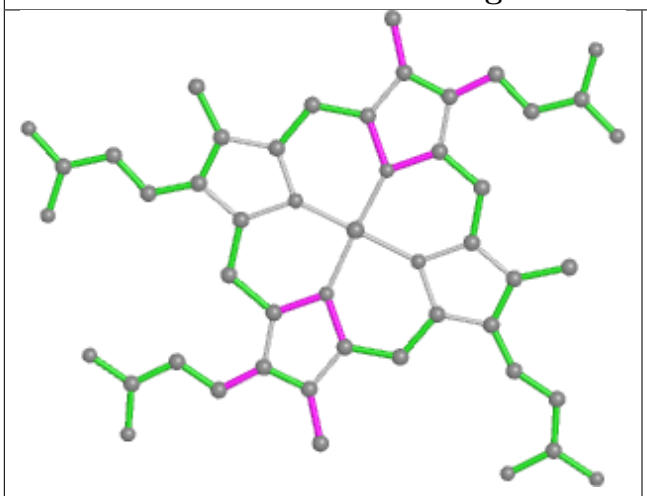


Torsions

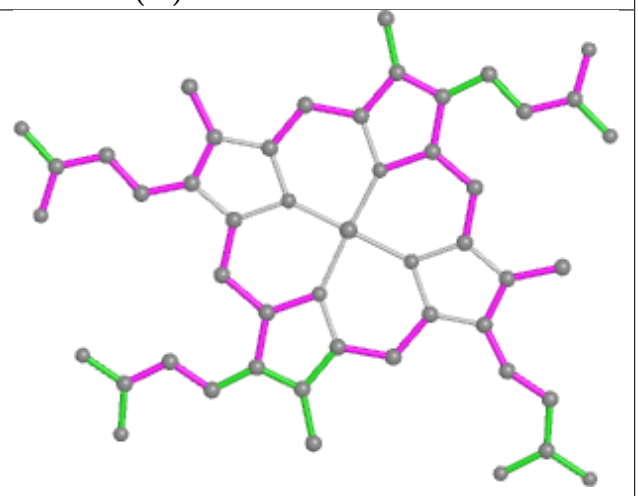


Rings

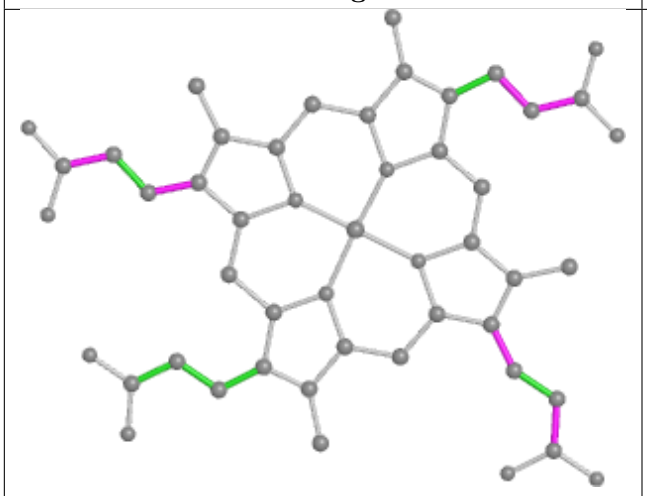
Ligand FEC C 1207 (B)



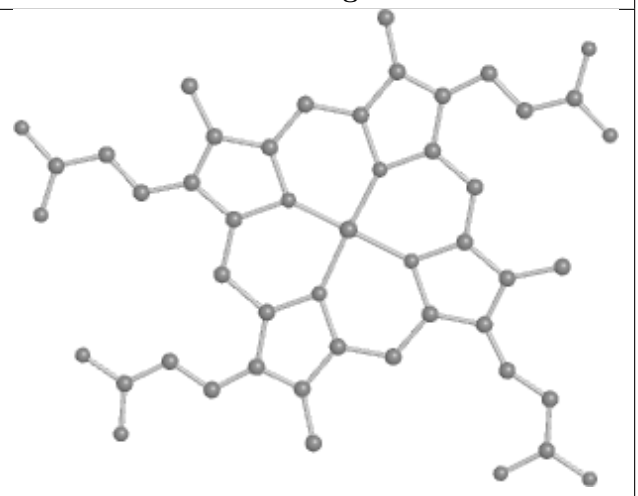
Bond lengths



Bond angles

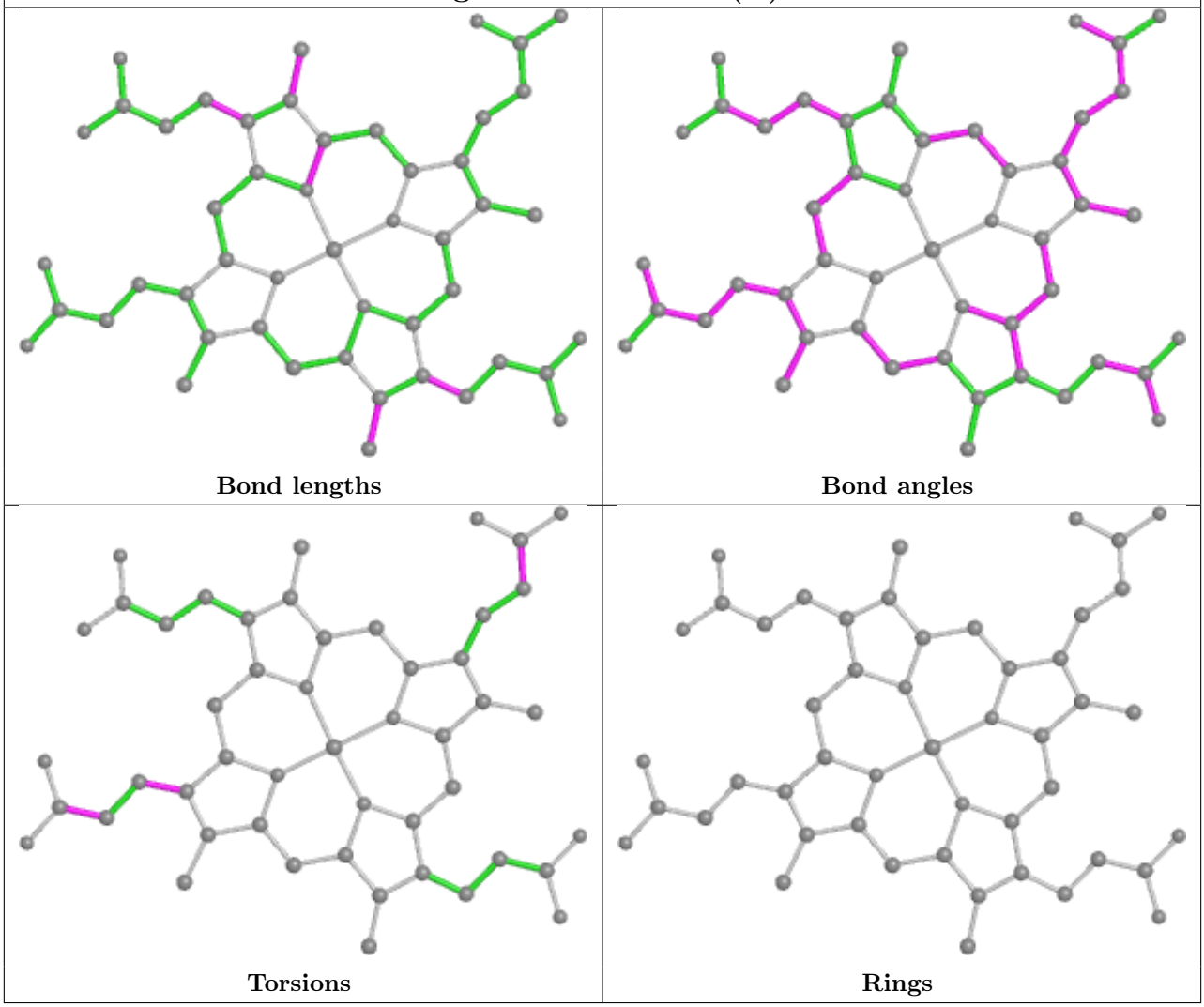


Torsions



Rings

Ligand FEC G 1607 (A)



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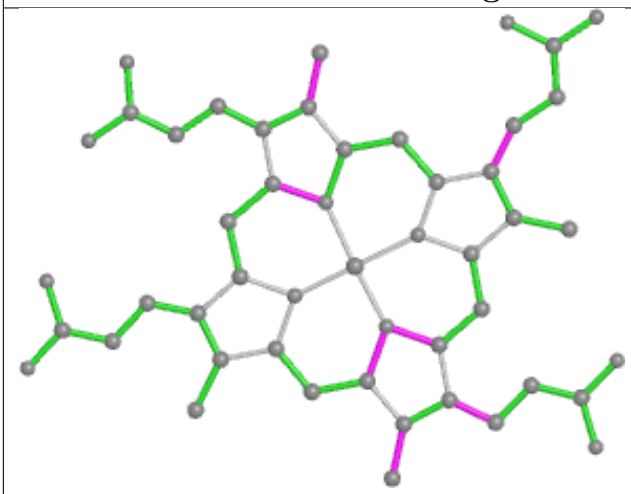
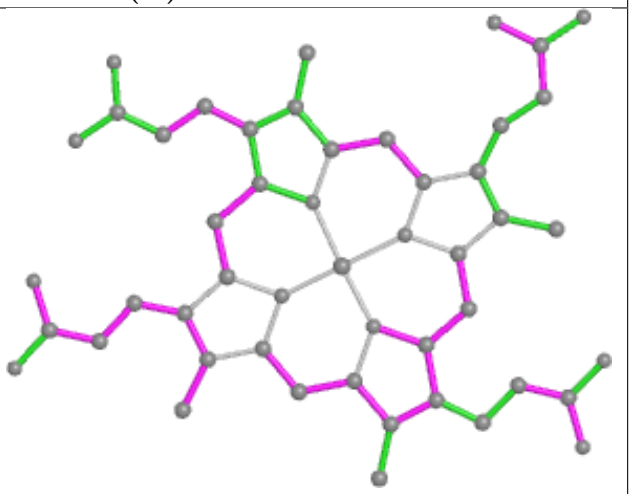
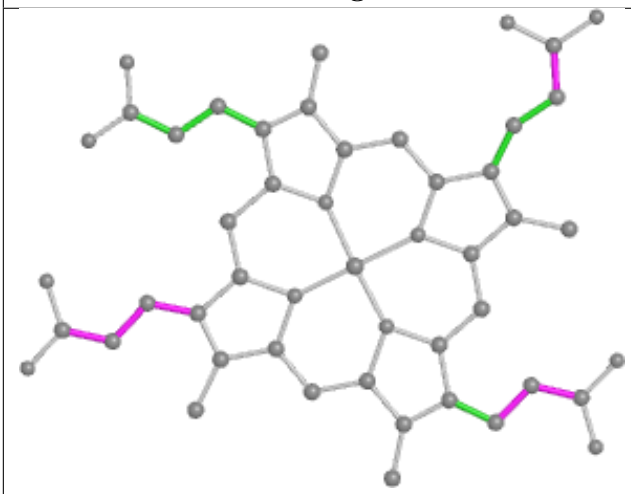


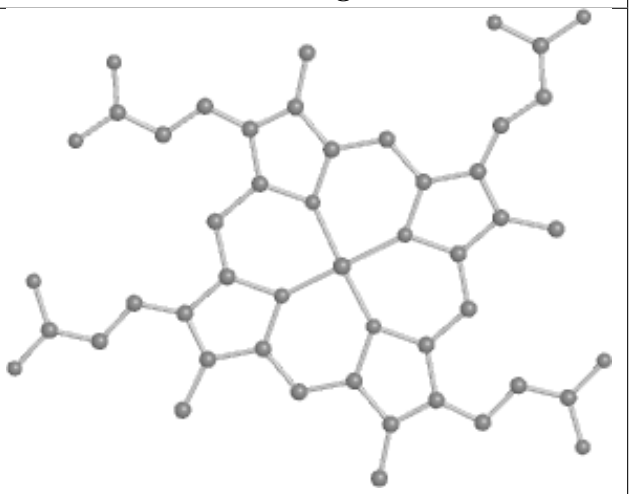
Bond lengths



Bond angles

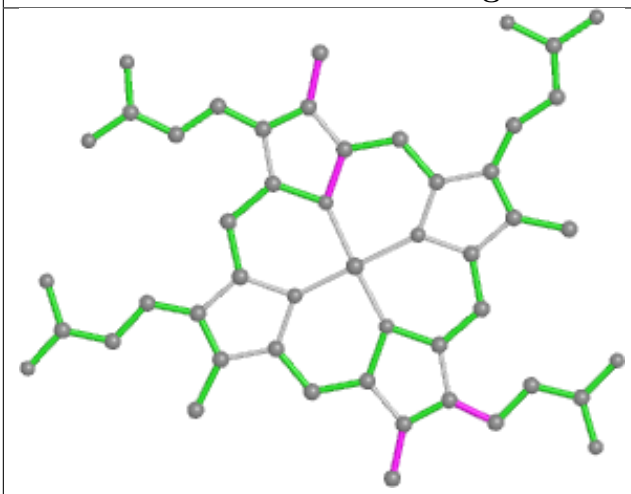


Torsions

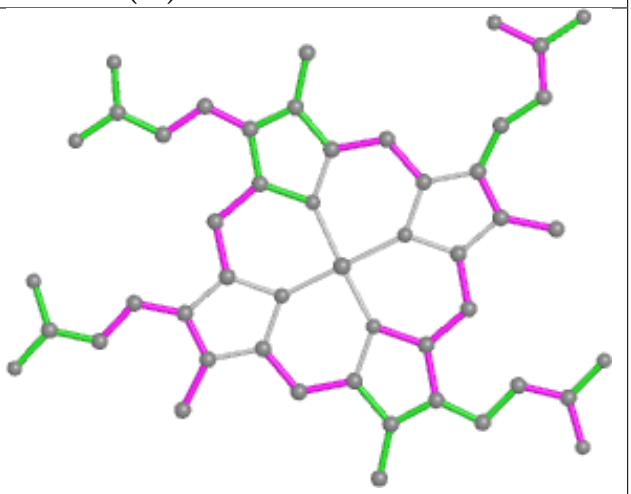


Rings

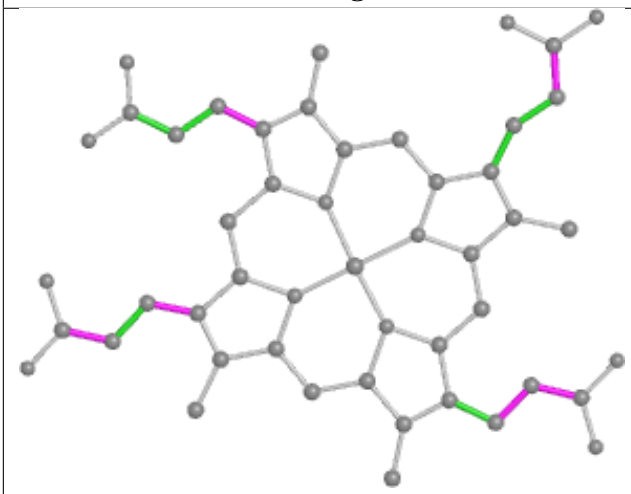
Ligand FEC A 1007 (A)



Bond lengths



Bond angles



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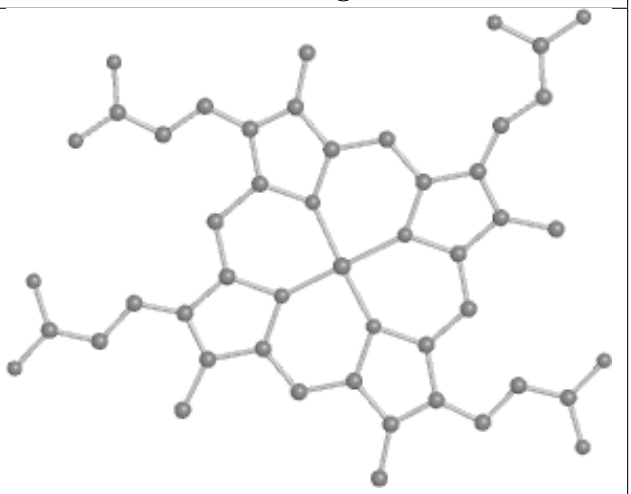
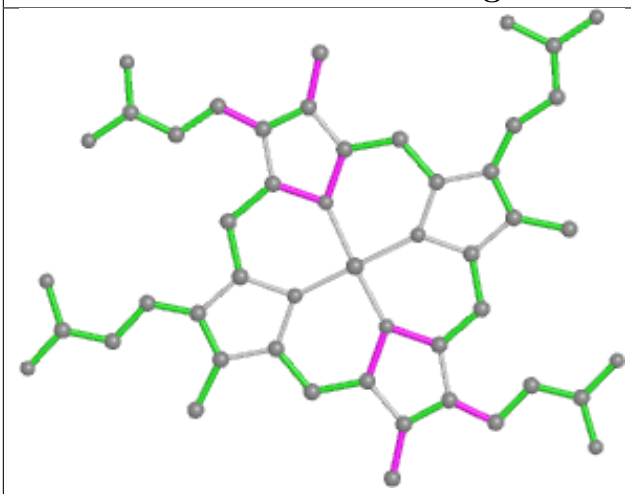
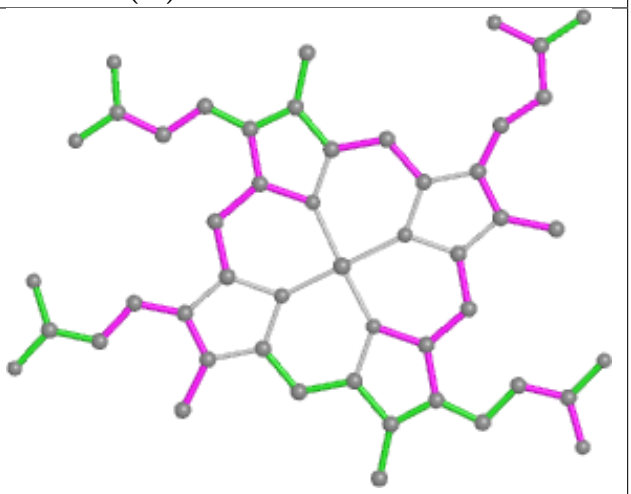


Rings

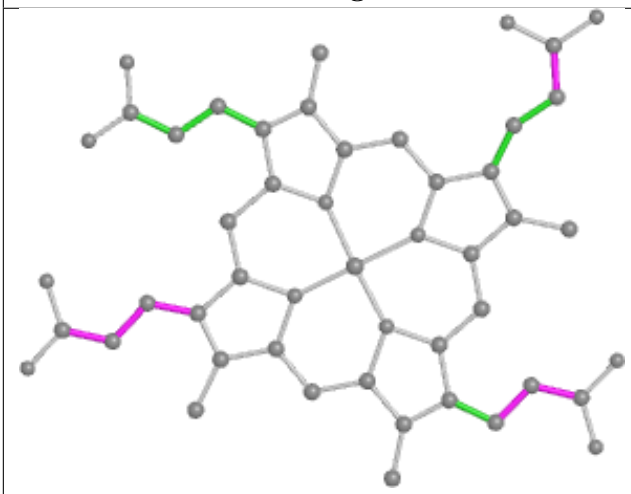
Ligand FEC A 1007 (B)



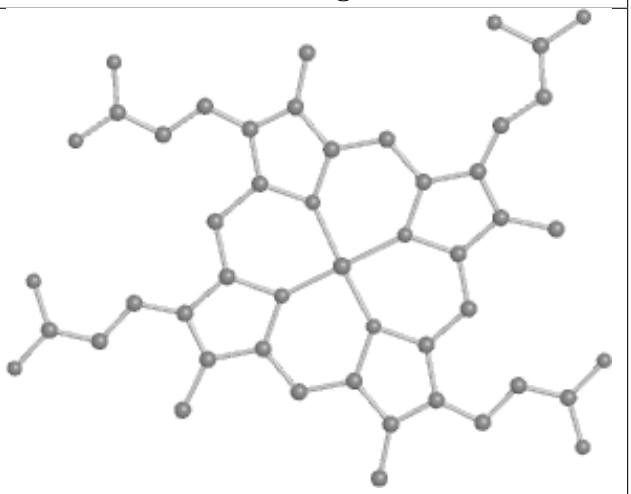
Bond lengths



Bond angles

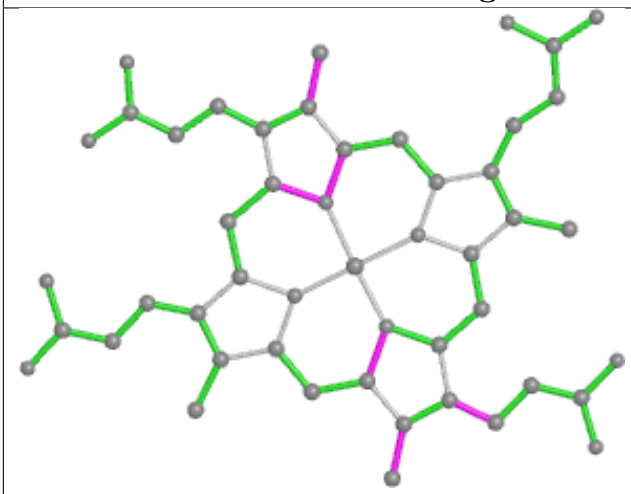


Torsions

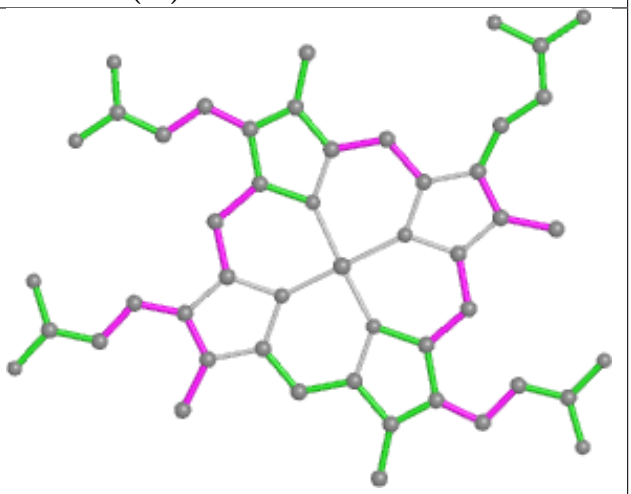


Rings

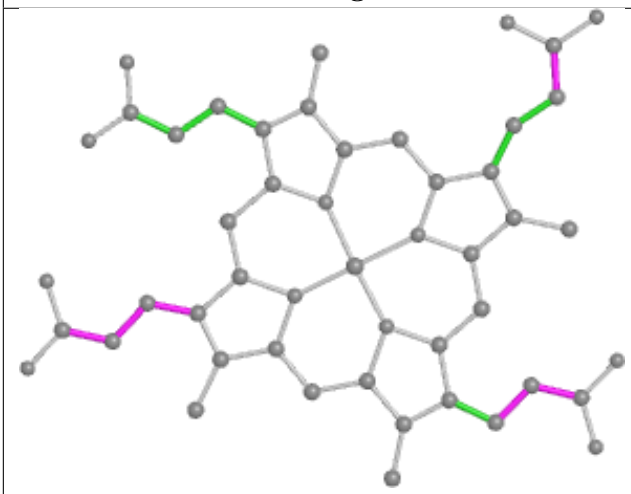
Ligand FEC M 2207 (A)



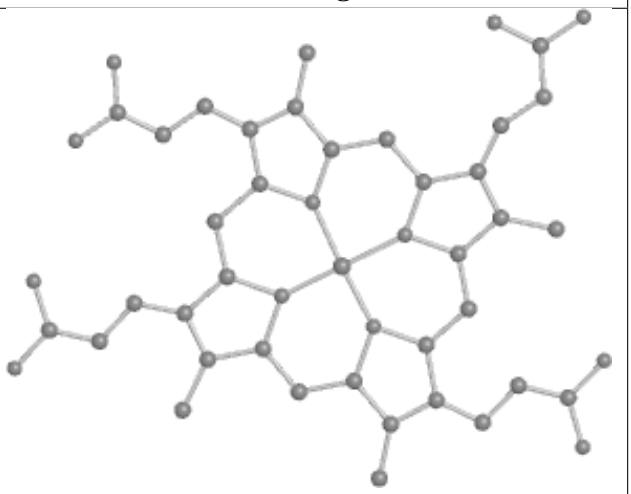
Bond lengths



Bond angles

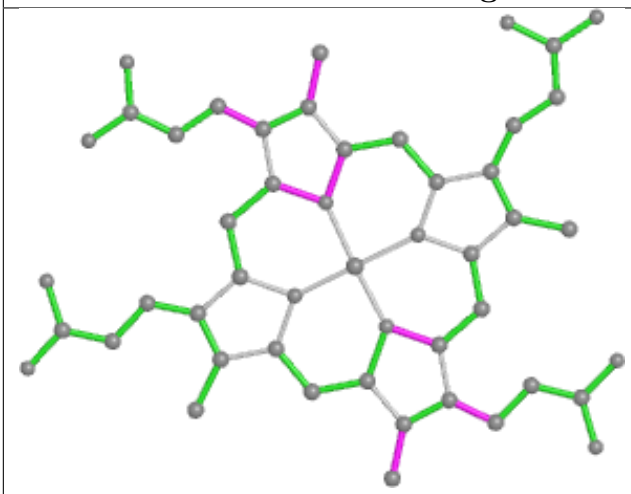


Torsions

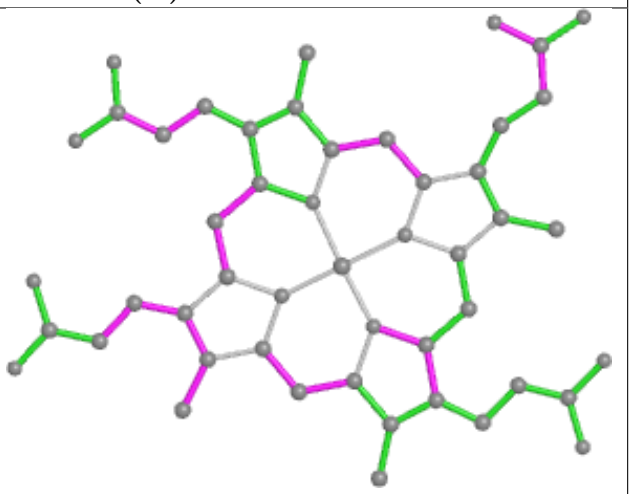


Rings

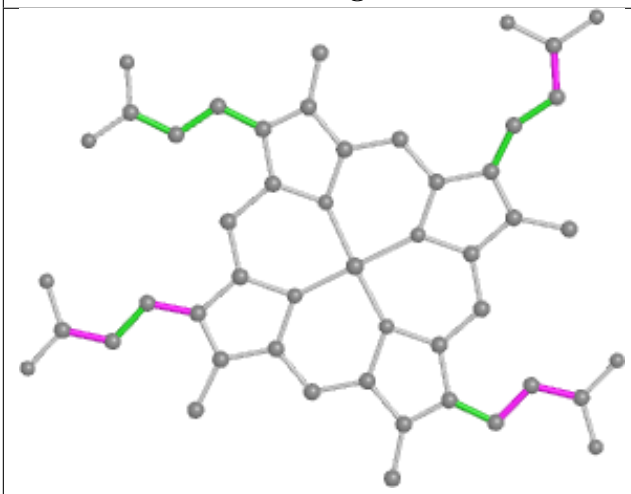
Ligand FEC M 2207 (B)



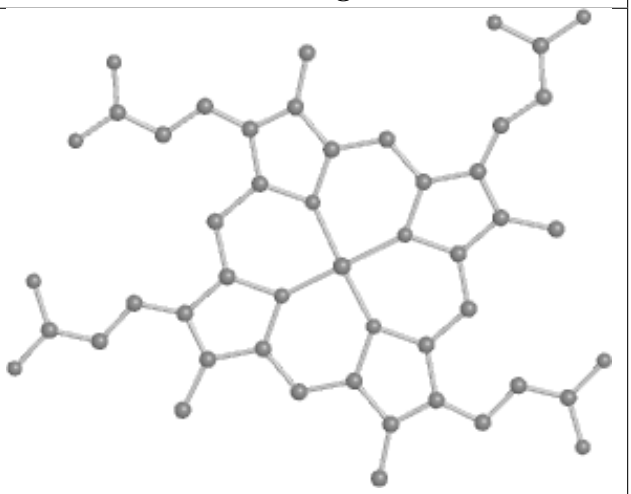
Bond lengths



Bond angles

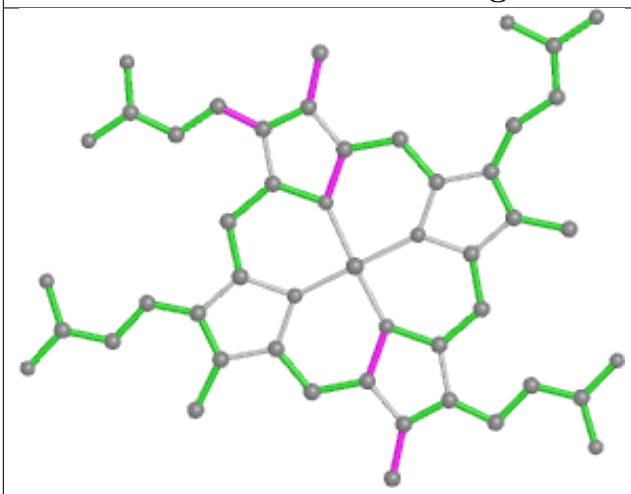


Torsions

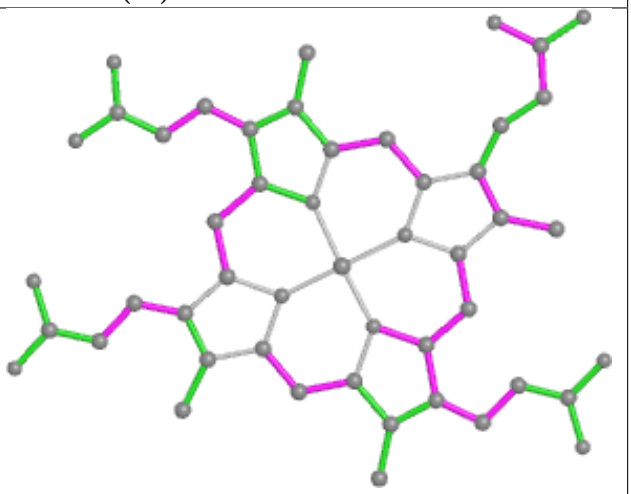


Rings

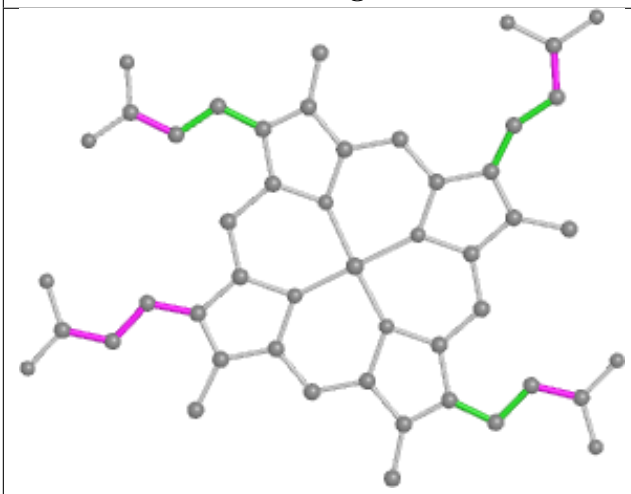
Ligand FEC I 1805 (A)



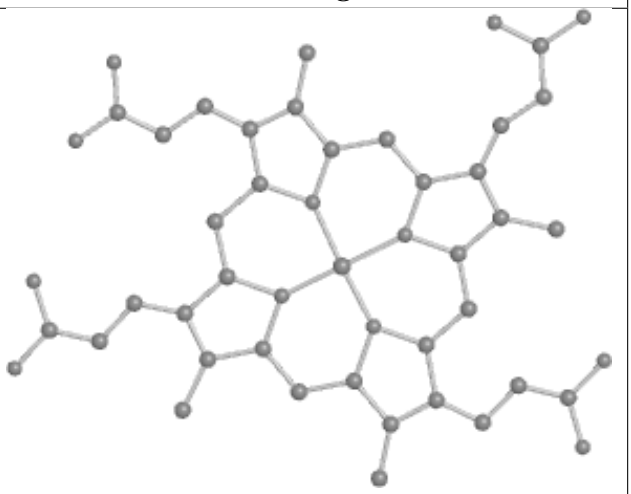
Bond lengths



Bond angles

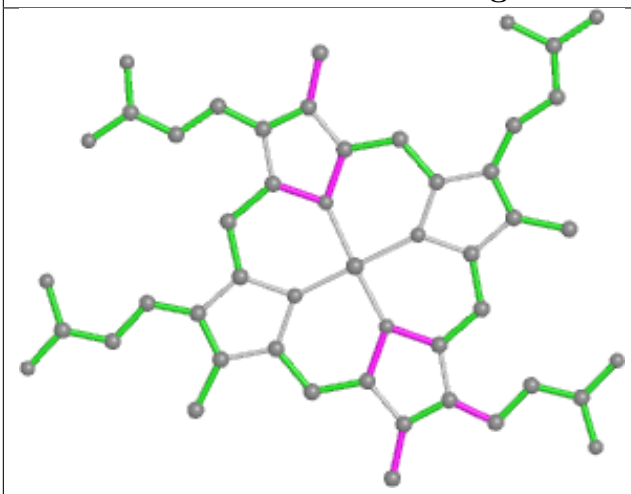


Torsions

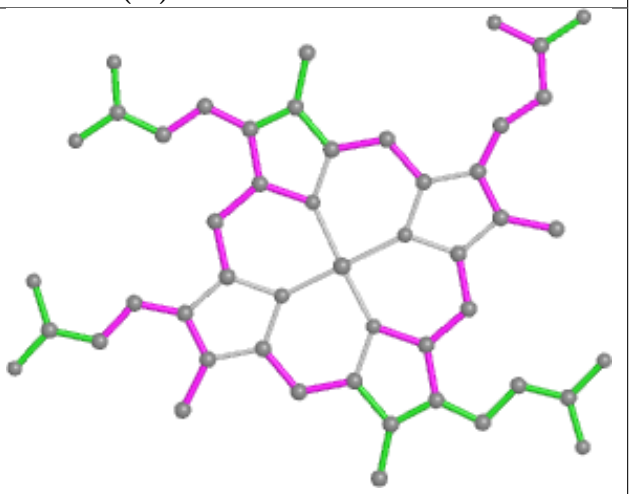


Rings

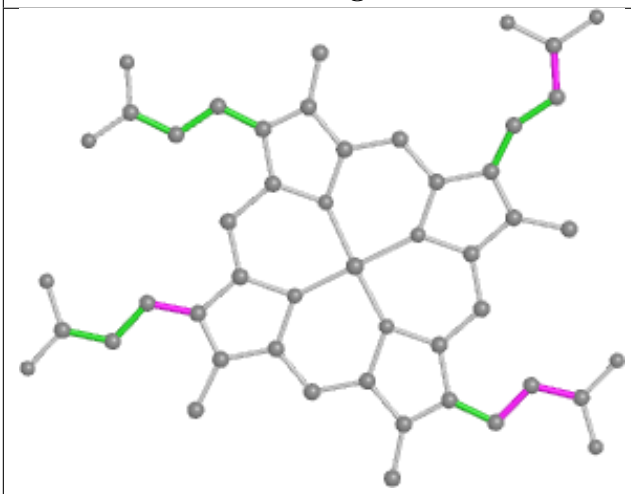
Ligand FEC I 1805 (B)



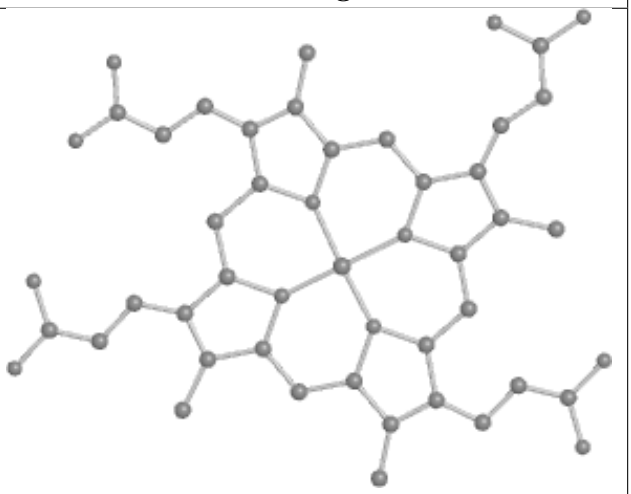
Bond lengths



Bond angles

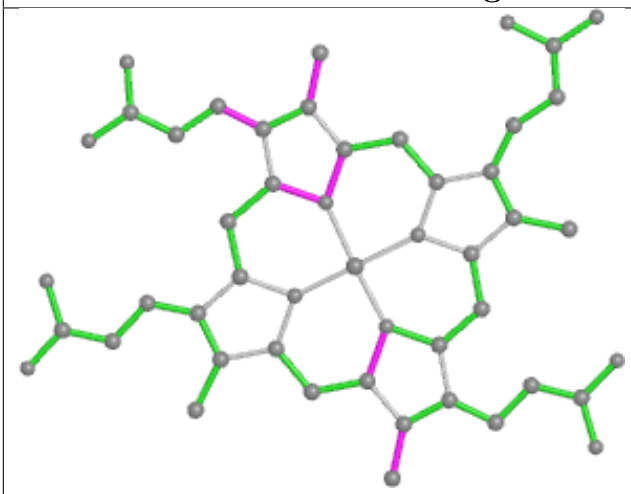


Torsions

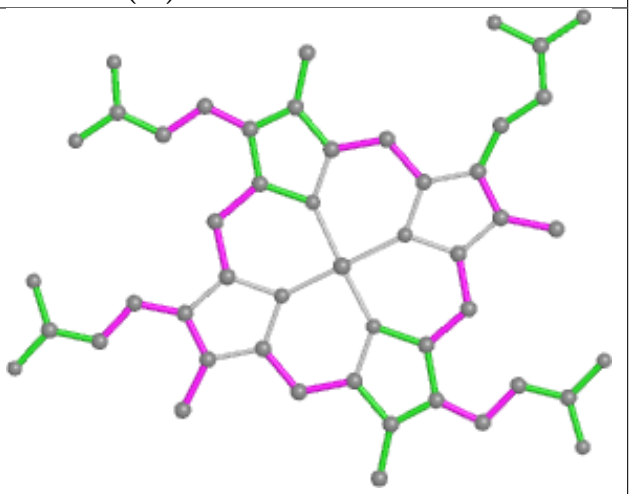


Rings

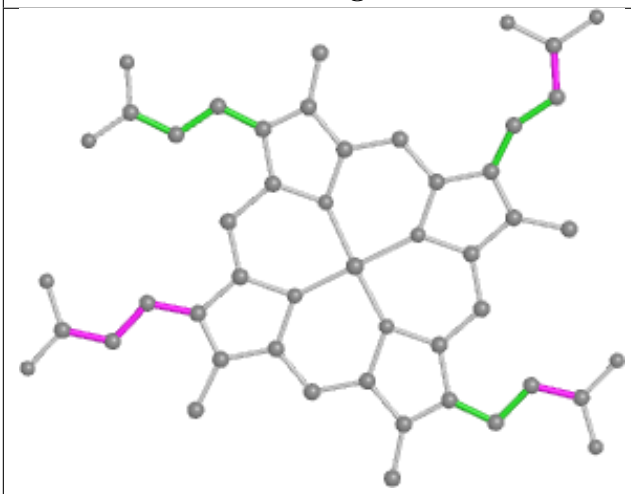
Ligand FEC P 2507 (A)



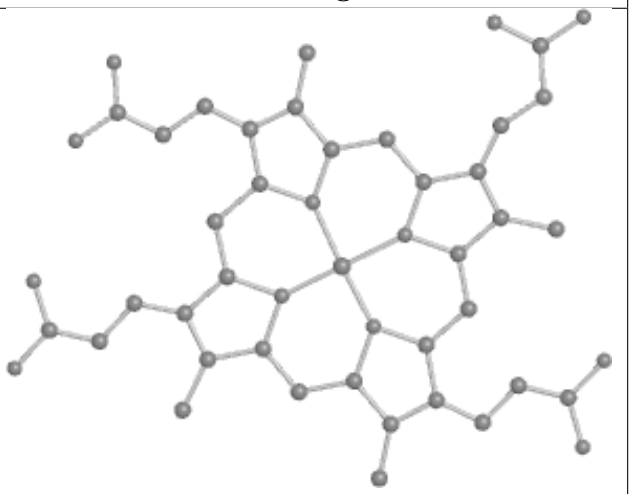
Bond lengths



Bond angles

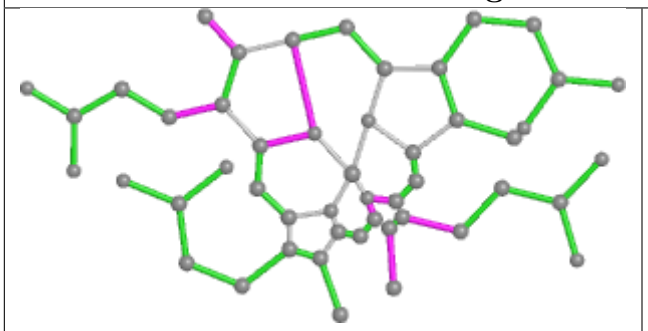


Torsions

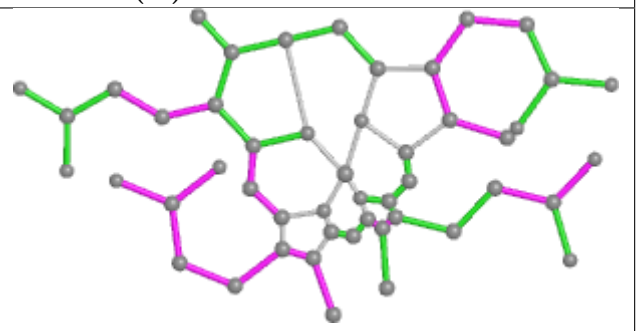


Rings

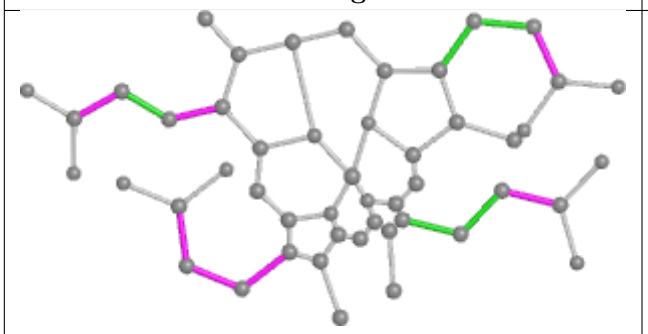
Ligand FEC P 2507 (B)



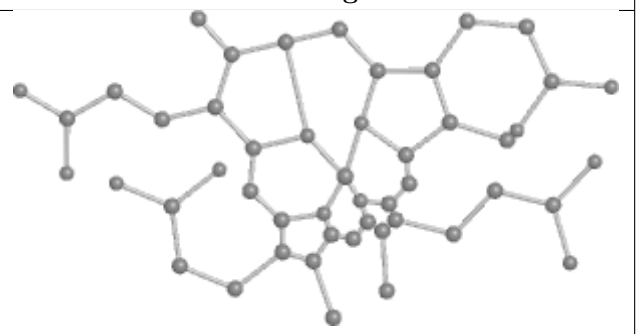
Bond lengths



Bond angles

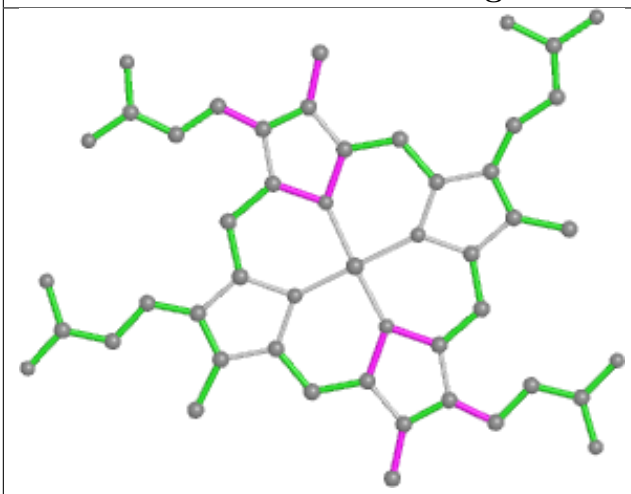


Torsions

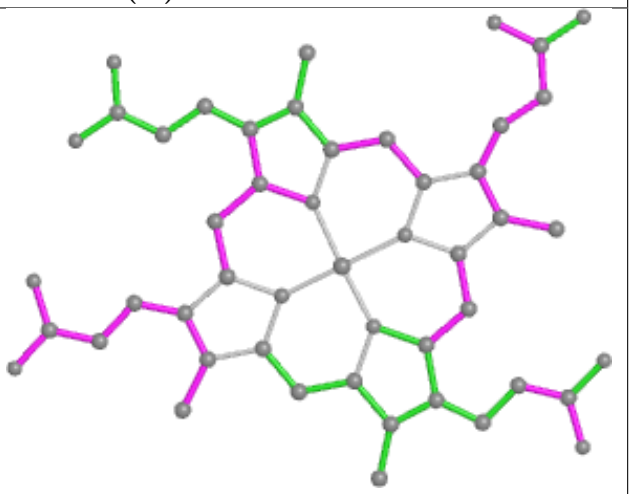


Rings

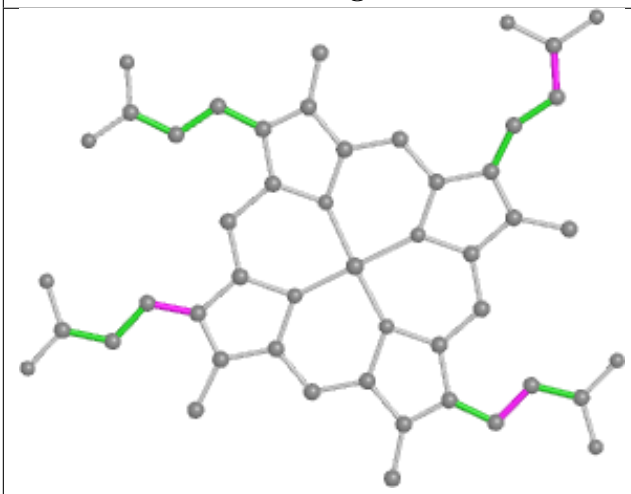
Ligand FEC E 1407 (B)



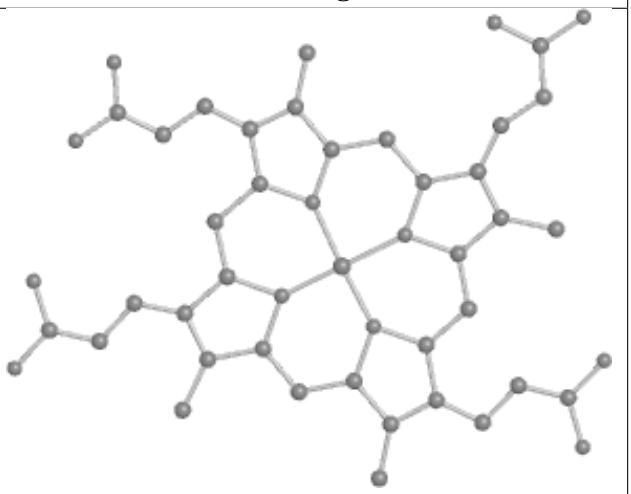
Bond lengths



Bond angles

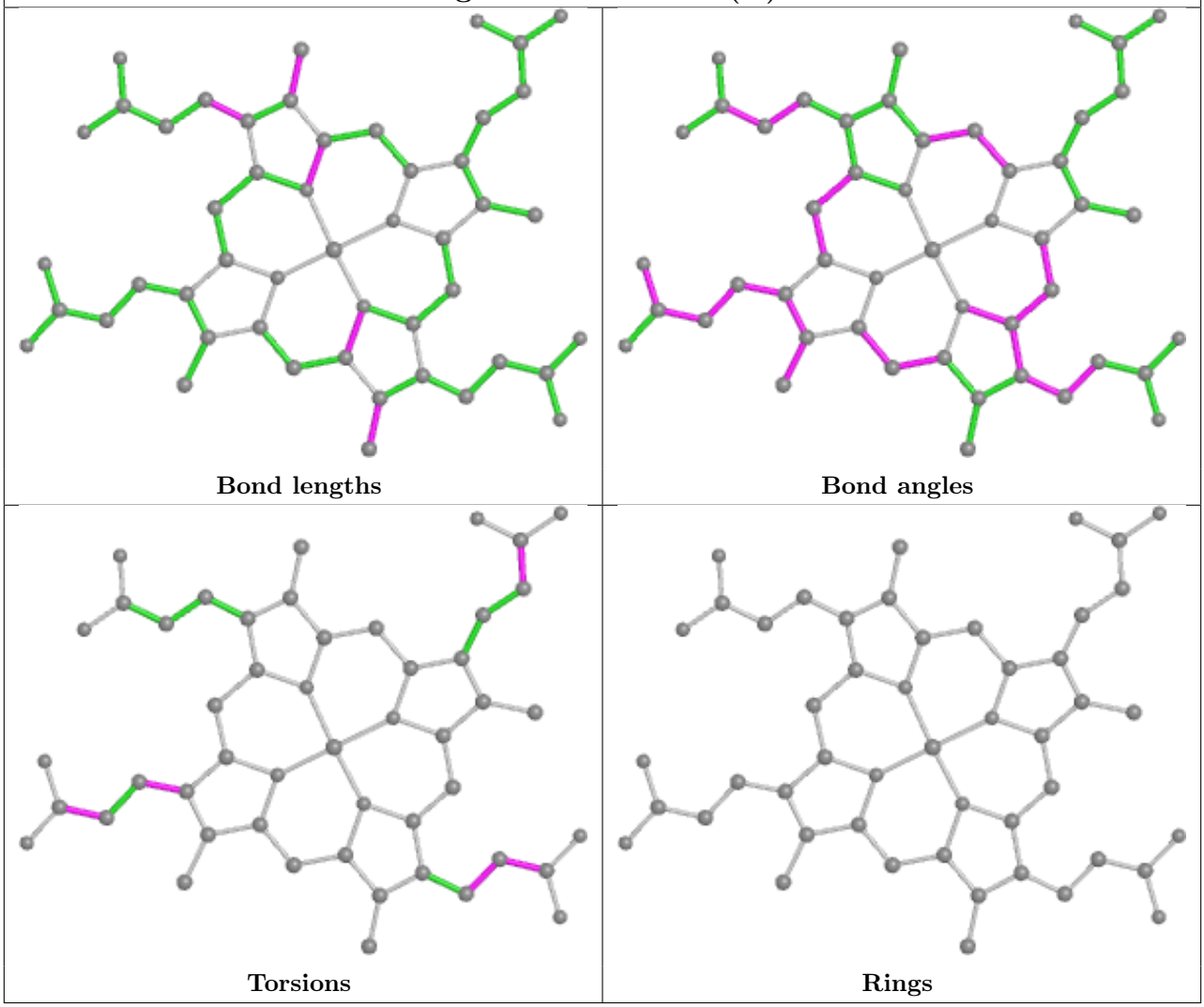


Torsions



Rings

Ligand FEC E 1407 (A)



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	169/179 (94%)	-0.21	5 (2%)	50	54	17, 26, 42, 66	0
1	B	169/179 (94%)	-0.20	4 (2%)	59	63	17, 25, 47, 66	0
1	C	169/179 (94%)	-0.31	8 (4%)	31	33	18, 26, 42, 64	0
1	D	169/179 (94%)	-0.22	4 (2%)	59	63	17, 26, 43, 66	0
1	E	169/179 (94%)	-0.28	6 (3%)	42	46	18, 26, 45, 64	0
1	F	169/179 (94%)	-0.32	6 (3%)	42	46	18, 26, 44, 66	0
1	G	169/179 (94%)	-0.25	6 (3%)	42	46	17, 26, 42, 66	0
1	H	170/179 (94%)	-0.28	7 (4%)	37	40	17, 26, 48, 68	0
1	I	170/179 (94%)	-0.29	4 (2%)	59	63	17, 26, 43, 66	0
1	J	169/179 (94%)	-0.31	5 (2%)	50	54	18, 26, 42, 66	0
1	K	169/179 (94%)	-0.29	3 (1%)	68	71	17, 26, 42, 64	0
1	L	170/179 (94%)	-0.22	8 (4%)	31	33	17, 26, 44, 66	0
1	M	170/179 (94%)	-0.29	5 (2%)	51	56	16, 25, 44, 66	0
1	N	169/179 (94%)	-0.27	3 (1%)	68	71	17, 25, 44, 64	0
1	O	169/179 (94%)	-0.23	4 (2%)	59	63	18, 26, 42, 64	0
1	P	170/179 (94%)	-0.38	3 (1%)	68	71	17, 26, 48, 66	0
All	All	2709/2864 (94%)	-0.27	81 (2%)	50	54	16, 26, 46, 68	0

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	168	SER	6.9
1	B	166	THR	6.7
1	I	166	THR	6.6
1	A	166	THR	6.3
1	N	168	SER	6.1

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Mol	Chain	Res	Type	RSRZ
1	G	166	THR	6.0
1	J	168	SER	5.8
1	G	168	SER	5.7
1	H	166	THR	5.7
1	F	168	SER	5.5
1	M	168	SER	5.4
1	C	168	SER	5.2
1	A	168	SER	5.1
1	P	168	SER	5.0
1	O	168	SER	4.8
1	K	166	THR	4.7
1	H	168	SER	4.6
1	F	166	THR	4.5
1	J	166	THR	4.5
1	E	166	THR	4.4
1	L	166	THR	4.3
1	K	168	SER	4.3
1	L	168	SER	4.2
1	C	166	THR	4.1
1	D	166	THR	4.1
1	O	166	THR	4.1
1	D	168	SER	4.1
1	E	167	ALA	4.0
1	I	169	LYS	3.8
1	C	165	GLY	3.8
1	C	7	ASP	3.7
1	B	168	SER	3.5
1	F	167	ALA	3.4
1	D	4	ASN	3.2
1	H	81	LYS	3.2
1	M	166	THR	3.2
1	I	168	SER	3.2
1	P	167	ALA	3.1
1	P	166	THR	3.0
1	H	169	LYS	3.0
1	M	3	GLY	2.9
1	G	165	GLY	2.9
1	H	165	GLY	2.9
1	K	27	ILE	2.8
1	H	7	ASP	2.7
1	G	167	ALA	2.7
1	G	150	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	N	169	LYS	2.6
1	J	4	ASN	2.6
1	M	169	LYS	2.5
1	N	166	THR	2.5
1	J	85	GLY	2.5
1	L	150	GLY	2.5
1	C	169	LYS	2.4
1	A	27	ILE	2.4
1	A	169	LYS	2.4
1	B	4	ASN	2.4
1	M	167	ALA	2.4
1	F	169	LYS	2.3
1	L	165	GLY	2.3
1	L	27	ILE	2.3
1	D	169	LYS	2.3
1	O	4	ASN	2.3
1	H	4	ASN	2.3
1	B	6	GLU	2.3
1	G	27	ILE	2.3
1	E	4	ASN	2.2
1	L	167	ALA	2.2
1	F	4	ASN	2.2
1	J	81	LYS	2.2
1	E	81	LYS	2.2
1	A	31	MET	2.2
1	C	167	ALA	2.1
1	C	27	ILE	2.1
1	O	167	ALA	2.1
1	F	6	GLU	2.1
1	E	27	ILE	2.1
1	L	151	ASP	2.1
1	I	172	VAL	2.0
1	C	4	ASN	2.0
1	L	169	LYS	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
3	SO4	J	1901	5/5	0.70	0.25	66,67,67,69	0
3	SO4	I	1704	5/5	0.76	0.35	36,37,38,38	0
3	SO4	H	1702	5/5	0.76	0.47	72,72,73,73	0
3	SO4	L	2104	5/5	0.77	0.34	78,78,78,79	5
3	SO4	M	2202	5/5	0.78	0.42	73,73,73,74	0
3	SO4	G	1601	5/5	0.82	0.23	74,74,74,75	0
3	SO4	D	1301	5/5	0.84	0.24	58,59,60,60	0
3	SO4	D	1303	5/5	0.85	0.43	39,44,45,50	0
3	SO4	O	2406	5/5	0.85	0.18	41,44,46,47	5
3	SO4	K	2001	5/5	0.86	0.22	51,53,53,54	0
3	SO4	L	2101	5/5	0.87	0.15	64,64,65,65	0
3	SO4	C	1201	5/5	0.88	0.16	65,65,67,67	0
3	SO4	E	1304	5/5	0.88	0.22	65,65,67,67	0
3	SO4	E	1406	5/5	0.88	0.26	62,67,67,70	0
3	SO4	B	1104	5/5	0.89	0.13	73,73,74,75	0
3	SO4	H	1701	5/5	0.89	0.19	54,54,55,56	0
3	SO4	M	2206	5/5	0.89	0.32	58,60,67,70	0
3	SO4	I	1801	5/5	0.89	0.29	61,61,62,63	0
3	SO4	P	2501	5/5	0.89	0.15	62,62,63,63	0
3	SO4	M	2203	5/5	0.90	0.41	62,63,63,63	0
3	SO4	F	1502	5/5	0.90	0.35	69,69,69,71	0
3	SO4	B	1101	5/5	0.90	0.14	66,66,67,67	0
3	SO4	K	2006	5/5	0.90	0.23	52,55,60,61	0
3	SO4	A	1006	5/5	0.91	0.40	56,67,69,74	0
3	SO4	E	1403	5/5	0.91	0.35	44,47,49,52	0
3	SO4	A	1001	5/5	0.91	0.16	53,54,54,55	0
3	SO4	N	2301	5/5	0.91	0.19	62,63,63,63	0
3	SO4	N	2306	5/5	0.91	0.31	60,65,69,71	0
3	SO4	F	1501	5/5	0.91	0.26	66,66,67,67	0
3	SO4	P	1504	5/5	0.91	0.13	78,78,78,79	0
3	SO4	A	1003	5/5	0.91	0.27	73,73,73,74	0
3	SO4	H	1706	5/5	0.92	0.23	47,55,58,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	SO4	C	1204	5/5	0.92	0.19	58,59,60,60	5
3	SO4	G	1603	5/5	0.92	0.16	73,73,74,75	0
3	SO4	L	2106	5/5	0.92	0.33	60,65,69,72	0
3	SO4	C	1206	5/5	0.92	0.14	46,46,47,49	5
3	SO4	B	1103	5/5	0.92	0.19	70,71,72,74	0
3	SO4	J	1904	5/5	0.93	0.19	61,61,62,63	5
3	SO4	P	2503	5/5	0.93	0.24	42,43,47,49	5
3	SO4	P	2506	5/5	0.93	0.31	57,63,66,67	0
3	SO4	K	2003	5/5	0.94	0.22	69,69,69,71	0
3	SO4	B	1106	5/5	0.94	0.34	64,66,74,75	0
3	SO4	I	1802	5/5	0.94	0.17	36,37,38,38	0
3	SO4	L	2102	5/5	0.94	0.15	78,78,78,79	5
3	SO4	I	1804	5/5	0.94	0.26	62,65,67,69	0
3	SO4	N	2303	5/5	0.94	0.24	64,68,70,72	0
3	SO4	J	1906	5/5	0.95	0.28	50,51,59,59	0
3	SO4	D	1306	5/5	0.95	0.45	45,45,48,48	0
3	SO4	O	2403	5/5	0.95	0.26	63,66,67,68	0
3	SO4	M	2201	5/5	0.95	0.19	51,51,52,53	0
3	SO4	I	1803	5/5	0.95	0.24	67,67,70,70	0
3	SO4	B	1005	5/5	0.95	0.27	51,53,55,61	0
3	SO4	G	1606	5/5	0.95	0.33	58,65,67,73	0
3	SO4	F	1506	5/5	0.95	0.23	65,67,68,69	0
3	SO4	H	1703	5/5	0.96	0.17	40,43,48,48	5
2	FE2	A	201	1/1	0.96	0.04	34,34,34,34	0
3	SO4	C	1203	5/5	0.96	0.19	56,58,62,64	0
4	FEC	C	1207[A]	49/49	0.96	0.20	15,20,30,37	49
4	FEC	C	1207[B]	49/49	0.96	0.20	12,20,32,35	49
4	FEC	E	1407[A]	49/49	0.96	0.18	16,20,31,36	49
4	FEC	E	1407[B]	49/49	0.96	0.18	15,20,29,36	49
4	FEC	I	1805[A]	49/49	0.96	0.17	15,20,31,36	49
4	FEC	I	1805[B]	49/49	0.96	0.17	13,21,30,33	49
4	FEC	L	2107[A]	49/49	0.96	0.22	15,20,31,36	49
4	FEC	L	2107[B]	49/49	0.96	0.22	13,20,28,30	49
4	FEC	M	2207[A]	49/49	0.96	0.19	15,20,31,37	49
4	FEC	M	2207[B]	49/49	0.96	0.19	12,20,29,32	49
2	FE2	E	200	1/1	0.97	0.05	34,34,34,34	0
2	FE2	F	201	1/1	0.97	0.04	35,35,35,35	0
4	FEC	A	1007[A]	49/49	0.97	0.22	15,20,31,36	49
4	FEC	A	1007[B]	49/49	0.97	0.22	9,19,28,34	49
4	FEC	G	1607[A]	49/49	0.97	0.20	15,20,31,36	49
4	FEC	G	1607[B]	49/49	0.97	0.20	9,20,32,38	49
4	FEC	P	2507[A]	49/49	0.97	0.19	15,20,31,35	49

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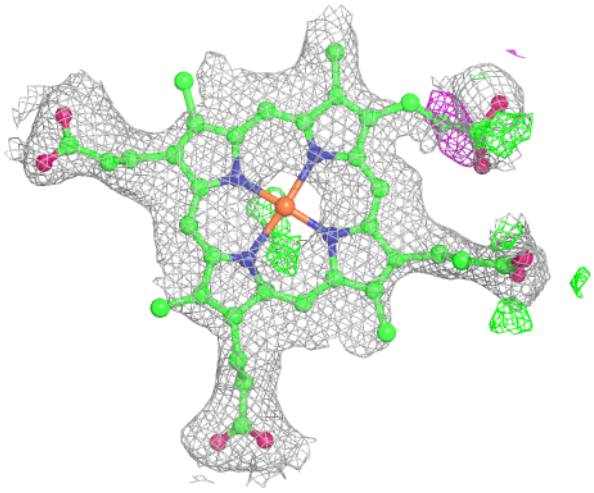
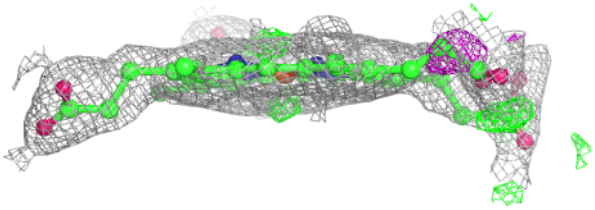
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	FEC	P	2507[B]	49/49	0.97	0.19	14,20,29,36	49
2	FE2	C	201	1/1	0.98	0.04	36,36,36,36	0
2	FE2	G	200	1/1	0.98	0.07	32,32,32,32	0
2	FE2	J	201	1/1	0.98	0.04	36,36,36,36	0
2	FE2	L	201	1/1	0.98	0.05	32,32,32,32	0
2	FE2	M	201	1/1	0.98	0.04	33,33,33,33	0
2	FE2	N	200	1/1	0.98	0.07	29,29,29,29	0
2	FE2	D	200	1/1	0.99	0.06	32,32,32,32	0
2	FE2	K	200	1/1	0.99	0.05	30,30,30,30	0
2	FE2	K	201	1/1	0.99	0.03	36,36,36,36	0
2	FE2	D	201	1/1	0.99	0.04	34,34,34,34	0
2	FE2	M	200	1/1	0.99	0.06	29,29,29,29	0
2	FE2	B	200	1/1	0.99	0.07	29,29,29,29	0
2	FE2	E	201	1/1	0.99	0.02	35,35,35,35	0
2	FE2	N	201	1/1	0.99	0.05	34,34,34,34	0
2	FE2	O	200	1/1	0.99	0.07	34,34,34,34	0
2	FE2	O	201	1/1	0.99	0.02	37,37,37,37	0
2	FE2	P	200	1/1	0.99	0.05	32,32,32,32	0
2	FE2	P	201	1/1	0.99	0.03	34,34,34,34	0
2	FE2	F	200	1/1	0.99	0.05	33,33,33,33	0
2	FE2	B	201	1/1	0.99	0.05	31,31,31,31	0
2	FE2	A	200	1/1	0.99	0.06	31,31,31,31	0
2	FE2	G	201	1/1	0.99	0.03	33,33,33,33	0
2	FE2	H	200	1/1	0.99	0.04	31,31,31,31	0
2	FE2	H	201	1/1	0.99	0.03	34,34,34,34	0
2	FE2	I	200	1/1	0.99	0.05	30,30,30,30	0
2	FE2	I	201	1/1	0.99	0.03	33,33,33,33	0
2	FE2	J	200	1/1	0.99	0.05	33,33,33,33	0
2	FE2	L	200	1/1	1.00	0.06	30,30,30,30	0
2	FE2	C	200	1/1	1.00	0.03	31,31,31,31	0

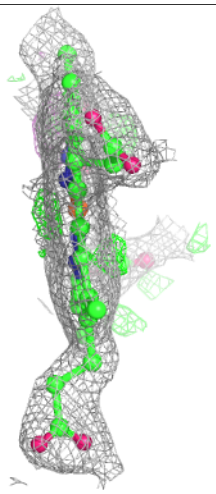
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around FEC C 1207 (A):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

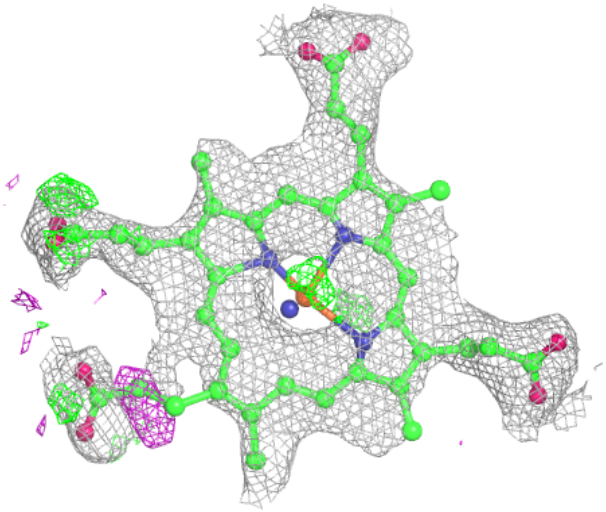


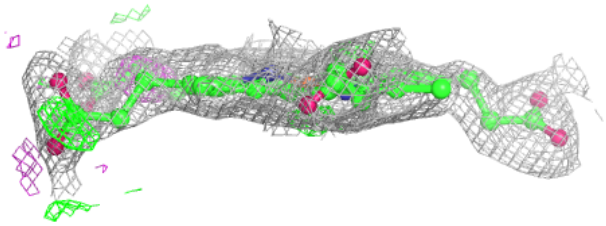


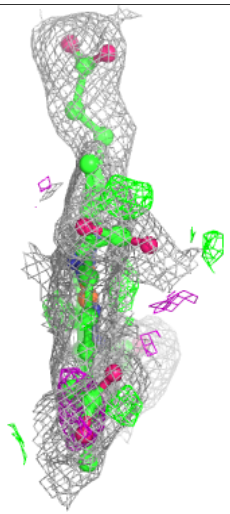


Electron density around FEC C 1207 (B):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

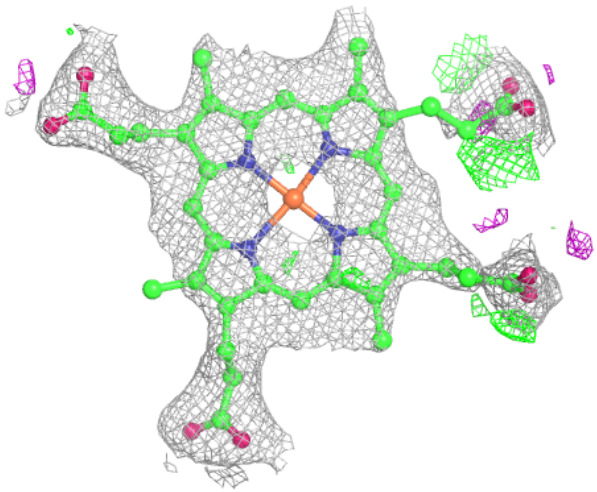


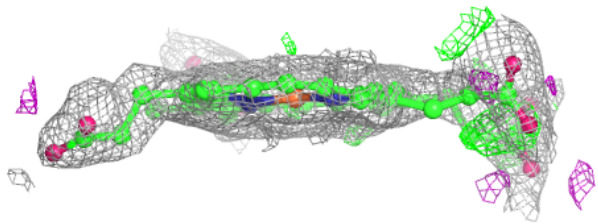


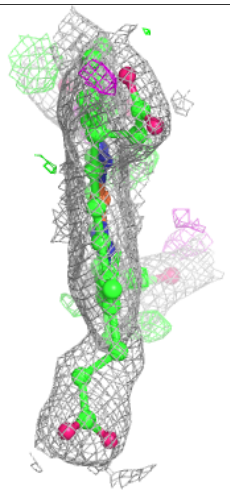


Electron density around FEC E 1407 (A):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

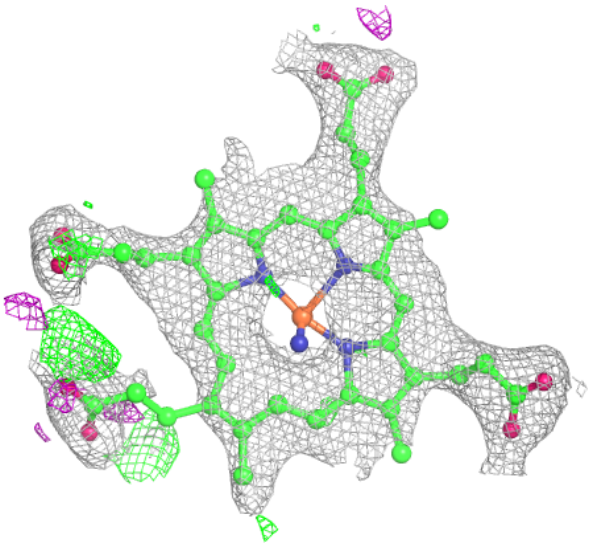


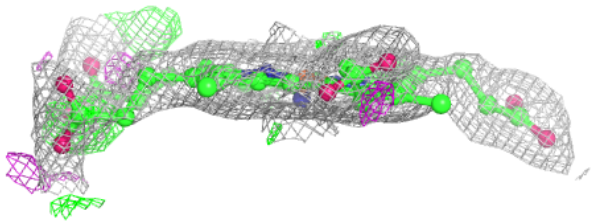


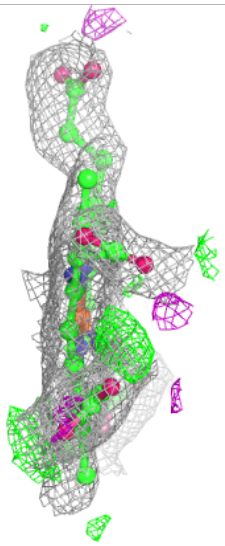


Electron density around FEC E 1407 (B):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

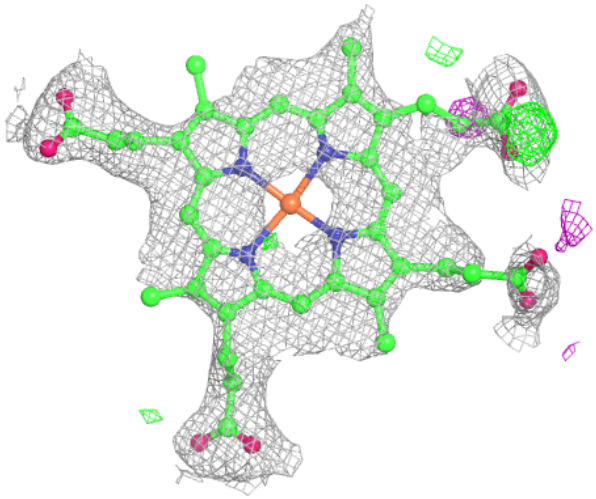


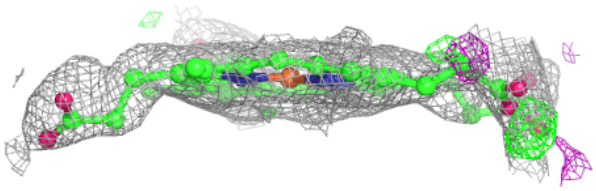


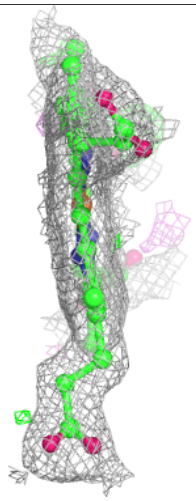


Electron density around FEC I 1805 (A):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

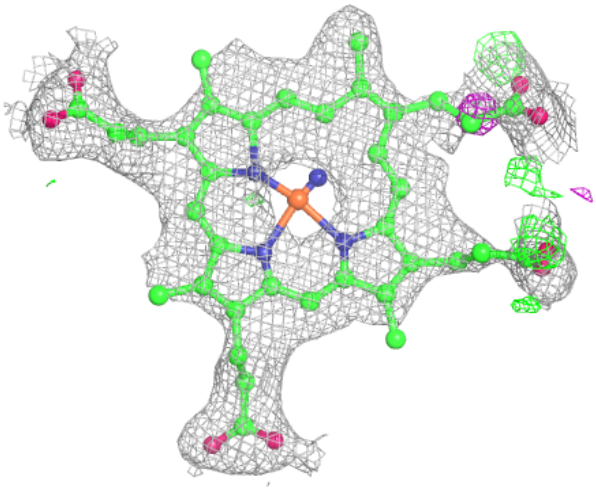


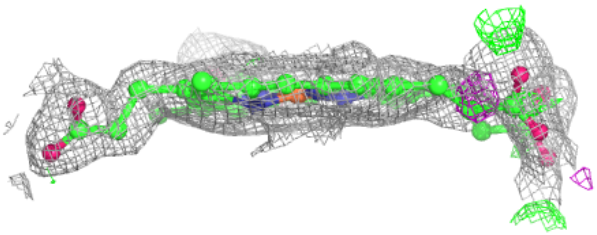


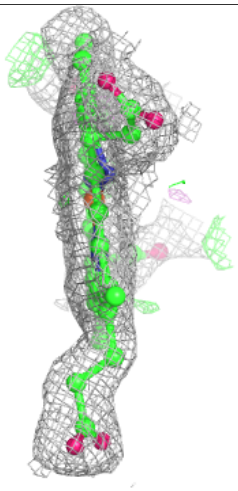


Electron density around FEC I 1805 (B):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

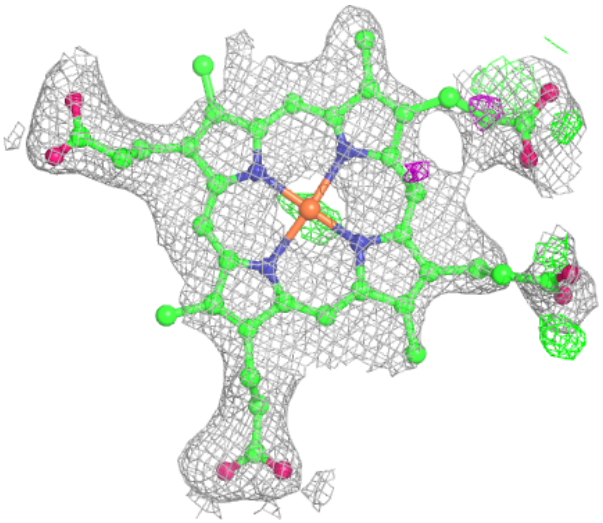


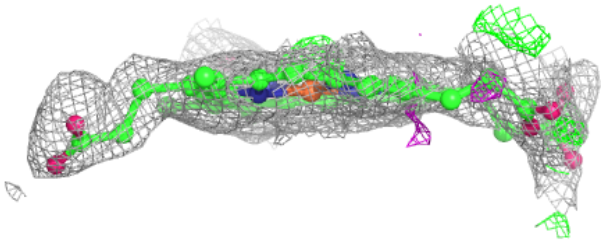




Electron density around FEC L 2107 (A):

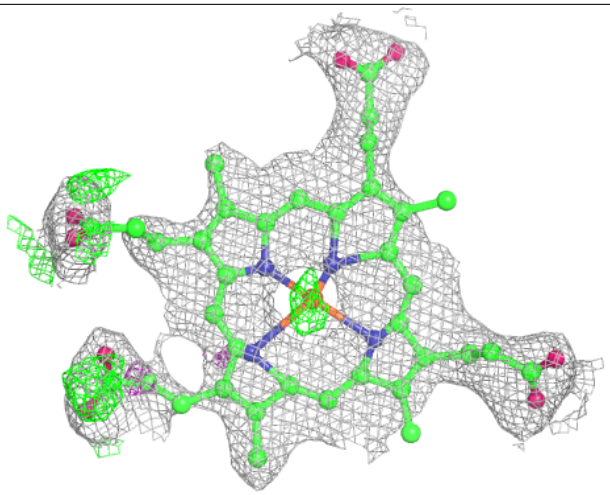
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

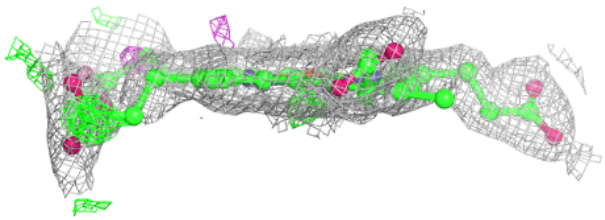


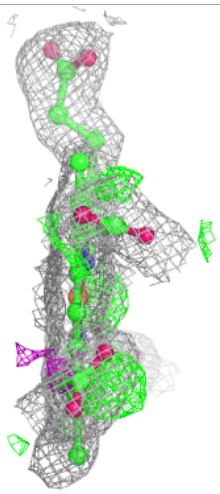


Electron density around FEC L 2107 (B):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

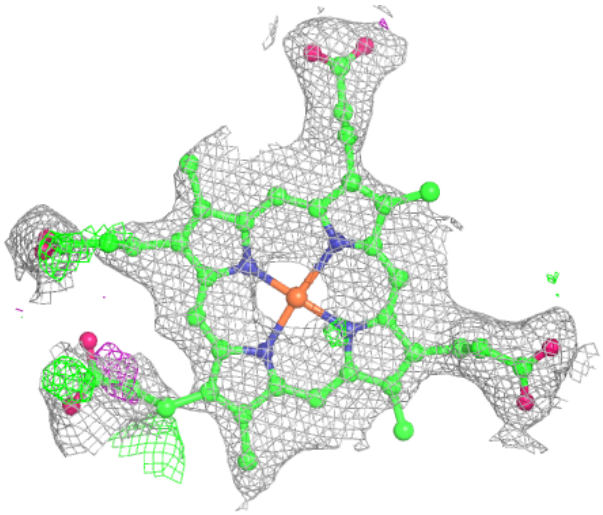


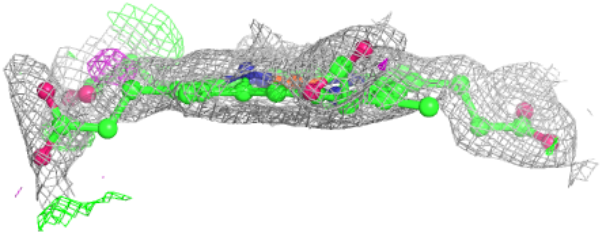


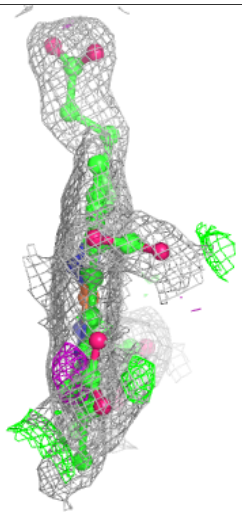


Electron density around FEC M 2207 (A):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

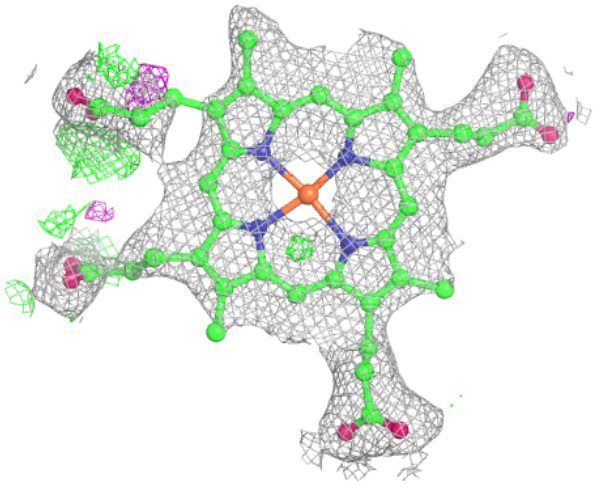


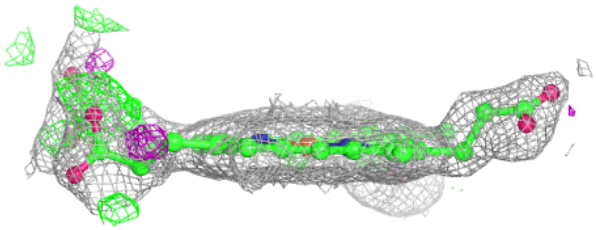


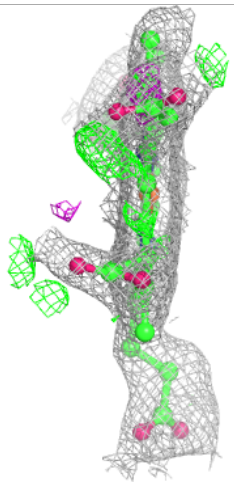


Electron density around FEC M 2207 (B):

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

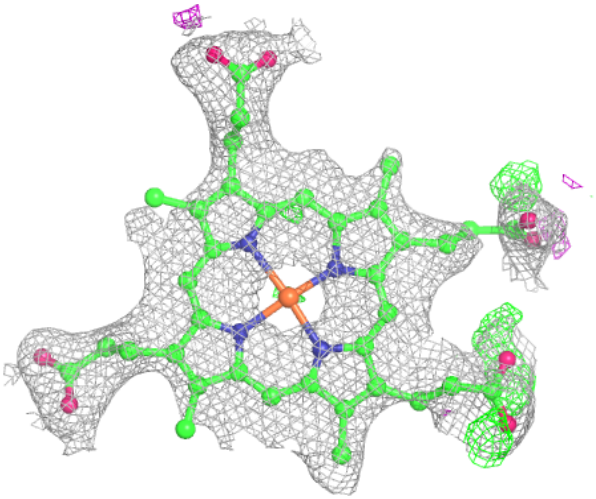


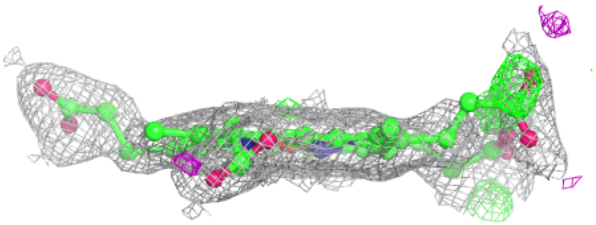


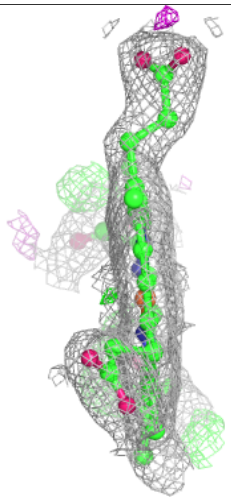


Electron density around FEC A 1007 (A):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

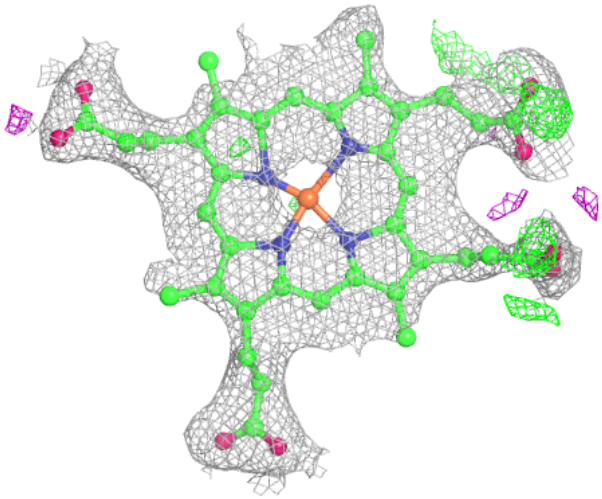


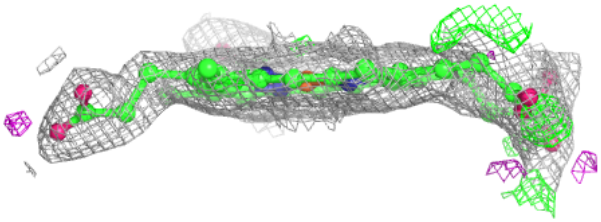


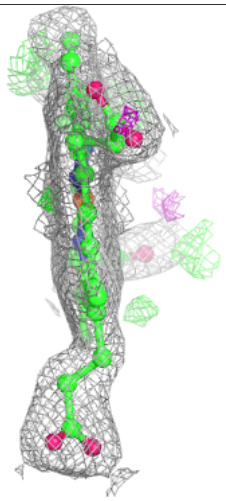


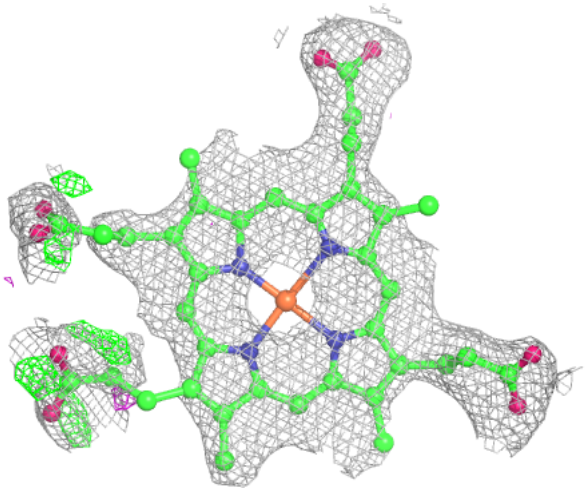
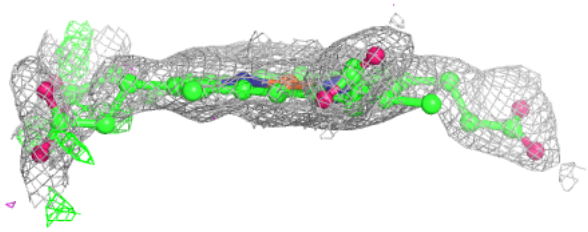
Electron density around FEC A 1007 (B):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



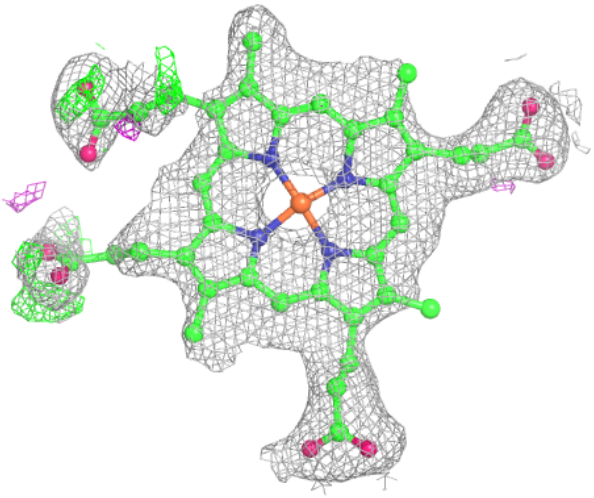


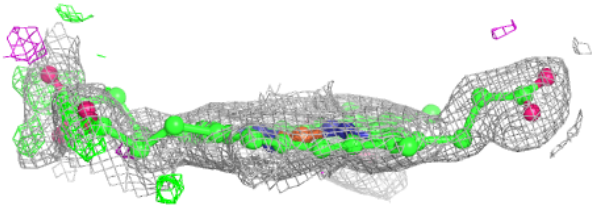


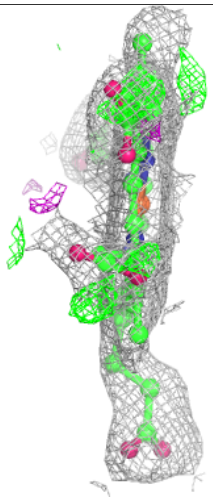
Electron density around FEC G 1607 (A): 2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)	
	

Electron density around FEC G 1607 (B):

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

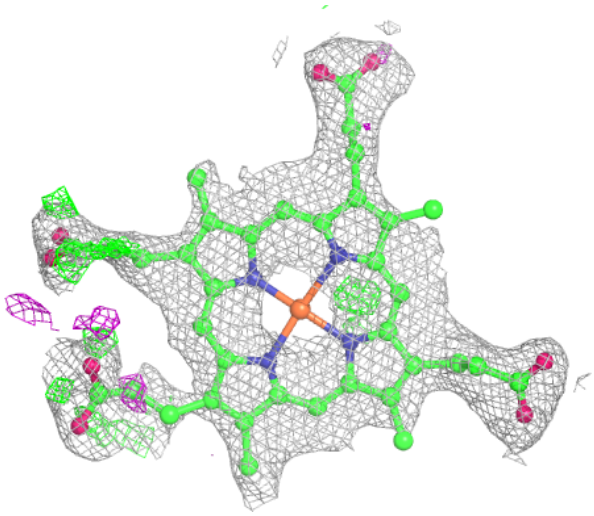


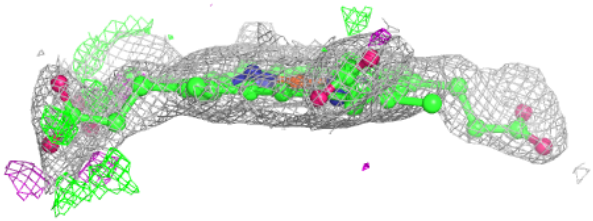


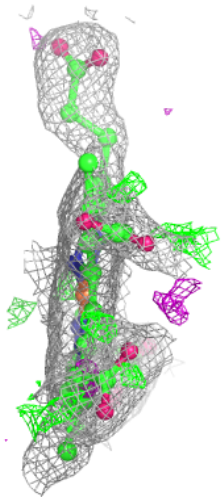


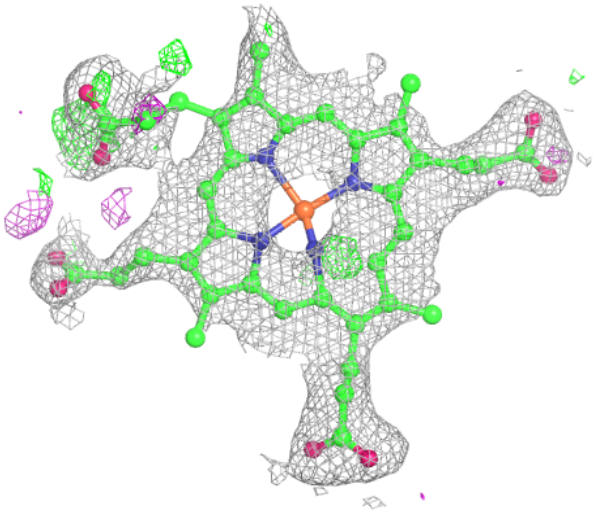
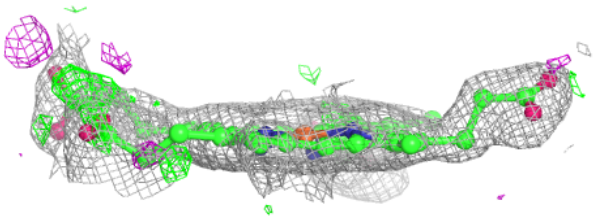
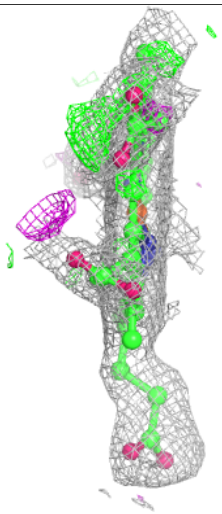
Electron density around FEC P 2507 (A):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







Electron density around FEC P 2507 (B): 2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)	
	

6.5 Other polymers (i)

There are no such residues in this entry.