Full wwPDB X-ray Structure Validation Report (i)

Oct 17, 2021 – 05:56 AM EDT

PDB ID	:	1MG2
Title	:	MUTATION OF ALPHA PHE55 OF METHYLAMINE DEHYDROGENASE ALTERS THE REORGANIZATION ENERGY AND ELECTRONIC COUPLING FOR ITS ELECTRON TRANSFER REACTION WITH AMICYANIN
Authors	:	Sun, D.; Chen, Z.W.; Mathews, F.S.; Davidson, V.L.
Deposited on	:	2002-08-14
Resolution	:	2.25 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 following versions of software and data (see references (i)) were used in the production of this report:

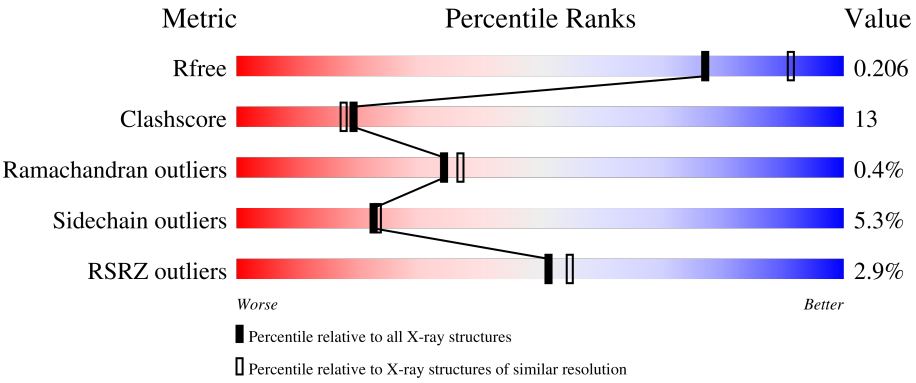
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 2.25 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	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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	390	2% 73% 23%
1	E	390	2% 73% 23%
1	I	390	2% 75% 21%
1	M	390	2% 74% 22%
2	B	131	% 70% 22% 5%

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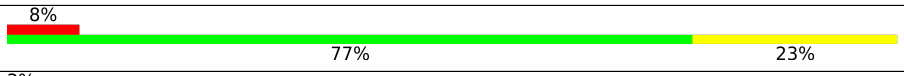
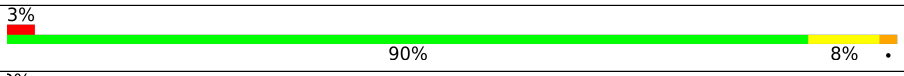
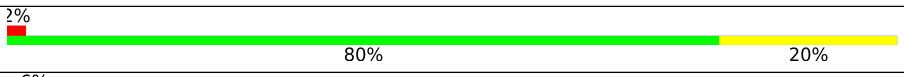
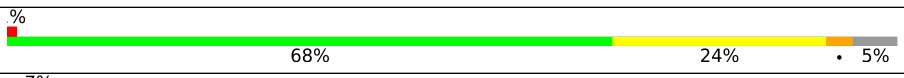
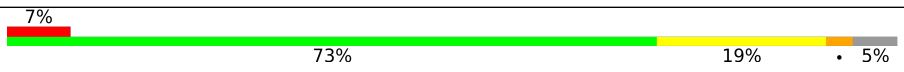
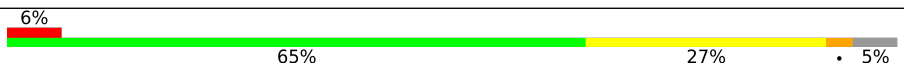
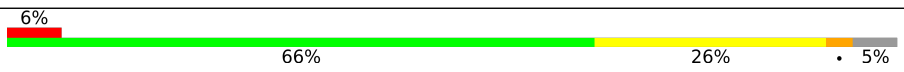
Mol	Chain	Length	Quality of chain
2	F	131	
2	J	131	
2	N	131	
3	C	105	
3	G	105	
3	K	105	
3	O	105	
4	D	155	
4	H	155	
4	L	155	
4	P	155	

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 25377 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 Methylamine dehydrogenase, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	382	Total	C	N	O	S	0	0	0
			2961	1872	509	572	8			
1	E	382	Total	C	N	O	S	0	0	0
			2961	1872	509	572	8			
1	I	382	Total	C	N	O	S	0	0	0
			2961	1872	509	572	8			
1	M	382	Total	C	N	O	S	0	0	0
			2961	1872	509	572	8			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	55	ALA	PHE	engineered mutation	UNP P29894
A	312	PHE	LEU	SEE REMARK 999	UNP P29894
A	313	VAL	LEU	SEE REMARK 999	UNP P29894
E	55	ALA	PHE	engineered mutation	UNP P29894
E	312	PHE	LEU	SEE REMARK 999	UNP P29894
E	313	VAL	LEU	SEE REMARK 999	UNP P29894
I	55	ALA	PHE	engineered mutation	UNP P29894
I	312	PHE	LEU	SEE REMARK 999	UNP P29894
I	313	VAL	LEU	SEE REMARK 999	UNP P29894
M	55	ALA	PHE	engineered mutation	UNP P29894
M	312	PHE	LEU	SEE REMARK 999	UNP P29894
M	313	VAL	LEU	SEE REMARK 999	UNP P29894

- Molecule 2 is a protein called Methylamine dehydrogenase, light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	125	Total	C	N	O	S	0	0	0
			956	590	161	192	13			
2	F	125	Total	C	N	O	S	0	0	0
			956	590	161	192	13			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	J	125	Total	C	N	O	S	0	0	0
			956	590	161	192	13			
2	N	125	Total	C	N	O	S	0	0	0
			956	590	161	192	13			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	57	TRQ	TRP	modified residue	UNP P22619
F	57	TRQ	TRP	modified residue	UNP P22619
J	57	TRQ	TRP	modified residue	UNP P22619
N	57	TRQ	TRP	modified residue	UNP P22619

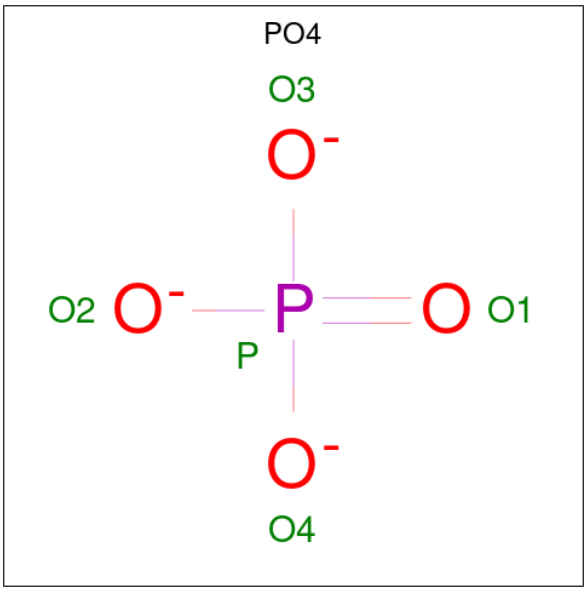
- Molecule 3 is a protein called Amicyanin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	105	Total	C	N	O	S	0	0	0
			807	516	133	152	6			
3	G	105	Total	C	N	O	S	0	0	0
			807	516	133	152	6			
3	K	105	Total	C	N	O	S	0	0	0
			807	516	133	152	6			
3	O	105	Total	C	N	O	S	0	0	0
			807	516	133	152	6			

- Molecule 4 is a protein called CYTOCHROME C-L.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	147	Total	C	N	O	S	0	0	0
			1144	724	182	230	8			
4	H	147	Total	C	N	O	S	0	0	0
			1144	724	182	230	8			
4	L	147	Total	C	N	O	S	0	0	0
			1144	724	182	230	8			
4	P	147	Total	C	N	O	S	0	0	0
			1144	724	182	230	8			

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total O P 5 4 1	0	0
5	B	1	Total O P 5 4 1	0	0
5	E	1	Total O P 5 4 1	0	0
5	F	1	Total O P 5 4 1	0	0
5	I	1	Total O P 5 4 1	0	0
5	J	1	Total O P 5 4 1	0	0
5	M	1	Total O P 5 4 1	0	0
5	N	1	Total O P 5 4 1	0	0

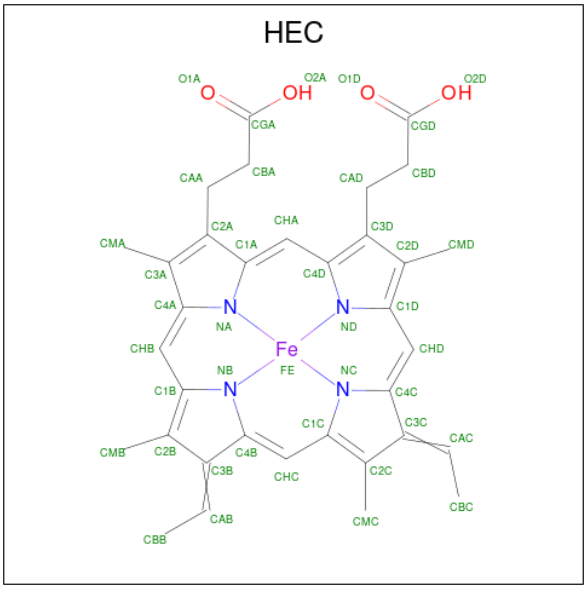
- Molecule 6 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	C	1	Total Cu 1 1	0	0
6	G	1	Total Cu 1 1	0	0
6	K	1	Total Cu 1 1	0	0
6	O	1	Total Cu 1 1	0	0

- Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	D	1	Total Na 1 1	0	0
7	H	1	Total Na 1 1	0	0
7	L	1	Total Na 1 1	0	0
7	P	1	Total Na 1 1	0	0

- Molecule 8 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	D	1	Total C Fe N O 43 34 1 4 4	0	0
8	H	1	Total C Fe N O 43 34 1 4 4	0	0
8	L	1	Total C Fe N O 43 34 1 4 4	0	0
8	P	1	Total C Fe N O 43 34 1 4 4	0	0

- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	218	Total O 218 218	0	0

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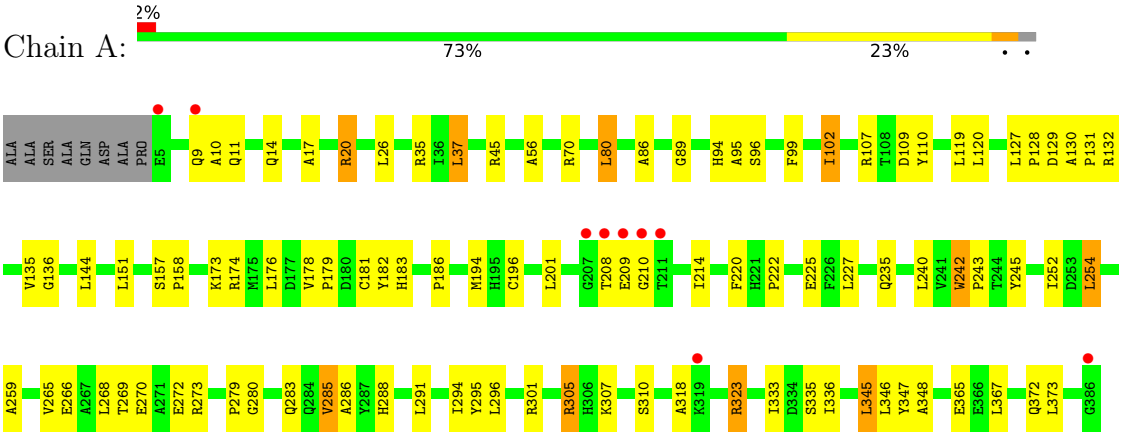
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	B	74	Total O 74 74	0	0
9	C	46	Total O 46 46	0	0
9	D	78	Total O 78 78	0	0
9	E	223	Total O 223 223	0	0
9	F	97	Total O 97 97	0	0
9	G	57	Total O 57 57	0	0
9	H	55	Total O 55 55	0	0
9	I	224	Total O 224 224	0	0
9	J	93	Total O 93 93	0	0
9	K	56	Total O 56 56	0	0
9	L	52	Total O 52 52	0	0
9	M	245	Total O 245 245	0	0
9	N	78	Total O 78 78	0	0
9	O	34	Total O 34 34	0	0
9	P	55	Total O 55 55	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.

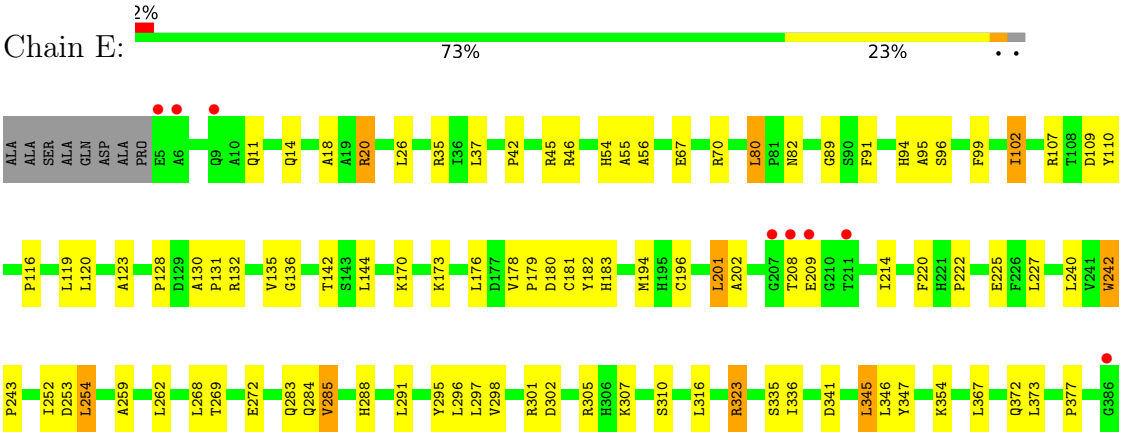
• Molecule 1: Methylamine dehydrogenase, heavy chain

Chain A:



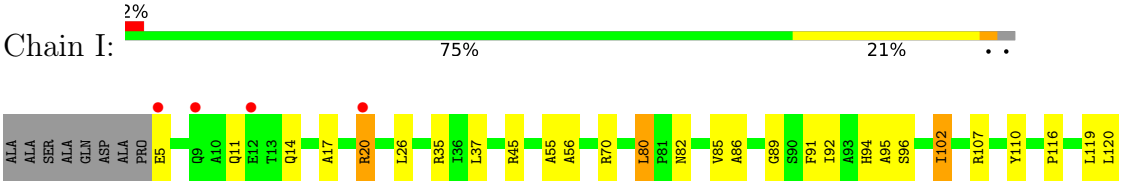
• Molecule 1: Methylamine dehydrogenase, heavy chain

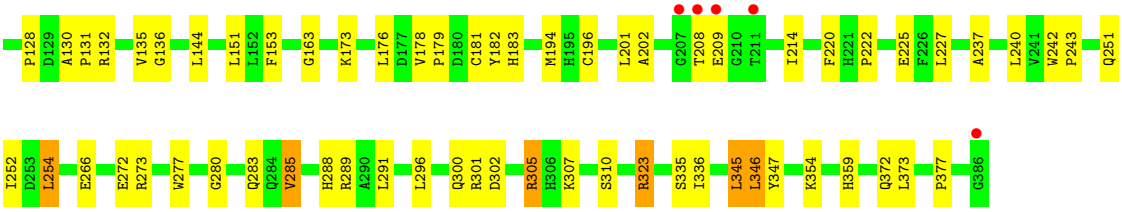
Chain E:



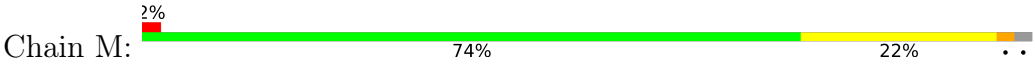
• Molecule 1: Methylamine dehydrogenase, heavy chain

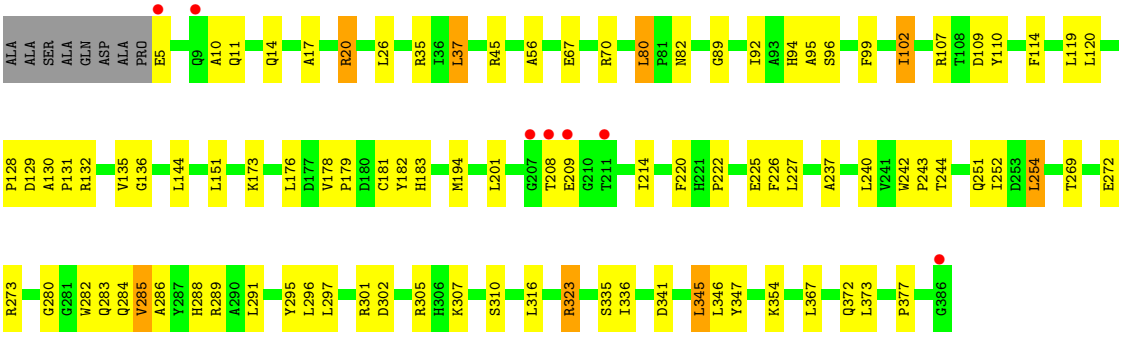
Chain I:





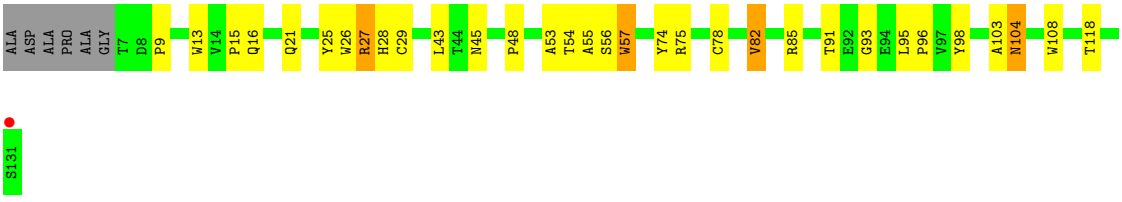
• Molecule 1: Methylamine dehydrogenase, heavy chain



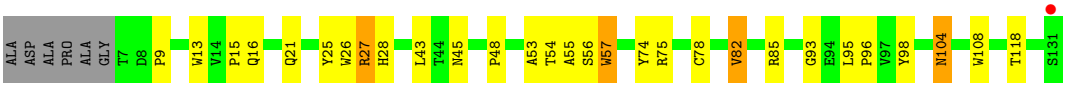


• Molecule 2: Methylamine dehydrogenase, light chain

• Molecule 2: Methylamine dehydrogenase, light chain

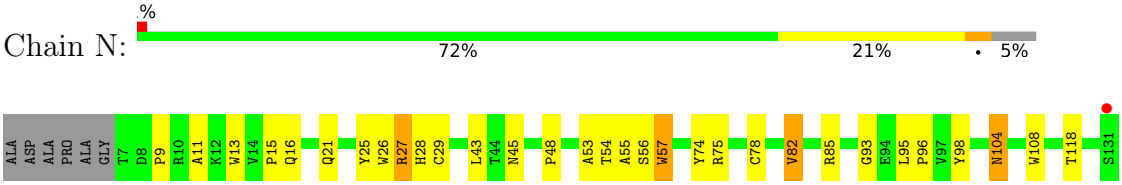


• Molecule 2: Methylamine dehydrogenase, light chain



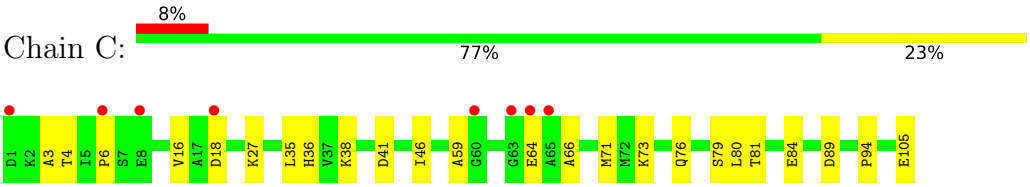
• Molecule 2: Methylamine dehydrogenase, light chain

Chain N:



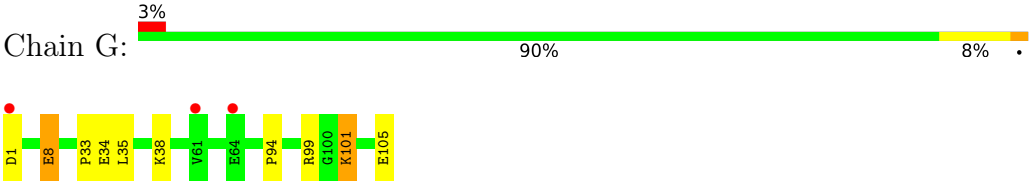
• Molecule 3: Amicyanin

Chain C:



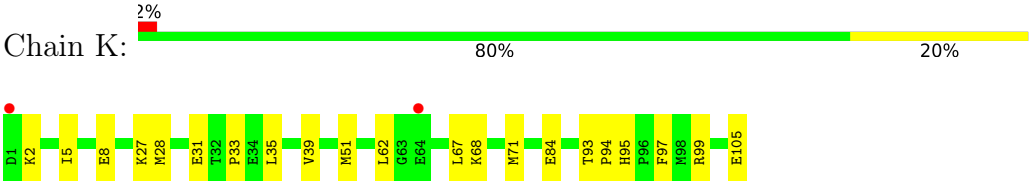
• Molecule 3: Amicyanin

Chain G:



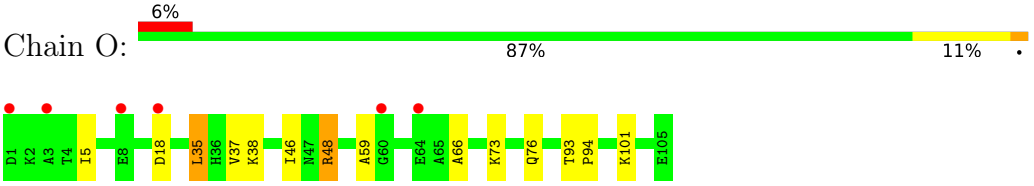
• Molecule 3: Amicyanin

Chain K:



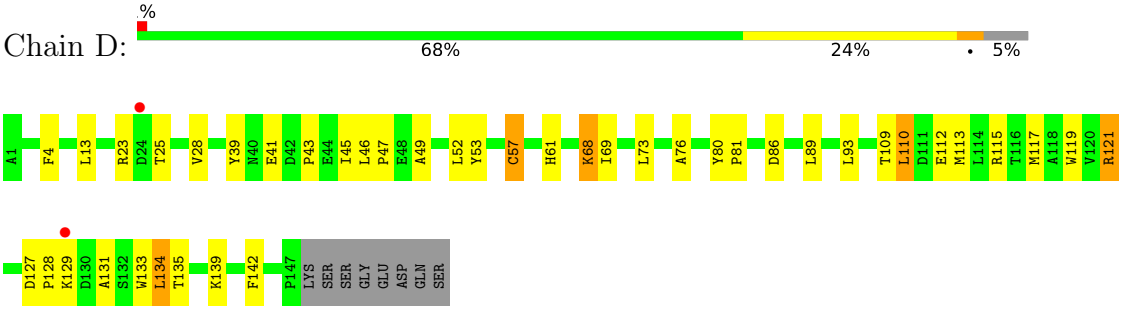
• Molecule 3: Amicyanin

Chain O:



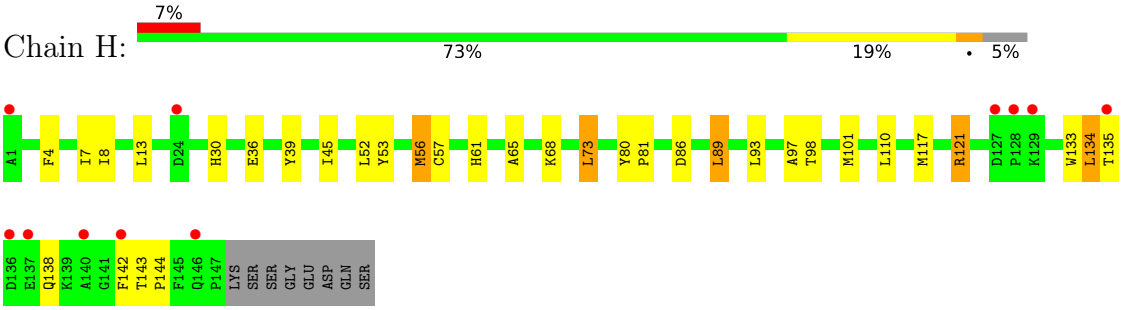
• Molecule 4: CYTOCHROME C-L

Chain D:



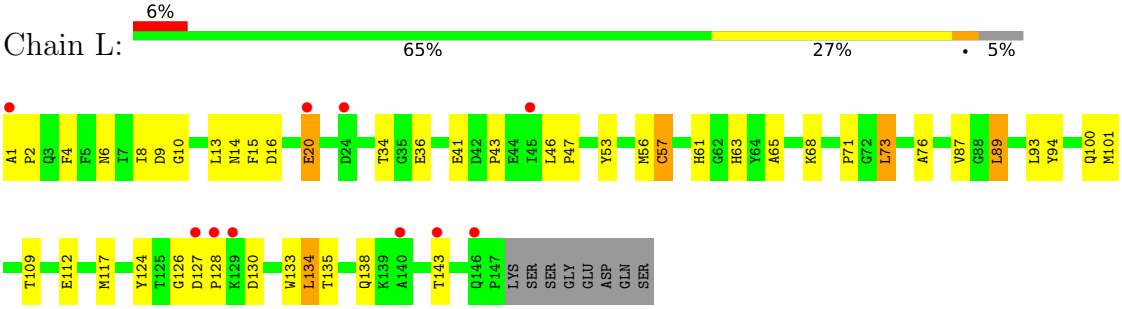
• Molecule 4: CYTOCHROME C-L

Chain H:



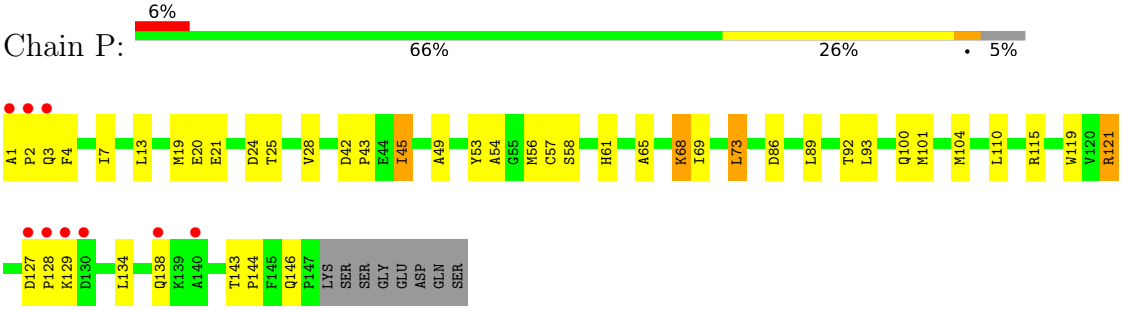
• Molecule 4: CYTOCHROME C-L

Chain L:



• Molecule 4: CYTOCHROME C-L

Chain P:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	79.12Å 188.20Å 127.10Å 90.00° 99.24° 90.00°	Depositor
Resolution (Å)	50.00 – 2.25 48.91 – 2.20	Depositor EDS
% Data completeness (in resolution range)	86.9 (50.00-2.25) 83.5 (48.91-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.67 (at 2.20Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.173 , 0.210 0.169 , 0.206	Depositor DCC
R_{free} test set	15487 reflections (9.99%)	wwPDB-VP
Wilson B-factor (Å^2)	17.8	Xtriage
Anisotropy	0.542	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 48.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	25377	wwPDB-VP
Average B, all atoms (Å^2)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.66% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, NA, HEC, TRQ, CU

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	0.32	0/3037	0.64	0/4139
1	E	0.32	0/3037	0.64	0/4139
1	I	0.34	0/3037	0.65	0/4139
1	M	0.33	0/3037	0.65	0/4139
2	B	0.34	0/964	0.61	0/1315
2	F	0.34	0/964	0.61	0/1315
2	J	0.34	0/964	0.61	0/1315
2	N	0.35	0/964	0.61	0/1315
3	C	0.33	0/828	0.56	0/1124
3	G	0.33	0/828	0.59	0/1124
3	K	0.34	0/828	0.61	0/1124
3	O	0.32	0/828	0.59	0/1124
4	D	0.37	0/1179	0.65	1/1605 (0.1%)
4	H	0.36	0/1179	0.67	1/1605 (0.1%)
4	L	0.35	1/1179 (0.1%)	0.63	1/1605 (0.1%)
4	P	0.35	1/1179 (0.1%)	0.63	1/1605 (0.1%)
All	All	0.34	2/24032 (0.0%)	0.63	4/32732 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	P	61	HIS	CE1-NE2	5.49	1.45	1.32
4	L	61	HIS	CE1-NE2	5.26	1.44	1.32

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	L	61	HIS	ND1-CG-CD2	8.07	120.10	108.80
4	P	61	HIS	ND1-CG-CD2	8.07	120.09	108.80
4	D	61	HIS	ND1-CG-CD2	8.03	120.03	108.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	H	61	HIS	ND1-CG-CD2	7.95	119.93	108.80

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	2961	0	2843	90	0
1	E	2961	0	2843	82	0
1	I	2961	0	2843	78	0
1	M	2961	0	2843	89	0
2	B	956	0	869	35	0
2	F	956	0	869	33	0
2	J	956	0	869	32	0
2	N	956	0	869	34	0
3	C	807	0	794	15	0
3	G	807	0	794	7	0
3	K	807	0	794	16	0
3	O	807	0	794	11	0
4	D	1144	0	1038	26	0
4	H	1144	0	1038	23	0
4	L	1144	0	1038	31	0
4	P	1144	0	1038	29	0
5	A	5	0	0	1	0
5	B	5	0	0	0	0
5	E	5	0	0	0	0
5	F	5	0	0	0	0
5	I	5	0	0	1	0
5	J	5	0	0	1	0
5	M	5	0	0	0	0
5	N	5	0	0	0	0
6	C	1	0	0	0	0
6	G	1	0	0	0	0
6	K	1	0	0	0	0
6	O	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	D	1	0	0	0	0
7	H	1	0	0	0	0
7	L	1	0	0	0	0
7	P	1	0	0	0	0
8	D	43	0	30	1	0
8	H	43	0	30	4	0
8	L	43	0	30	2	0
8	P	43	0	30	4	0
9	A	218	0	0	8	0
9	B	74	0	0	2	0
9	C	46	0	0	0	0
9	D	78	0	0	0	0
9	E	223	0	0	5	0
9	F	97	0	0	2	0
9	G	57	0	0	1	0
9	H	55	0	0	2	0
9	I	224	0	0	6	0
9	J	93	0	0	2	0
9	K	56	0	0	2	0
9	L	52	0	0	2	0
9	M	245	0	0	4	0
9	N	78	0	0	2	0
9	O	34	0	0	0	0
9	P	55	0	0	0	0
All	All	25377	0	22296	564	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

All (564) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:20:ARG:HB2	1:I:20:ARG:HH21	1.20	1.05
4:H:7:ILE:HG13	4:H:8:ILE:HD12	1.38	1.03
1:A:20:ARG:HB2	1:A:20:ARG:HH21	1.20	1.00
2:J:21:GLN:HE22	1:M:11:GLN:HG3	1.22	1.00
2:N:25:TYR:CE2	2:N:27:ARG:HG3	2.00	0.96
2:B:25:TYR:CE2	2:B:27:ARG:HG3	2.00	0.95
2:J:57:TRQ:HB2	2:J:108:TRP:NE1	1.82	0.95
2:J:25:TYR:CE2	2:J:27:ARG:HG3	2.00	0.95
2:N:57:TRQ:HB2	2:N:108:TRP:NE1	1.81	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:25:TYR:CE2	2:F:27:ARG:HG3	2.00	0.94
2:B:57:TRQ:HB2	2:B:108:TRP:NE1	1.84	0.92
2:F:57:TRQ:HB2	2:F:108:TRP:NE1	1.83	0.92
1:A:288:HIS:HD2	1:A:291:LEU:H	1.14	0.92
2:J:21:GLN:NE2	1:M:11:GLN:HG3	1.85	0.91
1:I:288:HIS:HD2	1:I:291:LEU:H	1.20	0.88
1:E:222:PRO:HG2	1:E:225:GLU:HB2	1.58	0.86
1:M:173:LYS:HE2	1:M:173:LYS:HA	1.59	0.84
1:M:288:HIS:HD2	1:M:291:LEU:H	1.21	0.84
1:I:45:ARG:HD2	1:I:345:LEU:HD22	1.59	0.83
1:A:173:LYS:HE2	1:A:173:LYS:HA	1.59	0.82
1:E:288:HIS:HD2	1:E:291:LEU:H	1.26	0.81
4:D:133:TRP:CD1	4:D:134:LEU:HD13	2.14	0.81
1:M:20:ARG:HH21	1:M:20:ARG:HB2	1.45	0.81
2:B:21:GLN:HE22	1:E:11:GLN:HG2	1.45	0.79
1:M:179:PRO:HD3	1:M:214:ILE:HD13	1.64	0.79
2:J:57:TRQ:HB2	2:J:108:TRP:HE1	1.46	0.78
1:M:222:PRO:HG2	1:M:225:GLU:HB2	1.65	0.78
1:E:173:LYS:HE2	1:E:173:LYS:HA	1.65	0.77
1:I:178:VAL:HG11	1:I:194:MET:SD	2.25	0.77
2:B:57:TRQ:HB2	2:B:108:TRP:HE1	1.50	0.77
2:F:57:TRQ:HB2	2:F:108:TRP:HE1	1.48	0.77
2:N:55:ALA:HB1	3:O:94:PRO:HB3	1.67	0.77
2:N:57:TRQ:HB2	2:N:108:TRP:HE1	1.48	0.76
3:O:73:LYS:H	3:O:76:GLN:NE2	1.83	0.76
1:A:45:ARG:HD2	1:A:345:LEU:HD22	1.66	0.76
1:I:179:PRO:HD3	1:I:214:ILE:HD13	1.67	0.76
2:B:45:ASN:HB3	1:E:37:LEU:HD13	1.68	0.75
1:A:288:HIS:CD2	1:A:291:LEU:H	2.02	0.74
1:E:178:VAL:HG11	1:E:194:MET:SD	2.28	0.74
3:G:34:GLU:HG3	3:G:101:LYS:HD2	1.70	0.73
1:A:35:ARG:H	2:F:45:ASN:HD22	1.37	0.73
1:E:45:ARG:HD2	1:E:345:LEU:HD22	1.69	0.73
1:E:132:ARG:HD2	9:E:1100:HOH:O	1.88	0.73
4:H:7:ILE:HG13	4:H:8:ILE:CD1	2.18	0.73
1:I:35:ARG:H	2:N:45:ASN:HD22	1.37	0.72
3:C:64:GLU:H	3:C:64:GLU:CD	1.93	0.72
1:A:178:VAL:HG11	1:A:194:MET:SD	2.30	0.71
2:J:25:TYR:HE2	2:J:27:ARG:HG3	1.55	0.71
4:L:4:PHE:HB3	4:L:13:LEU:HD12	1.72	0.71
4:P:134:LEU:HG	4:P:138:GLN:HB3	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:222:PRO:HG2	1:I:225:GLU:HB2	1.72	0.71
1:I:119:LEU:HD22	2:N:48:PRO:HB2	1.73	0.71
3:C:38:LYS:HG2	3:C:41:ASP:OD2	1.90	0.71
1:A:222:PRO:HG2	1:A:225:GLU:HB2	1.71	0.71
1:M:301:ARG:NH1	1:M:310:SER:OG	2.24	0.70
4:H:4:PHE:HB3	4:H:13:LEU:HD12	1.74	0.70
1:M:132:ARG:HD2	9:M:1104:HOH:O	1.91	0.70
1:A:179:PRO:HD3	1:A:214:ILE:HD13	1.74	0.69
1:I:20:ARG:HH21	1:I:20:ARG:CB	2.01	0.69
1:A:20:ARG:HH21	1:A:20:ARG:CB	2.03	0.69
2:B:25:TYR:HE2	2:B:27:ARG:HG3	1.57	0.69
1:E:95:ALA:HB1	1:E:132:ARG:HD3	1.74	0.69
1:A:301:ARG:NH1	1:A:310:SER:OG	2.26	0.69
1:A:135:VAL:HG22	1:A:136:GLY:N	2.08	0.68
2:B:45:ASN:HD22	1:E:35:ARG:H	1.42	0.68
1:E:178:VAL:HG13	1:E:179:PRO:HD2	1.75	0.68
1:E:301:ARG:NH1	1:E:310:SER:OG	2.26	0.68
4:P:21:GLU:H	4:P:21:GLU:CD	1.96	0.68
4:H:93:LEU:HD21	8:H:200:HEC:HMB2	1.76	0.67
1:A:17:ALA:HA	1:A:20:ARG:HH22	1.59	0.67
2:F:25:TYR:HE2	2:F:27:ARG:HG3	1.57	0.67
1:I:17:ALA:HA	1:I:20:ARG:HH22	1.58	0.67
1:A:323:ARG:HD3	9:A:1447:HOH:O	1.94	0.67
3:G:8:GLU:CD	3:G:8:GLU:H	1.97	0.67
4:L:109:THR:OG1	4:L:112:GLU:HG3	1.96	0.66
4:P:93:LEU:HD21	8:P:200:HEC:HMB2	1.76	0.66
2:J:48:PRO:HB2	1:M:119:LEU:HD22	1.76	0.66
2:F:13:TRP:HZ3	9:F:2501:HOH:O	1.78	0.66
1:I:17:ALA:HA	1:I:20:ARG:NH2	2.11	0.66
3:O:5:ILE:N	3:O:5:ILE:HD12	2.11	0.66
1:M:307:LYS:HZ2	2:N:104:ASN:HD21	1.42	0.65
2:N:25:TYR:HE2	2:N:27:ARG:HG3	1.55	0.65
1:A:201:LEU:HD13	1:A:220:PHE:CE1	2.31	0.65
1:A:178:VAL:HG13	1:A:179:PRO:HD2	1.78	0.65
1:A:372:GLN:HB2	2:F:85:ARG:HD2	1.79	0.65
2:J:21:GLN:NE2	1:M:11:GLN:CG	2.60	0.64
1:M:288:HIS:CD2	1:M:291:LEU:H	2.11	0.64
1:A:95:ALA:HB1	1:A:132:ARG:HD3	1.79	0.64
1:A:17:ALA:HA	1:A:20:ARG:NH2	2.12	0.64
4:L:133:TRP:CD1	4:L:134:LEU:HD13	2.33	0.64
1:M:178:VAL:HG11	1:M:194:MET:SD	2.37	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:ALA:HA	2:B:82:VAL:CG2	2.29	0.63
1:I:132:ARG:HD2	9:I:1034:HOH:O	1.98	0.63
1:I:372:GLN:HB2	2:N:85:ARG:HD2	1.79	0.63
1:I:173:LYS:HE2	1:I:173:LYS:HA	1.79	0.63
4:P:1:ALA:N	4:P:2:PRO:HD2	2.14	0.63
9:B:2682:HOH:O	3:C:71:MET:HE2	1.99	0.63
1:I:56:ALA:HA	2:J:82:VAL:CG2	2.29	0.63
1:M:252:ILE:N	1:M:252:ILE:HD12	2.14	0.63
1:A:56:ALA:HA	2:B:82:VAL:HG23	1.81	0.62
1:E:179:PRO:HD3	1:E:214:ILE:HD13	1.81	0.62
2:J:45:ASN:HD22	1:M:35:ARG:H	1.46	0.62
3:O:73:LYS:H	3:O:76:GLN:HE21	1.46	0.62
1:M:178:VAL:HG13	1:M:179:PRO:HD2	1.81	0.62
2:B:85:ARG:HD2	1:E:372:GLN:HB2	1.81	0.62
1:E:178:VAL:HG13	1:E:179:PRO:CD	2.29	0.62
1:A:132:ARG:HD2	9:A:1008:HOH:O	1.99	0.61
1:I:56:ALA:HA	2:J:82:VAL:HG23	1.82	0.61
1:M:45:ARG:HD2	1:M:345:LEU:HD22	1.81	0.61
1:I:37:LEU:HD13	2:N:45:ASN:HB3	1.82	0.61
2:J:85:ARG:HD2	1:M:372:GLN:HB2	1.83	0.61
1:I:272:GLU:CD	1:I:323:ARG:HH12	2.04	0.61
1:M:96:SER:HB3	1:M:110:TYR:CZ	2.36	0.61
1:M:107:ARG:HD2	1:M:130:ALA:CB	2.31	0.61
1:A:252:ILE:HD12	1:A:252:ILE:N	2.16	0.61
1:M:17:ALA:HA	1:M:20:ARG:NH2	2.16	0.61
4:H:142:PHE:HA	9:H:2615:HOH:O	2.01	0.60
4:H:121:ARG:HD3	4:H:133:TRP:CD1	2.36	0.60
1:E:56:ALA:HA	2:F:82:VAL:CG2	2.32	0.60
4:P:93:LEU:HD22	4:P:104:MET:HG3	1.83	0.60
1:A:11:GLN:HB2	2:F:21:GLN:HE22	1.65	0.60
1:I:301:ARG:NH1	1:I:310:SER:OG	2.34	0.60
2:B:48:PRO:HB2	1:E:119:LEU:HD22	1.82	0.60
4:L:127:ASP:OD2	4:L:128:PRO:HD2	2.02	0.60
1:I:89:GLY:HA2	9:I:1231:HOH:O	2.01	0.59
1:E:252:ILE:HG22	1:E:254:LEU:HD13	1.84	0.59
1:M:272:GLU:OE2	1:M:323:ARG:NH1	2.35	0.59
3:K:5:ILE:HD12	3:K:5:ILE:N	2.17	0.59
4:H:93:LEU:CD2	8:H:200:HEC:HMB2	2.32	0.59
1:M:307:LYS:HZ2	2:N:104:ASN:ND2	2.00	0.59
1:I:178:VAL:HG13	1:I:179:PRO:HD2	1.84	0.58
1:M:80:LEU:HD13	9:M:1009:HOH:O	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:36:HIS:CD2	4:D:69:ILE:HD12	2.38	0.58
4:D:133:TRP:HD1	4:D:134:LEU:HD13	1.63	0.58
1:M:107:ARG:HD3	1:M:109:ASP:OD1	2.03	0.58
4:L:135:THR:OG1	4:L:138:GLN:HG3	2.04	0.58
1:E:56:ALA:HA	2:F:82:VAL:HG23	1.86	0.58
1:E:288:HIS:CD2	1:E:291:LEU:H	2.16	0.58
2:J:55:ALA:HB1	3:K:94:PRO:HB3	1.85	0.58
1:M:17:ALA:HA	1:M:20:ARG:HH22	1.68	0.58
4:L:14:ASN:OD1	4:L:16:ASP:HB2	2.02	0.58
1:A:286:ALA:HB3	1:A:295:TYR:HB2	1.85	0.57
4:D:68:LYS:HG2	4:D:69:ILE:N	2.18	0.57
3:K:33:PRO:HG3	9:K:2185:HOH:O	2.04	0.57
1:M:135:VAL:HG22	1:M:136:GLY:N	2.19	0.57
1:A:272:GLU:CD	1:A:323:ARG:HH12	2.08	0.57
1:M:307:LYS:NZ	2:N:104:ASN:HD21	2.01	0.57
1:A:96:SER:HB3	1:A:110:TYR:CZ	2.39	0.57
4:D:46:LEU:HB2	4:D:47:PRO:HD3	1.85	0.57
2:N:53:ALA:O	2:N:75:ARG:HD2	2.04	0.57
1:M:297:LEU:HD22	1:M:310:SER:HB2	1.87	0.57
2:B:21:GLN:NE2	1:E:11:GLN:HG2	2.18	0.57
4:H:133:TRP:CD1	4:H:134:LEU:HD13	2.39	0.57
1:E:128:PRO:O	1:E:131:PRO:HD3	2.04	0.57
4:H:53:TYR:CE1	4:H:57:CYS:HB2	2.40	0.57
1:M:227:LEU:HB3	1:M:242:TRP:NE1	2.19	0.57
1:E:135:VAL:HG22	1:E:136:GLY:N	2.20	0.57
1:E:208:THR:HG23	1:E:209:GLU:HG2	1.86	0.56
1:A:14:GLN:NE2	1:A:70:ARG:HH21	2.04	0.56
1:E:201:LEU:HD13	1:E:220:PHE:CE1	2.41	0.56
2:F:53:ALA:O	2:F:75:ARG:HD2	2.05	0.56
1:I:11:GLN:HB3	2:N:21:GLN:HE22	1.69	0.56
1:I:91:PHE:HA	1:I:116:PRO:HD3	1.86	0.56
1:M:56:ALA:HA	2:N:82:VAL:CG2	2.36	0.56
1:M:99:PHE:CE1	1:M:107:ARG:HG3	2.41	0.56
1:A:336:ILE:HA	1:A:347:TYR:O	2.06	0.56
3:K:39:VAL:HG23	3:K:105:GLU:OXT	2.05	0.56
3:K:2:LYS:HE2	3:K:84:GLU:OE2	2.05	0.56
1:M:82:ASN:HD22	1:M:132:ARG:NH2	2.04	0.56
1:E:80:LEU:HD13	9:E:1015:HOH:O	2.06	0.56
4:H:135:THR:OG1	4:H:138:GLN:HG3	2.06	0.56
2:J:53:ALA:O	2:J:75:ARG:HD2	2.06	0.55
4:P:93:LEU:HD21	8:P:200:HEC:CMB	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:128:PRO:CG	4:P:144:PRO:HG3	2.36	0.55
1:I:128:PRO:O	1:I:131:PRO:HD3	2.06	0.55
1:M:182:TYR:O	1:M:183:HIS:HB2	2.07	0.55
2:B:104:ASN:HD22	2:B:104:ASN:C	2.10	0.55
1:M:56:ALA:HA	2:N:82:VAL:HG23	1.89	0.55
4:P:25:THR:OG1	4:P:28:VAL:HG23	2.06	0.55
4:L:41:GLU:O	4:L:43:PRO:HD3	2.07	0.55
2:B:53:ALA:O	2:B:75:ARG:HD2	2.07	0.55
1:I:272:GLU:OE2	1:I:323:ARG:NH1	2.39	0.55
1:M:107:ARG:HD2	1:M:130:ALA:HB1	1.89	0.55
1:E:89:GLY:HA2	9:E:1074:HOH:O	2.06	0.55
1:M:307:LYS:NZ	2:N:104:ASN:ND2	2.56	0.54
1:A:119:LEU:HD22	2:F:48:PRO:HB2	1.88	0.54
2:F:55:ALA:HB1	3:G:94:PRO:HB3	1.89	0.54
1:M:301:ARG:HG3	1:M:302:ASP:O	2.06	0.54
1:M:201:LEU:HD13	1:M:220:PHE:CE1	2.42	0.54
1:M:283:GLN:HB2	1:M:335:SER:HB3	1.90	0.54
1:M:10:ALA:O	1:M:14:GLN:HG3	2.08	0.54
1:E:99:PHE:CE1	1:E:107:ARG:HG3	2.43	0.54
1:I:323:ARG:HD3	9:I:1988:HOH:O	2.08	0.54
2:J:104:ASN:C	2:J:104:ASN:HD22	2.10	0.54
2:B:13:TRP:CZ3	2:B:15:PRO:HB3	2.43	0.54
2:N:13:TRP:CZ3	2:N:15:PRO:HB3	2.43	0.54
4:D:41:GLU:O	4:D:43:PRO:HD3	2.08	0.54
1:E:102:ILE:N	1:E:102:ILE:HD12	2.23	0.54
1:E:178:VAL:HG12	1:E:179:PRO:O	2.08	0.53
1:A:107:ARG:HD3	1:A:109:ASP:OD1	2.07	0.53
1:M:14:GLN:NE2	1:M:70:ARG:HH21	2.04	0.53
1:A:305:ARG:HD3	2:B:9:PRO:O	2.08	0.53
3:C:59:ALA:N	3:C:66:ALA:HB2	2.23	0.53
4:L:8:ILE:HG13	4:L:9:ASP:N	2.24	0.53
1:M:272:GLU:CD	1:M:323:ARG:HH12	2.11	0.53
2:J:13:TRP:CZ3	2:J:15:PRO:HB3	2.43	0.53
4:L:6:ASN:OD1	4:L:8:ILE:HG12	2.09	0.53
4:P:20:GLU:CD	4:P:20:GLU:H	2.12	0.53
4:H:86:ASP:OD1	4:H:121:ARG:HD2	2.09	0.53
1:I:96:SER:HB3	1:I:110:TYR:CZ	2.44	0.53
1:A:135:VAL:CG2	1:A:136:GLY:N	2.72	0.53
1:I:243:PRO:HG2	1:I:285:VAL:CG2	2.39	0.52
1:A:272:GLU:OE2	1:A:323:ARG:NH1	2.42	0.52
9:A:1119:HOH:O	2:B:103:ALA:HB1	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:13:TRP:CZ3	2:F:15:PRO:HB3	2.44	0.52
2:F:104:ASN:C	2:F:104:ASN:HD22	2.13	0.52
1:M:237:ALA:HB2	1:M:289:ARG:HG3	1.91	0.52
1:I:178:VAL:HG12	1:I:179:PRO:O	2.09	0.52
2:N:13:TRP:HZ3	9:N:1263:HOH:O	1.92	0.52
1:A:99:PHE:CE1	1:A:107:ARG:HG3	2.45	0.52
2:B:45:ASN:CB	1:E:37:LEU:HD13	2.38	0.52
1:E:283:GLN:HB2	1:E:335:SER:CB	2.40	0.52
2:N:104:ASN:C	2:N:104:ASN:HD22	2.10	0.52
1:A:208:THR:HG23	1:A:209:GLU:HG2	1.92	0.52
2:B:56:SER:HB2	2:B:74:TYR:O	2.10	0.52
1:E:268:LEU:HD21	1:E:298:VAL:HG11	1.92	0.52
1:E:182:TYR:CD1	1:E:182:TYR:N	2.78	0.52
1:E:307:LYS:HZ2	2:F:104:ASN:ND2	2.08	0.52
1:A:178:VAL:HG13	1:A:179:PRO:CD	2.40	0.52
4:P:54:ALA:HA	4:P:58:SER:HB2	1.92	0.52
1:I:252:ILE:HG22	1:I:254:LEU:HD13	1.91	0.51
1:A:107:ARG:HD2	1:A:130:ALA:CB	2.40	0.51
1:E:107:ARG:HD3	1:E:109:ASP:OD1	2.10	0.51
4:H:101:MET:HB2	8:H:200:HEC:C1D	2.40	0.51
3:K:62:LEU:HD12	3:K:67:LEU:HD23	1.91	0.51
1:I:305:ARG:HD3	2:J:9:PRO:O	2.11	0.51
3:C:16:VAL:HG21	3:C:46:ILE:HD11	1.91	0.51
1:E:305:ARG:HD3	2:F:9:PRO:O	2.11	0.51
1:A:179:PRO:HB2	1:A:181:CYS:SG	2.51	0.51
1:I:283:GLN:HB2	1:I:335:SER:HB3	1.91	0.51
1:M:285:VAL:HG13	1:M:296:LEU:HD13	1.92	0.51
1:A:266:GLU:HG2	1:A:273:ARG:NH2	2.26	0.51
1:E:283:GLN:HB2	1:E:335:SER:HB3	1.92	0.51
1:I:20:ARG:HB2	1:I:20:ARG:NH2	2.06	0.51
1:E:297:LEU:HD22	1:E:310:SER:HB2	1.93	0.51
2:F:56:SER:HB2	2:F:74:TYR:O	2.11	0.51
4:P:7:ILE:HD13	4:P:92:THR:OG1	2.11	0.51
1:M:178:VAL:HG13	1:M:179:PRO:CD	2.41	0.51
1:A:37:LEU:HD13	2:F:45:ASN:HB3	1.91	0.51
2:B:13:TRP:HZ3	9:B:1133:HOH:O	1.94	0.50
1:E:336:ILE:HA	1:E:347:TYR:O	2.11	0.50
1:I:227:LEU:HB3	1:I:242:TRP:CD1	2.46	0.50
1:I:288:HIS:CD2	1:I:291:LEU:H	2.11	0.50
1:I:354:LYS:HA	1:I:377:PRO:HG3	1.93	0.50
4:D:25:THR:OG1	4:D:28:VAL:HG23	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:93:GLY:O	2:B:95:LEU:HD13	2.12	0.50
4:D:127:ASP:OD2	4:D:129:LYS:HB3	2.10	0.50
4:P:4:PHE:HB3	4:P:13:LEU:HD12	1.93	0.50
1:I:102:ILE:N	1:I:102:ILE:HD12	2.27	0.50
1:I:151:LEU:C	1:I:151:LEU:HD23	2.31	0.50
1:I:227:LEU:HB3	1:I:242:TRP:NE1	2.26	0.50
2:J:45:ASN:HB3	1:M:37:LEU:HD13	1.92	0.50
4:P:128:PRO:HG3	4:P:144:PRO:HG3	1.93	0.50
4:D:93:LEU:HD21	8:D:200:HEC:HMB2	1.94	0.50
1:M:178:VAL:HG12	1:M:179:PRO:O	2.11	0.50
1:M:336:ILE:HA	1:M:347:TYR:O	2.11	0.50
1:E:14:GLN:NE2	1:E:70:ARG:HH21	2.10	0.50
1:E:307:LYS:HZ2	2:F:104:ASN:HD21	1.59	0.50
1:I:82:ASN:HD22	1:I:132:ARG:NH2	2.10	0.50
1:I:135:VAL:HG22	1:I:136:GLY:N	2.26	0.50
2:J:93:GLY:O	2:J:95:LEU:HD13	2.12	0.50
1:E:180:ASP:OD2	3:G:99:ARG:NH1	2.44	0.50
1:M:227:LEU:HB3	1:M:242:TRP:CD1	2.47	0.50
1:I:208:THR:HG23	1:I:209:GLU:HG2	1.94	0.49
4:L:133:TRP:HD1	4:L:134:LEU:HD13	1.75	0.49
3:C:79:SER:O	3:C:80:LEU:HD23	2.11	0.49
1:I:243:PRO:HG2	1:I:285:VAL:HG21	1.93	0.49
2:N:56:SER:HB2	2:N:74:TYR:O	2.12	0.49
1:A:280:GLY:HA3	1:A:301:ARG:CZ	2.42	0.49
1:E:252:ILE:N	1:E:252:ILE:HD12	2.27	0.49
1:M:95:ALA:HB1	1:M:132:ARG:HD3	1.93	0.49
1:I:182:TYR:O	1:I:183:HIS:HB2	2.13	0.49
2:J:56:SER:HB2	2:J:74:TYR:O	2.12	0.49
1:E:272:GLU:OE2	1:E:323:ARG:NH1	2.46	0.49
2:F:25:TYR:HB3	2:F:28:HIS:CD2	2.48	0.49
3:G:38:LYS:HA	3:G:105:GLU:OXT	2.13	0.49
1:I:336:ILE:HA	1:I:347:TYR:O	2.13	0.49
4:L:20:GLU:H	4:L:20:GLU:CD	2.16	0.49
1:A:252:ILE:HG22	1:A:254:LEU:HD13	1.93	0.49
1:A:254:LEU:HD12	1:A:259:ALA:HA	1.94	0.49
2:B:25:TYR:HB3	2:B:28:HIS:CD2	2.48	0.48
1:M:102:ILE:HD12	1:M:102:ILE:N	2.28	0.48
3:O:93:THR:HB	3:O:94:PRO:HD3	1.95	0.48
1:A:178:VAL:HG12	1:A:179:PRO:O	2.13	0.48
1:M:107:ARG:HD2	1:M:130:ALA:HB2	1.95	0.48
2:N:25:TYR:HB3	2:N:28:HIS:CD2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:93:GLY:O	2:F:95:LEU:HD13	2.13	0.48
4:L:101:MET:HB2	8:L:200:HEC:C1D	2.43	0.48
1:I:307:LYS:NZ	2:J:104:ASN:HD21	2.12	0.48
4:L:15:PHE:HA	4:L:94:TYR:OH	2.14	0.48
4:P:127:ASP:OD2	4:P:129:LYS:HG2	2.13	0.48
2:B:55:ALA:HB1	3:C:94:PRO:HB3	1.95	0.48
4:H:56:MET:HE3	4:H:56:MET:HA	1.96	0.48
4:H:65:ALA:HB1	4:H:73:LEU:HB2	1.95	0.48
1:I:80:LEU:HD13	9:I:1003:HOH:O	2.13	0.48
1:I:178:VAL:HG13	1:I:179:PRO:CD	2.43	0.48
1:M:354:LYS:HA	1:M:377:PRO:HG3	1.96	0.48
1:A:20:ARG:HB2	1:A:20:ARG:NH2	2.05	0.48
1:I:280:GLY:HA3	1:I:301:ARG:CZ	2.44	0.48
1:I:85:VAL:HG13	1:I:92:ILE:HG22	1.95	0.48
1:I:307:LYS:NZ	2:J:104:ASN:ND2	2.62	0.47
4:L:109:THR:HG23	4:L:112:GLU:OE1	2.14	0.47
1:E:42:PRO:HA	1:E:46:ARG:HD3	1.96	0.47
1:I:301:ARG:HG3	1:I:302:ASP:O	2.14	0.47
1:A:333:ILE:HD12	1:A:348:ALA:HB1	1.95	0.47
1:E:91:PHE:HA	1:E:116:PRO:HD3	1.95	0.47
1:A:285:VAL:HG13	1:A:296:LEU:HD13	1.97	0.47
1:I:266:GLU:HG2	1:I:273:ARG:NH2	2.29	0.47
4:P:53:TYR:CE1	4:P:57:CYS:HB2	2.49	0.47
4:D:39:TYR:CD1	4:D:45:ILE:HG13	2.49	0.47
1:E:96:SER:HB3	1:E:110:TYR:CZ	2.49	0.47
1:E:201:LEU:HD13	1:E:220:PHE:HE1	1.79	0.47
1:A:86:ALA:HB1	5:A:408:PO4:O3	2.14	0.47
8:H:200:HEC:HMC3	9:H:1646:HOH:O	2.14	0.47
3:K:99:ARG:HD3	9:K:1406:HOH:O	2.14	0.47
4:L:93:LEU:HD11	8:L:200:HEC:HMB2	1.96	0.47
4:L:124:TYR:CZ	4:L:126:GLY:HA3	2.50	0.47
1:M:243:PRO:HG2	1:M:285:VAL:CG2	2.44	0.47
2:N:85:ARG:NH1	9:N:1403:HOH:O	2.46	0.47
4:H:8:ILE:HD13	4:H:97:ALA:HA	1.96	0.47
1:M:273:ARG:HH21	1:M:273:ARG:HG3	1.79	0.47
1:A:45:ARG:HG2	9:A:2133:HOH:O	2.14	0.47
1:I:251:GLN:HG3	9:I:1083:HOH:O	2.14	0.47
1:M:251:GLN:HG3	9:M:1526:HOH:O	2.15	0.47
3:O:59:ALA:N	3:O:66:ALA:HB2	2.30	0.47
2:F:103:ALA:HB1	9:F:1097:HOH:O	2.15	0.46
1:I:196:CYS:SG	1:I:202:ALA:HB2	2.56	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:57:TRQ:CB	2:J:108:TRP:NE1	2.68	0.46
1:M:20:ARG:HH21	1:M:20:ARG:CB	2.23	0.46
1:M:252:ILE:HG22	1:M:254:LEU:HD13	1.97	0.46
1:A:285:VAL:HG13	1:A:296:LEU:CD1	2.46	0.46
1:A:307:LYS:NZ	2:B:104:ASN:HD21	2.12	0.46
2:J:25:TYR:HB3	2:J:28:HIS:CD2	2.49	0.46
2:N:93:GLY:O	2:N:95:LEU:HD13	2.16	0.46
1:A:245:TYR:O	1:A:279:PRO:HD2	2.16	0.46
1:I:283:GLN:HB2	1:I:335:SER:CB	2.45	0.46
1:A:107:ARG:CZ	1:A:130:ALA:HB1	2.46	0.46
2:F:25:TYR:CE2	2:F:27:ARG:CG	2.89	0.46
4:H:39:TYR:CD1	4:H:45:ILE:HG12	2.51	0.46
1:I:5:GLU:O	1:I:5:GLU:HG2	2.16	0.46
4:L:20:GLU:CD	4:L:20:GLU:N	2.69	0.46
2:N:78:CYS:HB3	2:N:118:THR:O	2.15	0.46
4:L:53:TYR:CE1	4:L:57:CYS:HB2	2.51	0.46
1:M:89:GLY:HA2	9:M:1114:HOH:O	2.14	0.46
1:A:135:VAL:HG22	1:A:136:GLY:H	1.80	0.46
3:C:36:HIS:HD2	4:D:69:ILE:HD12	1.79	0.46
1:E:272:GLU:CD	1:E:323:ARG:HH12	2.19	0.46
4:H:89:LEU:HD13	4:H:117:MET:HG2	1.98	0.46
1:I:35:ARG:H	2:N:45:ASN:ND2	2.11	0.46
1:I:86:ALA:HB1	5:I:405:PO4:O4	2.16	0.46
2:J:78:CYS:HB3	2:J:118:THR:O	2.16	0.46
1:M:286:ALA:HB3	1:M:295:TYR:HB2	1.97	0.46
1:E:107:ARG:CZ	1:E:130:ALA:HB1	2.46	0.46
1:M:5:GLU:HG2	1:M:5:GLU:O	2.16	0.46
1:A:9:GLN:HE21	1:A:9:GLN:HA	1.80	0.46
2:B:25:TYR:CE2	2:B:27:ARG:CG	2.88	0.46
1:A:80:LEU:HD13	9:A:1004:HOH:O	2.16	0.46
3:C:27:LYS:HE3	4:D:76:ALA:HB3	1.97	0.46
1:I:182:TYR:N	1:I:182:TYR:CD1	2.84	0.46
1:I:277:TRP:CE2	1:I:300:GLN:HG3	2.51	0.46
2:J:96:PRO:HB2	2:J:98:TYR:CE2	2.51	0.46
4:P:54:ALA:O	4:P:58:SER:HB3	2.15	0.46
4:P:68:LYS:HD2	4:P:69:ILE:HG12	1.98	0.46
1:A:10:ALA:O	1:A:14:GLN:HG3	2.16	0.45
4:D:131:ALA:HB1	4:D:134:LEU:HD22	1.98	0.45
2:F:78:CYS:HB3	2:F:118:THR:O	2.17	0.45
1:I:354:LYS:HA	1:I:377:PRO:CG	2.45	0.45
1:A:182:TYR:O	1:A:183:HIS:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:243:PRO:HG2	1:E:285:VAL:CG2	2.46	0.45
4:L:71:PRO:O	4:L:73:LEU:HD13	2.15	0.45
4:P:86:ASP:OD1	4:P:121:ARG:HD2	2.16	0.45
1:E:182:TYR:O	1:E:183:HIS:HB2	2.15	0.45
1:E:285:VAL:HG13	1:E:296:LEU:HD13	1.98	0.45
4:L:127:ASP:HB3	4:L:130:ASP:OD2	2.16	0.45
2:B:57:TRQ:CB	2:B:108:TRP:NE1	2.71	0.45
1:I:107:ARG:HD2	1:I:130:ALA:CB	2.46	0.45
1:A:102:ILE:HD12	1:A:102:ILE:N	2.30	0.45
2:B:78:CYS:HB3	2:B:118:THR:O	2.17	0.45
4:P:19:MET:HB3	4:P:21:GLU:OE2	2.17	0.45
1:E:284:GLN:O	1:E:296:LEU:HD12	2.16	0.45
1:M:305:ARG:HD3	2:N:9:PRO:O	2.16	0.45
1:A:107:ARG:HD2	1:A:130:ALA:HB1	1.97	0.45
4:D:128:PRO:HG3	4:D:142:PHE:HD2	1.81	0.45
1:E:45:ARG:NH2	1:E:67:GLU:OE2	2.49	0.45
1:E:253:ASP:HB2	1:E:262:LEU:HD11	1.98	0.45
4:L:34:THR:OG1	4:L:36:GLU:HG2	2.16	0.45
2:B:96:PRO:HB2	2:B:98:TYR:CE2	2.52	0.45
2:F:96:PRO:HB2	2:F:98:TYR:CE2	2.51	0.45
2:J:54:THR:O	2:J:75:ARG:HD3	2.17	0.45
1:M:92:ILE:HG13	1:M:114:PHE:HB2	1.99	0.45
1:M:129:ASP:O	1:M:130:ALA:C	2.55	0.45
2:N:96:PRO:HB2	2:N:98:TYR:CE2	2.52	0.45
1:A:227:LEU:HB3	1:A:242:TRP:NE1	2.31	0.45
4:P:49:ALA:HB1	4:P:119:TRP:HB2	1.99	0.45
1:A:266:GLU:HG2	1:A:273:ARG:CZ	2.46	0.45
4:D:121:ARG:HD3	4:D:133:TRP:CD1	2.52	0.45
1:I:237:ALA:HB2	1:I:289:ARG:HG3	1.98	0.45
1:M:316:LEU:HD23	1:M:316:LEU:N	2.31	0.44
1:A:270:GLU:HG2	9:A:1706:HOH:O	2.17	0.44
1:A:307:LYS:NZ	2:B:104:ASN:ND2	2.66	0.44
1:E:307:LYS:NZ	2:F:104:ASN:ND2	2.66	0.44
1:I:181:CYS:HA	1:I:196:CYS:HA	1.98	0.44
1:M:341:ASP:OD2	1:M:341:ASP:N	2.49	0.44
1:M:92:ILE:CG1	1:M:114:PHE:HB2	2.47	0.44
4:L:89:LEU:HD13	4:L:117:MET:HG2	1.99	0.44
1:E:295:TYR:N	1:E:295:TYR:CD1	2.86	0.44
3:O:5:ILE:N	3:O:5:ILE:CD1	2.80	0.44
3:O:35:LEU:HD22	3:O:37:VAL:HG13	1.99	0.44
1:A:129:ASP:O	1:A:130:ALA:C	2.55	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:53:TYR:CE1	4:D:57:CYS:HB2	2.51	0.44
1:E:180:ASP:CG	3:G:99:ARG:HH12	2.20	0.44
1:E:181:CYS:HA	1:E:196:CYS:HA	1.99	0.44
1:I:11:GLN:NE2	9:I:2068:HOH:O	2.50	0.44
4:P:65:ALA:HB1	4:P:73:LEU:HB2	2.00	0.44
1:A:9:GLN:HA	1:A:9:GLN:NE2	2.33	0.44
1:A:127:LEU:HA	1:A:128:PRO:HD3	1.88	0.44
3:K:27:LYS:HE3	4:L:76:ALA:HB3	2.00	0.44
4:L:87:VAL:HG23	9:L:1808:HOH:O	2.18	0.44
2:N:25:TYR:CE2	2:N:27:ARG:CG	2.88	0.44
3:O:93:THR:HB	3:O:94:PRO:CD	2.48	0.44
3:G:33:PRO:HG3	9:G:1733:HOH:O	2.18	0.44
1:M:45:ARG:NH2	1:M:67:GLU:OE2	2.51	0.44
1:A:283:GLN:HB2	1:A:335:SER:HB3	1.99	0.43
1:I:95:ALA:HB1	1:I:132:ARG:HD3	1.99	0.43
5:J:403:PO4:O4	3:K:68:LYS:NZ	2.47	0.43
1:M:45:ARG:CD	1:M:345:LEU:HD22	2.48	0.43
4:L:1:ALA:N	4:L:2:PRO:CD	2.81	0.43
4:H:80:TYR:HA	4:H:81:PRO:HD2	1.73	0.43
1:A:268:LEU:O	1:A:273:ARG:NH2	2.51	0.43
4:D:45:ILE:HD12	4:D:115:ARG:CZ	2.49	0.43
1:E:20:ARG:HG3	9:E:1924:HOH:O	2.18	0.43
1:E:227:LEU:HB3	1:E:242:TRP:NE1	2.33	0.43
1:E:354:LYS:HA	1:E:377:PRO:HG3	2.00	0.43
1:M:128:PRO:O	1:M:131:PRO:HD3	2.18	0.43
2:N:54:THR:O	2:N:75:ARG:HD3	2.18	0.43
4:P:143:THR:O	4:P:144:PRO:C	2.56	0.43
1:E:269:THR:OG1	1:E:272:GLU:HG3	2.18	0.43
2:J:26:TRP:CZ2	2:J:27:ARG:HD2	2.53	0.43
3:K:93:THR:HB	3:K:94:PRO:HD3	2.01	0.43
4:P:1:ALA:N	4:P:2:PRO:CD	2.81	0.43
3:C:4:THR:O	3:C:6:PRO:HD3	2.18	0.43
4:L:134:LEU:HG	4:L:138:GLN:HB3	2.00	0.43
4:P:134:LEU:HG	4:P:138:GLN:CB	2.42	0.43
1:A:227:LEU:HB3	1:A:242:TRP:CD1	2.54	0.43
2:B:26:TRP:CZ2	2:B:27:ARG:HD2	2.54	0.43
9:J:1711:HOH:O	3:K:71:MET:HE2	2.18	0.43
1:M:179:PRO:HB2	1:M:181:CYS:SG	2.58	0.43
1:M:251:GLN:C	1:M:252:ILE:HD12	2.38	0.43
4:P:45:ILE:HD11	4:P:115:ARG:CZ	2.49	0.43
1:A:265:VAL:HG12	1:A:266:GLU:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:GLU:HG3	9:A:1068:HOH:O	2.18	0.43
1:A:307:LYS:HZ2	2:B:104:ASN:HD21	1.67	0.43
3:K:28:MET:SD	3:K:51:MET:HG2	2.59	0.43
1:A:181:CYS:HA	1:A:196:CYS:HA	2.00	0.43
1:E:107:ARG:HD2	1:E:130:ALA:CB	2.49	0.43
1:A:35:ARG:H	2:F:45:ASN:ND2	2.11	0.43
1:A:182:TYR:N	1:A:182:TYR:CD1	2.87	0.43
1:E:123:ALA:HB2	1:E:170:LYS:HE3	2.00	0.43
2:F:26:TRP:CZ2	2:F:27:ARG:CD	3.02	0.43
1:I:227:LEU:HD12	1:I:227:LEU:N	2.33	0.43
1:I:307:LYS:HZ2	2:J:104:ASN:HD21	1.67	0.43
4:L:65:ALA:HB1	4:L:73:LEU:HB2	1.99	0.43
2:N:26:TRP:CZ2	2:N:27:ARG:HD2	2.54	0.43
3:O:101:LYS:HB2	3:O:101:LYS:NZ	2.34	0.43
4:P:101:MET:HB2	8:P:200:HEC:C1D	2.49	0.43
2:B:20:ILE:HD13	1:E:18:ALA:HB1	2.00	0.42
2:B:54:THR:O	2:B:75:ARG:HD3	2.19	0.42
4:D:80:TYR:HA	4:D:81:PRO:HD2	1.79	0.42
1:I:285:VAL:HG13	1:I:296:LEU:HD13	2.00	0.42
1:A:294:ILE:HG13	1:A:318:ALA:HB2	2.00	0.42
1:E:341:ASP:OD2	1:E:341:ASP:N	2.52	0.42
2:F:26:TRP:CZ2	2:F:27:ARG:HD2	2.54	0.42
3:K:31:GLU:O	4:L:71:PRO:HA	2.19	0.42
1:M:227:LEU:N	1:M:227:LEU:HD12	2.34	0.42
3:O:46:ILE:HG22	3:O:48:ARG:HD2	2.01	0.42
1:A:128:PRO:O	1:A:131:PRO:HD3	2.18	0.42
3:C:3:ALA:HA	3:C:81:THR:O	2.19	0.42
4:H:8:ILE:HG12	4:H:98:THR:HG22	2.01	0.42
1:I:107:ARG:CZ	1:I:130:ALA:HB1	2.49	0.42
1:I:153:PHE:CE2	1:I:163:GLY:HA3	2.54	0.42
4:D:23:ARG:HG2	4:D:110:LEU:HD22	2.02	0.42
1:I:55:ALA:O	2:J:82:VAL:HG22	2.19	0.42
3:K:93:THR:HB	3:K:94:PRO:CD	2.50	0.42
1:A:201:LEU:HD12	1:A:201:LEU:HA	1.93	0.42
1:A:365:GLU:O	1:A:367:LEU:HD13	2.19	0.42
1:E:82:ASN:HB3	1:E:142:THR:HB	2.01	0.42
2:J:26:TRP:CZ2	2:J:27:ARG:CD	3.03	0.42
4:L:100:GLN:HG3	9:L:1802:HOH:O	2.19	0.42
4:L:124:TYR:CE2	4:L:126:GLY:HA3	2.55	0.42
2:F:54:THR:O	2:F:75:ARG:HD3	2.20	0.42
1:M:305:ARG:HD2	2:N:11:ALA:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:307:LYS:NZ	2:F:104:ASN:HD21	2.17	0.42
2:J:13:TRP:HZ3	9:J:1013:HOH:O	2.03	0.42
3:K:2:LYS:HB2	3:K:62:LEU:HA	2.02	0.42
1:M:269:THR:OG1	1:M:272:GLU:HG3	2.19	0.42
3:K:95:HIS:HB3	3:K:97:PHE:CZ	2.55	0.42
1:M:107:ARG:CD	1:M:130:ALA:HB1	2.50	0.42
1:E:196:CYS:SG	1:E:202:ALA:HB2	2.59	0.42
1:M:282:TRP:O	1:M:284:GLN:HG3	2.19	0.42
1:A:269:THR:OG1	1:A:272:GLU:HG3	2.20	0.42
2:B:26:TRP:CZ2	2:B:27:ARG:CD	3.03	0.42
1:M:151:LEU:HD23	1:M:151:LEU:C	2.40	0.42
2:N:26:TRP:CZ2	2:N:27:ARG:CD	3.03	0.42
4:D:45:ILE:HD12	4:D:115:ARG:NH2	2.35	0.41
4:D:49:ALA:HB1	4:D:119:TRP:HB2	2.01	0.41
4:D:109:THR:OG1	4:D:112:GLU:HG3	2.20	0.41
1:E:42:PRO:HA	9:E:1233:HOH:O	2.20	0.41
4:H:30:HIS:CE1	4:H:36:GLU:HB3	2.55	0.41
1:M:182:TYR:CD1	1:M:182:TYR:N	2.88	0.41
1:A:107:ARG:NH2	1:A:130:ALA:HB1	2.34	0.41
1:A:174:ARG:NH1	1:A:210:GLY:O	2.44	0.41
4:H:133:TRP:NE1	4:H:134:LEU:HD13	2.34	0.41
1:I:179:PRO:HD3	1:I:214:ILE:CD1	2.46	0.41
1:I:346:LEU:HB3	1:I:359:HIS:HB2	2.03	0.41
1:M:283:GLN:HB2	1:M:335:SER:CB	2.51	0.41
2:N:57:TRQ:HZ3	2:N:108:TRP:HB2	2.03	0.41
1:A:151:LEU:C	1:A:151:LEU:HD23	2.40	0.41
1:A:186:PRO:HB2	1:A:235:GLN:OE1	2.20	0.41
1:E:227:LEU:HB3	1:E:242:TRP:CD1	2.55	0.41
4:H:117:MET:O	4:H:121:ARG:HG2	2.20	0.41
4:P:100:GLN:HB3	8:P:200:HEC:HBC2	2.02	0.41
4:D:113:MET:O	4:D:117:MET:HG3	2.19	0.41
1:E:178:VAL:CG1	1:E:179:PRO:N	2.83	0.41
1:E:262:LEU:N	1:E:262:LEU:HD12	2.36	0.41
1:E:301:ARG:HG3	1:E:302:ASP:O	2.20	0.41
1:A:89:GLY:HA2	9:A:1357:HOH:O	2.21	0.41
3:C:38:LYS:HA	3:C:105:GLU:OXT	2.21	0.41
1:A:243:PRO:HG2	1:A:285:VAL:CG2	2.51	0.41
4:H:143:THR:O	4:H:144:PRO:C	2.59	0.41
3:C:73:LYS:HB2	3:C:76:GLN:OE1	2.21	0.41
1:I:201:LEU:HD13	1:I:220:PHE:CE1	2.56	0.41
1:M:285:VAL:HG13	1:M:296:LEU:CD1	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:86:ASP:OD1	4:D:121:ARG:HD2	2.21	0.41
1:E:135:VAL:CG2	1:E:136:GLY:N	2.82	0.41
1:E:181:CYS:C	1:E:182:TYR:CD1	2.94	0.41
1:M:99:PHE:CZ	1:M:107:ARG:HG3	2.56	0.41
1:M:107:ARG:CZ	1:M:130:ALA:HB1	2.51	0.41
1:E:54:HIS:O	1:E:55:ALA:HB3	2.21	0.41
1:E:254:LEU:HD12	1:E:259:ALA:HA	2.02	0.41
4:P:146:GLN:HA	4:P:146:GLN:OE1	2.21	0.41
4:D:4:PHE:HB3	4:D:13:LEU:HD12	2.03	0.40
4:D:135:THR:O	4:D:139:LYS:HG3	2.21	0.40
4:L:46:LEU:HB2	4:L:47:PRO:HD3	2.03	0.40
1:M:208:THR:HG23	1:M:209:GLU:HG2	2.02	0.40
1:M:280:GLY:HA3	1:M:301:ARG:CZ	2.51	0.40
4:P:42:ASP:HA	4:P:43:PRO:HD2	1.88	0.40
1:M:354:LYS:HA	1:M:377:PRO:CG	2.51	0.40
1:A:157:SER:OG	1:A:158:PRO:HA	2.21	0.40
1:A:305:ARG:HD2	2:B:11:ALA:O	2.20	0.40
3:C:59:ALA:H	3:C:66:ALA:HB2	1.87	0.40
1:I:14:GLN:NE2	1:I:70:ARG:HH21	2.20	0.40
1:E:307:LYS:HD2	2:F:91:THR:HG21	2.04	0.40
1:I:107:ARG:HD2	1:I:130:ALA:HB1	2.04	0.40
1:M:226:PHE:O	1:M:244:THR:HA	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	380/390 (97%)	364 (96%)	15 (4%)	1 (0%)	41	46
1	E	380/390 (97%)	365 (96%)	14 (4%)	1 (0%)	41	46
1	I	380/390 (97%)	365 (96%)	14 (4%)	1 (0%)	41	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	M	380/390 (97%)	367 (97%)	12 (3%)	1 (0%)	41 46
2	B	122/131 (93%)	118 (97%)	4 (3%)	0	100 100
2	F	122/131 (93%)	118 (97%)	4 (3%)	0	100 100
2	J	122/131 (93%)	118 (97%)	4 (3%)	0	100 100
2	N	122/131 (93%)	116 (95%)	6 (5%)	0	100 100
3	C	103/105 (98%)	100 (97%)	3 (3%)	0	100 100
3	G	103/105 (98%)	101 (98%)	2 (2%)	0	100 100
3	K	103/105 (98%)	101 (98%)	2 (2%)	0	100 100
3	O	103/105 (98%)	97 (94%)	5 (5%)	1 (1%)	15 13
4	D	145/155 (94%)	139 (96%)	5 (3%)	1 (1%)	22 21
4	H	145/155 (94%)	133 (92%)	11 (8%)	1 (1%)	22 21
4	L	145/155 (94%)	136 (94%)	7 (5%)	2 (1%)	11 7
4	P	145/155 (94%)	134 (92%)	9 (6%)	2 (1%)	11 7
All	All	3000/3124 (96%)	2872 (96%)	117 (4%)	11 (0%)	34 37

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	68	LYS
4	H	68	LYS
4	L	10	GLY
4	P	68	LYS
1	A	102	ILE
1	E	102	ILE
1	I	102	ILE
4	L	68	LYS
4	P	3	GLN
3	O	18	ASP
1	M	102	ILE

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	307/311 (99%)	290 (94%)	17 (6%)	21	21
1	E	307/311 (99%)	289 (94%)	18 (6%)	19	19
1	I	307/311 (99%)	292 (95%)	15 (5%)	25	27
1	M	307/311 (99%)	291 (95%)	16 (5%)	23	24
2	B	104/106 (98%)	98 (94%)	6 (6%)	20	20
2	F	104/106 (98%)	98 (94%)	6 (6%)	20	20
2	J	104/106 (98%)	99 (95%)	5 (5%)	25	28
2	N	104/106 (98%)	98 (94%)	6 (6%)	20	20
3	C	85/85 (100%)	81 (95%)	4 (5%)	26	29
3	G	85/85 (100%)	81 (95%)	4 (5%)	26	29
3	K	85/85 (100%)	83 (98%)	2 (2%)	49	58
3	O	85/85 (100%)	82 (96%)	3 (4%)	36	43
4	D	118/125 (94%)	111 (94%)	7 (6%)	19	19
4	H	118/125 (94%)	111 (94%)	7 (6%)	19	19
4	L	118/125 (94%)	110 (93%)	8 (7%)	16	14
4	P	118/125 (94%)	111 (94%)	7 (6%)	19	19
All	All	2456/2508 (98%)	2325 (95%)	131 (5%)	22	23

All (131) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	ARG
1	A	26	LEU
1	A	37	LEU
1	A	80	LEU
1	A	94	HIS
1	A	120	LEU
1	A	144	LEU
1	A	176	LEU
1	A	240	LEU
1	A	242	TRP
1	A	254	LEU
1	A	285	VAL
1	A	305	ARG
1	A	323	ARG
1	A	345	LEU
1	A	346	LEU

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Mol	Chain	Res	Type
1	A	373	LEU
2	B	16	GLN
2	B	27	ARG
2	B	29	CYS
2	B	43	LEU
2	B	82	VAL
2	B	104	ASN
3	C	18	ASP
3	C	35	LEU
3	C	84	GLU
3	C	89	ASP
4	D	52	LEU
4	D	57	CYS
4	D	73	LEU
4	D	89	LEU
4	D	110	LEU
4	D	121	ARG
4	D	134	LEU
1	E	20	ARG
1	E	26	LEU
1	E	80	LEU
1	E	94	HIS
1	E	120	LEU
1	E	144	LEU
1	E	176	LEU
1	E	201	LEU
1	E	240	LEU
1	E	242	TRP
1	E	254	LEU
1	E	285	VAL
1	E	316	LEU
1	E	323	ARG
1	E	345	LEU
1	E	346	LEU
1	E	367	LEU
1	E	373	LEU
2	F	16	GLN
2	F	27	ARG
2	F	29	CYS
2	F	43	LEU
2	F	82	VAL
2	F	104	ASN

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Mol	Chain	Res	Type
3	G	1	ASP
3	G	8	GLU
3	G	35	LEU
3	G	101	LYS
4	H	52	LEU
4	H	56	MET
4	H	73	LEU
4	H	89	LEU
4	H	110	LEU
4	H	121	ARG
4	H	134	LEU
1	I	20	ARG
1	I	26	LEU
1	I	80	LEU
1	I	94	HIS
1	I	120	LEU
1	I	144	LEU
1	I	176	LEU
1	I	240	LEU
1	I	254	LEU
1	I	285	VAL
1	I	305	ARG
1	I	323	ARG
1	I	345	LEU
1	I	346	LEU
1	I	373	LEU
2	J	16	GLN
2	J	27	ARG
2	J	43	LEU
2	J	82	VAL
2	J	104	ASN
3	K	8	GLU
3	K	35	LEU
4	L	20	GLU
4	L	56	MET
4	L	57	CYS
4	L	63	HIS
4	L	73	LEU
4	L	89	LEU
4	L	134	LEU
4	L	143	THR
1	M	20	ARG

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Mol	Chain	Res	Type
1	M	26	LEU
1	M	37	LEU
1	M	80	LEU
1	M	94	HIS
1	M	120	LEU
1	M	144	LEU
1	M	176	LEU
1	M	240	LEU
1	M	254	LEU
1	M	285	VAL
1	M	323	ARG
1	M	345	LEU
1	M	346	LEU
1	M	367	LEU
1	M	373	LEU
2	N	16	GLN
2	N	27	ARG
2	N	29	CYS
2	N	43	LEU
2	N	82	VAL
2	N	104	ASN
3	O	35	LEU
3	O	38	LYS
3	O	48	ARG
4	P	24	ASP
4	P	45	ILE
4	P	56	MET
4	P	73	LEU
4	P	89	LEU
4	P	110	LEU
4	P	121	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (51) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	GLN
1	A	14	GLN
1	A	16	GLN
1	A	284	GLN
1	A	288	HIS
2	B	21	GLN
2	B	34	ASN

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Mol	Chain	Res	Type
2	B	45	ASN
2	B	104	ASN
4	D	146	GLN
1	E	9	GLN
1	E	14	GLN
1	E	16	GLN
1	E	82	ASN
1	E	284	GLN
1	E	288	HIS
2	F	21	GLN
2	F	34	ASN
2	F	45	ASN
2	F	104	ASN
4	H	30	HIS
4	H	63	HIS
4	H	100	GLN
4	H	146	GLN
1	I	9	GLN
1	I	14	GLN
1	I	16	GLN
1	I	30	GLN
1	I	82	ASN
1	I	284	GLN
1	I	288	HIS
2	J	21	GLN
2	J	34	ASN
2	J	45	ASN
2	J	104	ASN
4	L	3	GLN
1	M	9	GLN
1	M	11	GLN
1	M	14	GLN
1	M	16	GLN
1	M	82	ASN
1	M	235	GLN
1	M	284	GLN
1	M	288	HIS
2	N	21	GLN
2	N	34	ASN
2	N	45	ASN
2	N	104	ASN
3	O	76	GLN

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Mol	Chain	Res	Type
4	P	30	HIS
4	P	100	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\#\|Z\| > 2$
2	TRQ	F	57	2	13,17,18	4.64	3 (23%)	14,24,26	2.26	5 (35%)
2	TRQ	B	57	2	13,17,18	4.64	3 (23%)	14,24,26	2.28	5 (35%)
2	TRQ	J	57	2	13,17,18	4.64	3 (23%)	14,24,26	2.27	5 (35%)
2	TRQ	N	57	2	13,17,18	4.72	3 (23%)	14,24,26	2.25	4 (28%)

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
2	TRQ	F	57	2	-	0/4/19/21	0/2/2/2
2	TRQ	B	57	2	-	0/4/19/21	0/2/2/2
2	TRQ	J	57	2	-	0/4/19/21	0/2/2/2
2	TRQ	N	57	2	-	0/4/19/21	0/2/2/2

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	N	57	TRQ	CH2-CZ2	-14.70	1.37	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	57	TRQ	CH2-CZ2	-14.54	1.37	1.54
2	J	57	TRQ	CH2-CZ2	-14.53	1.37	1.54
2	F	57	TRQ	CH2-CZ2	-14.47	1.37	1.54
2	N	57	TRQ	CE2-CZ2	-7.46	1.40	1.50
2	F	57	TRQ	CE2-CZ2	-7.24	1.40	1.50
2	B	57	TRQ	CE2-CZ2	-7.18	1.40	1.50
2	J	57	TRQ	CE2-CZ2	-6.97	1.40	1.50
2	J	57	TRQ	CZ3-CE3	3.34	1.40	1.34
2	F	57	TRQ	CZ3-CE3	3.20	1.40	1.34
2	B	57	TRQ	CZ3-CE3	3.20	1.40	1.34
2	N	57	TRQ	CZ3-CE3	2.83	1.39	1.34

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	J	57	TRQ	CZ2-CE2-NE1	5.75	129.13	119.94
2	F	57	TRQ	CZ2-CE2-NE1	5.70	129.05	119.94
2	B	57	TRQ	CZ2-CE2-NE1	5.68	129.01	119.94
2	N	57	TRQ	CZ2-CE2-NE1	5.68	129.00	119.94
2	N	57	TRQ	O7-CZ2-CH2	3.84	123.52	119.00
2	B	57	TRQ	O7-CZ2-CH2	3.54	123.16	119.00
2	F	57	TRQ	O7-CZ2-CH2	3.34	122.94	119.00
2	J	57	TRQ	O7-CZ2-CH2	3.26	122.83	119.00
2	N	57	TRQ	O7-CZ2-CE2	-2.86	118.81	121.84
2	B	57	TRQ	O7-CZ2-CE2	-2.66	119.02	121.84
2	J	57	TRQ	O6-CH2-CZ2	2.47	120.19	118.51
2	F	57	TRQ	O7-CZ2-CE2	-2.42	119.28	121.84
2	F	57	TRQ	O6-CH2-CZ2	2.32	120.09	118.51
2	J	57	TRQ	O7-CZ2-CE2	-2.28	119.42	121.84
2	J	57	TRQ	CZ3-CH2-CZ2	2.09	121.57	118.72
2	B	57	TRQ	O6-CH2-CZ2	2.06	119.91	118.51
2	F	57	TRQ	CZ3-CH2-CZ2	2.05	121.52	118.72
2	N	57	TRQ	CZ3-CH2-CZ2	2.03	121.50	118.72
2	B	57	TRQ	CZ3-CH2-CZ2	2.02	121.48	118.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	57	TRQ	2	0
2	B	57	TRQ	3	0
2	J	57	TRQ	3	0
2	N	57	TRQ	3	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 20 ligands modelled in this entry, 8 are monoatomic - leaving 12 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	$\#\|Z\| > 2$
5	PO4	J	403	-	4,4,4	1.69	1 (25%)	6,6,6	0.43	0
5	PO4	E	406	-	4,4,4	1.65	0	6,6,6	0.43	0
8	HEC	P	200	4	26,50,50	1.94	2 (7%)	18,82,82	1.76	7 (38%)
5	PO4	N	404	-	4,4,4	1.68	0	6,6,6	0.43	0
5	PO4	I	405	-	4,4,4	1.68	0	6,6,6	0.42	0
5	PO4	B	402	-	4,4,4	1.71	0	6,6,6	0.43	0
5	PO4	F	401	-	4,4,4	1.66	0	6,6,6	0.44	0
8	HEC	D	200	4	26,50,50	1.96	2 (7%)	18,82,82	1.93	7 (38%)
8	HEC	H	200	4	26,50,50	2.00	2 (7%)	18,82,82	1.69	7 (38%)
8	HEC	L	200	4	26,50,50	1.98	3 (11%)	18,82,82	1.88	7 (38%)
5	PO4	M	407	-	4,4,4	1.65	0	6,6,6	0.43	0
5	PO4	A	408	-	4,4,4	1.88	3 (75%)	6,6,6	0.43	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
8	HEC	P	200	4	-	0/6/54/54	-
8	HEC	D	200	4	-	0/6/54/54	-
8	HEC	H	200	4	-	0/6/54/54	-
8	HEC	L	200	4	-	0/6/54/54	-

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	H	200	HEC	C3C-C2C	-6.58	1.33	1.40
8	L	200	HEC	C3C-C2C	-6.46	1.34	1.40
8	P	200	HEC	C3C-C2C	-6.31	1.34	1.40
8	D	200	HEC	C3C-C2C	-6.17	1.34	1.40
8	D	200	HEC	C3B-C2B	-4.54	1.36	1.40
8	H	200	HEC	C3B-C2B	-4.39	1.36	1.40
8	L	200	HEC	C3B-C2B	-4.21	1.36	1.40
8	P	200	HEC	C3B-C2B	-4.04	1.36	1.40
5	A	408	PO4	P-O2	-2.12	1.48	1.54
5	A	408	PO4	P-O3	-2.11	1.48	1.54
5	A	408	PO4	P-O4	-2.09	1.48	1.54
8	L	200	HEC	CMC-C2C	2.05	1.56	1.51
5	J	403	PO4	P-O4	-2.01	1.48	1.54

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	D	200	HEC	CBD-CAD-C3D	-4.14	104.84	112.49
8	L	200	HEC	CBD-CAD-C3D	-3.52	106.00	112.49
8	H	200	HEC	CMC-C2C-C3C	3.02	129.37	125.82
8	L	200	HEC	CAD-CBD-CGD	2.97	117.66	112.67
8	L	200	HEC	CMC-C2C-C3C	2.92	129.25	125.82
8	D	200	HEC	CMC-C2C-C3C	2.89	129.22	125.82
8	D	200	HEC	CAD-CBD-CGD	2.85	117.45	112.67
8	P	200	HEC	CMC-C2C-C3C	2.81	129.12	125.82
8	D	200	HEC	CMC-C2C-C1C	-2.80	124.17	128.46
8	H	200	HEC	CMC-C2C-C1C	-2.77	124.20	128.46
8	P	200	HEC	CMC-C2C-C1C	-2.67	124.36	128.46
8	L	200	HEC	CMC-C2C-C1C	-2.65	124.39	128.46
8	P	200	HEC	CBD-CAD-C3D	-2.61	107.68	112.49
8	P	200	HEC	CAA-CBA-CGA	2.53	116.92	112.67
8	H	200	HEC	CBD-CAD-C3D	-2.46	107.95	112.49
8	H	200	HEC	CMD-C2D-C1D	-2.42	124.74	128.46
8	P	200	HEC	CMD-C2D-C1D	-2.38	124.80	128.46
8	L	200	HEC	CMB-C2B-C3B	2.36	128.60	125.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	P	200	HEC	CMB-C2B-C1B	-2.34	124.87	128.46
8	L	200	HEC	CMB-C2B-C1B	-2.27	124.97	128.46
8	L	200	HEC	CMD-C2D-C1D	-2.26	124.99	128.46
8	P	200	HEC	CMB-C2B-C3B	2.23	128.44	125.82
8	D	200	HEC	CMB-C2B-C1B	-2.21	125.07	128.46
8	D	200	HEC	CMB-C2B-C3B	2.18	128.38	125.82
8	D	200	HEC	CMD-C2D-C1D	-2.13	125.19	128.46
8	H	200	HEC	CMB-C2B-C1B	-2.11	125.22	128.46
8	H	200	HEC	CAD-CBD-CGD	2.11	116.20	112.67
8	H	200	HEC	CMB-C2B-C3B	2.02	128.19	125.82

There are no chirality outliers.

There are no torsion outliers.

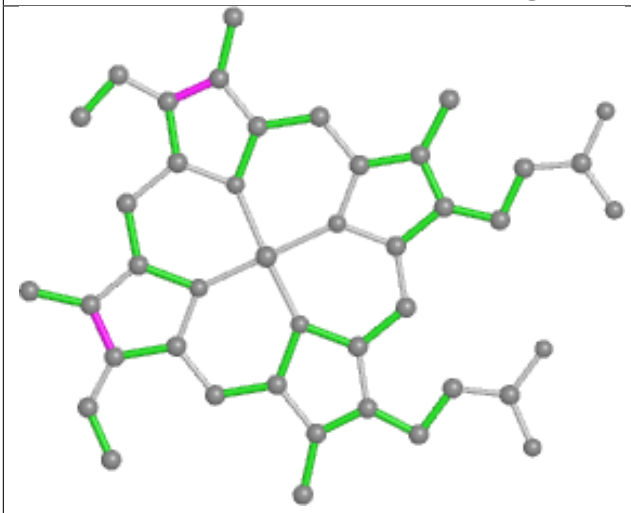
There are no ring outliers.

7 monomers are involved in 14 short contacts:

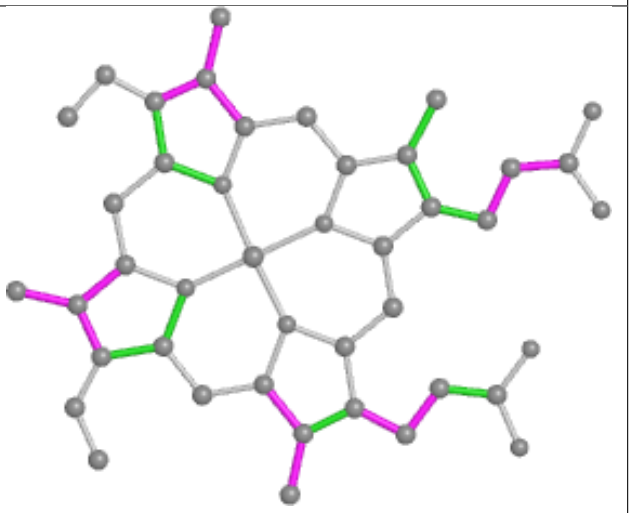
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	J	403	PO4	1	0
8	P	200	HEC	4	0
5	I	405	PO4	1	0
8	D	200	HEC	1	0
8	H	200	HEC	4	0
8	L	200	HEC	2	0
5	A	408	PO4	1	0

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.

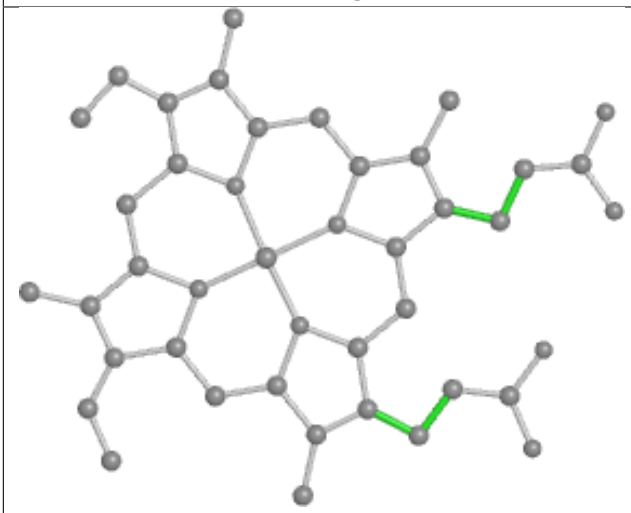
Ligand HEC P 200



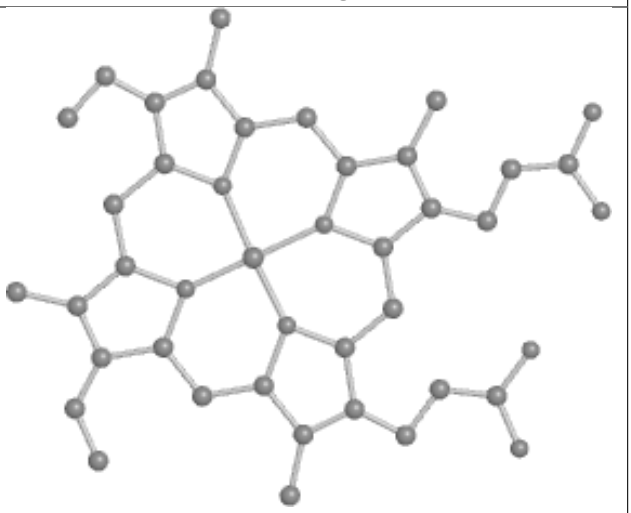
Bond lengths



Bond angles

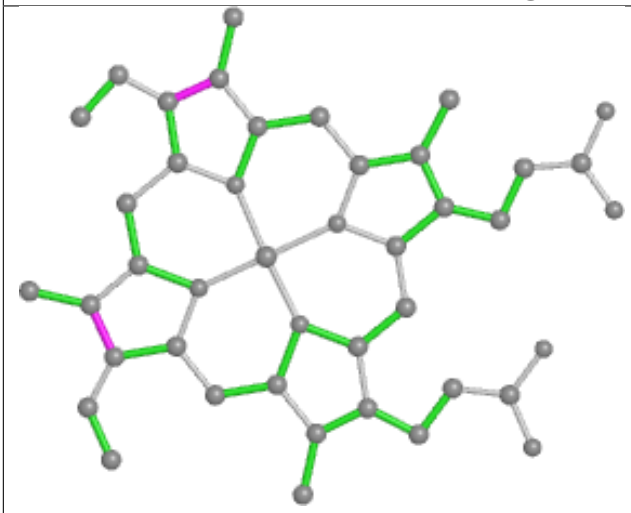


Torsions

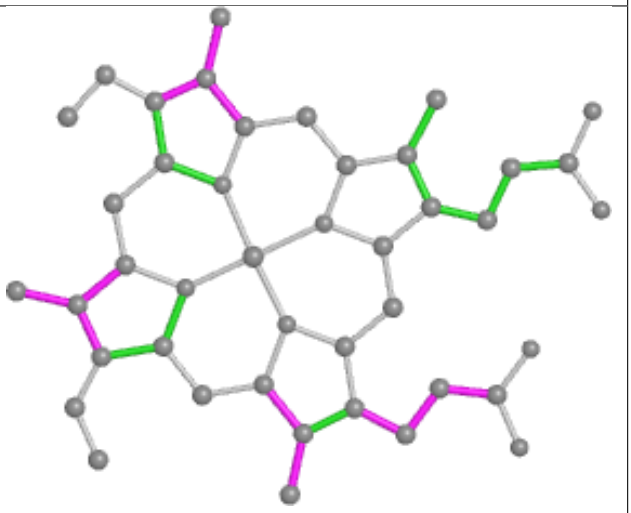


Rings

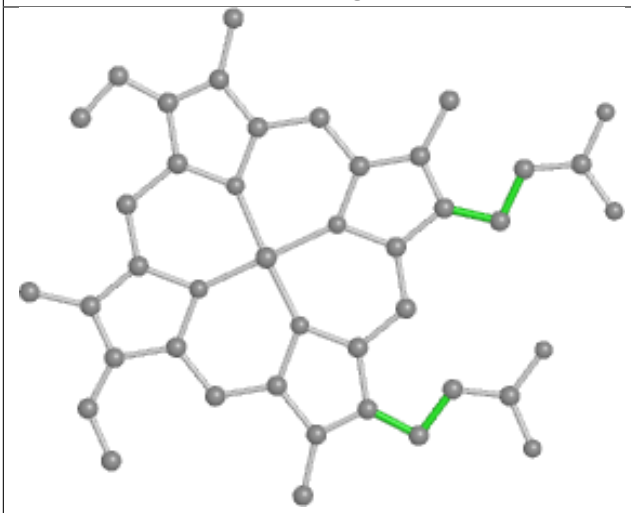
Ligand HEC D 200



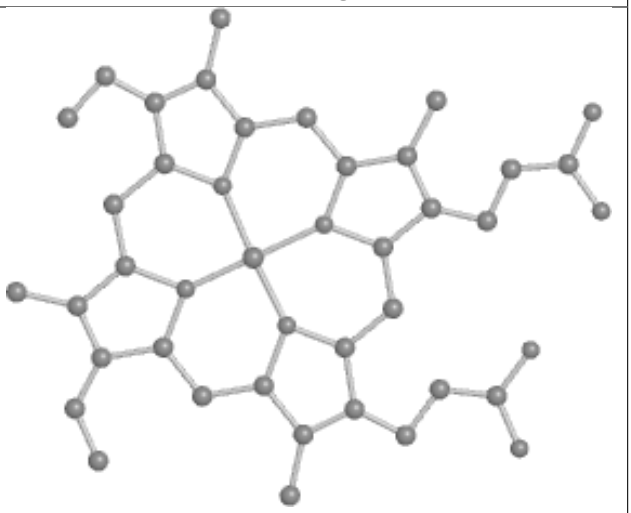
Bond lengths



Bond angles

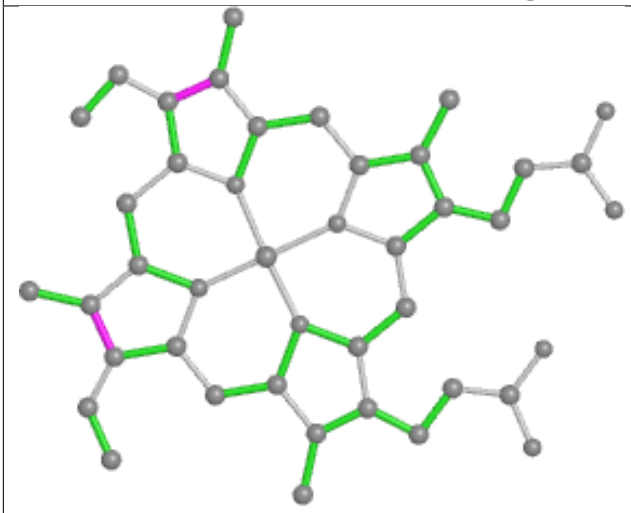


Torsions

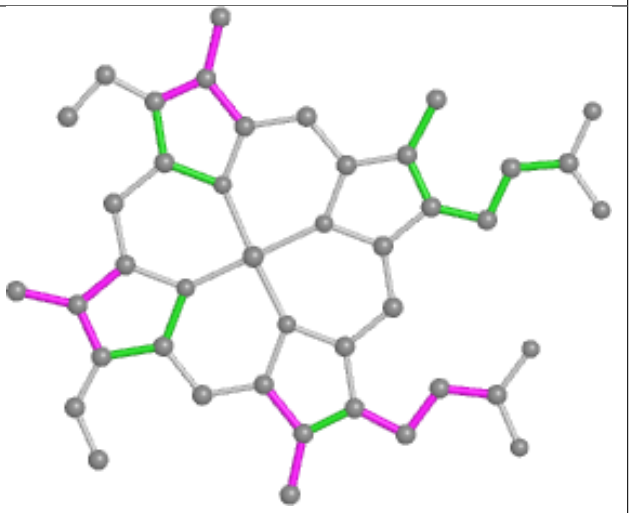


Rings

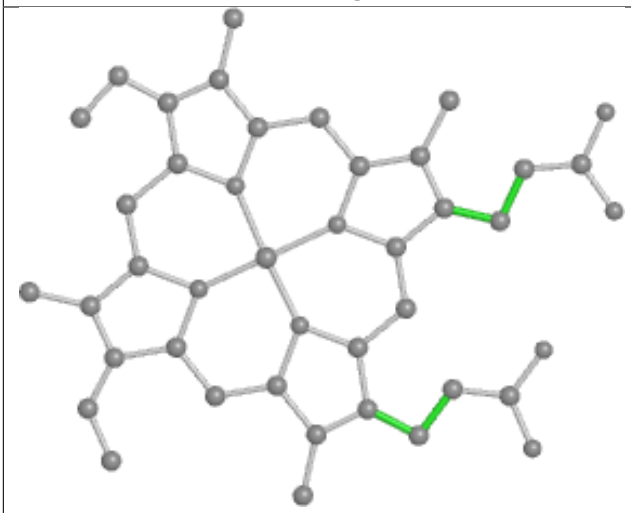
Ligand HEC H 200



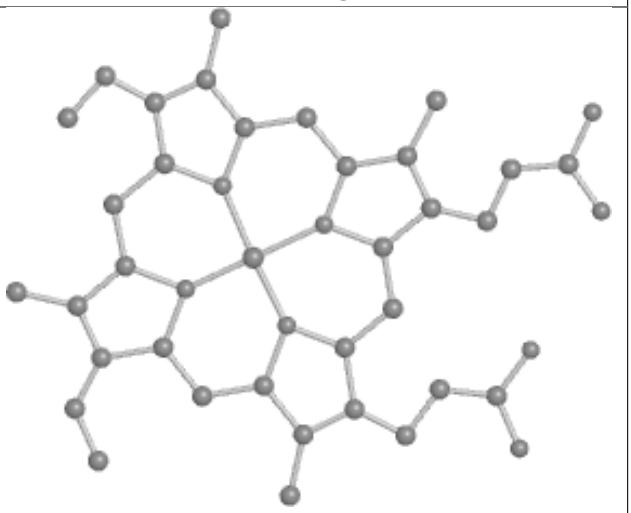
Bond lengths



Bond angles

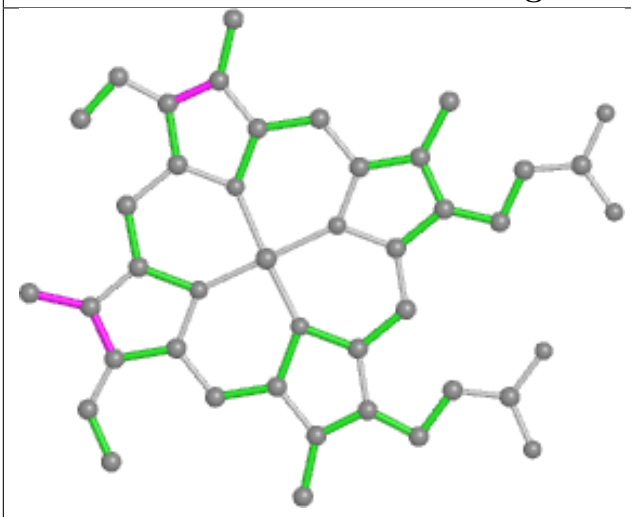


Torsions

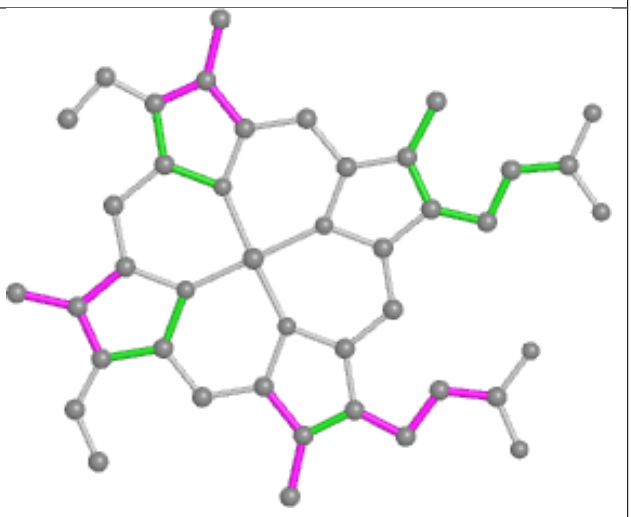


Rings

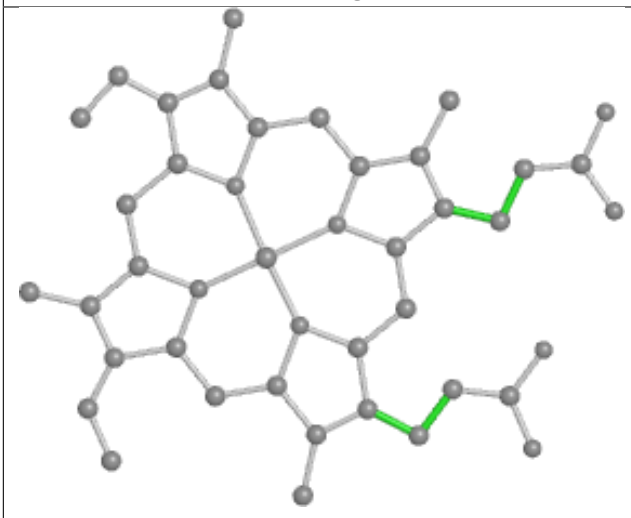
Ligand HEC L 200



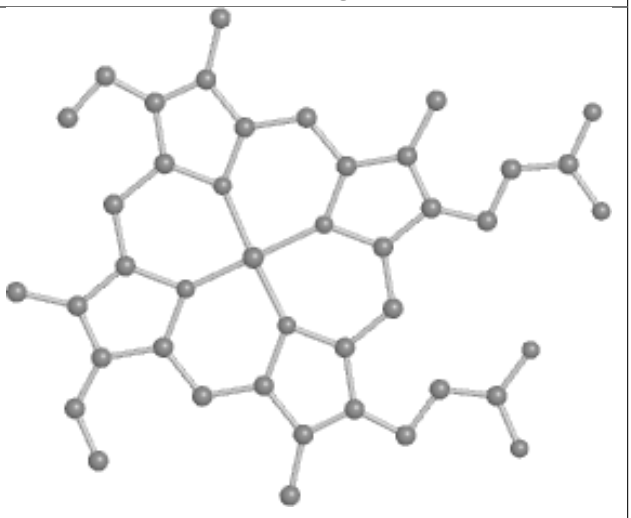
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	382/390 (97%)	-0.19	9 (2%)	59	62	9, 19, 40, 77	0
1	E	382/390 (97%)	-0.17	8 (2%)	63	66	9, 19, 38, 74	0
1	I	382/390 (97%)	-0.26	9 (2%)	59	62	6, 17, 38, 74	0
1	M	382/390 (97%)	-0.24	7 (1%)	68	71	8, 18, 36, 74	0
2	B	124/131 (94%)	-0.23	1 (0%)	86	87	11, 17, 30, 68	0
2	F	124/131 (94%)	-0.25	1 (0%)	86	87	10, 15, 27, 69	0
2	J	124/131 (94%)	-0.23	1 (0%)	86	87	7, 15, 27, 68	0
2	N	124/131 (94%)	-0.25	1 (0%)	86	87	11, 18, 29, 68	0
3	C	105/105 (100%)	0.24	8 (7%)	13	15	16, 28, 52, 61	0
3	G	105/105 (100%)	-0.27	3 (2%)	51	55	12, 21, 32, 51	0
3	K	105/105 (100%)	-0.28	2 (1%)	66	69	10, 20, 33, 51	0
3	O	105/105 (100%)	0.14	6 (5%)	23	25	16, 28, 53, 66	0
4	D	147/155 (94%)	-0.28	2 (1%)	75	77	13, 22, 47, 59	0
4	H	147/155 (94%)	-0.02	11 (7%)	14	15	15, 26, 57, 70	0
4	L	147/155 (94%)	0.07	10 (6%)	17	18	15, 31, 50, 58	0
4	P	147/155 (94%)	0.07	9 (6%)	21	23	14, 28, 61, 82	0
All	All	3032/3124 (97%)	-0.16	88 (2%)	51	55	6, 20, 45, 82	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	131	SER	7.8
4	P	129	LYS	7.5
2	F	131	SER	6.2
1	E	386	GLY	6.1
1	E	5	GLU	5.9

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Mol	Chain	Res	Type	RSRZ
1	E	208	THR	5.7
2	N	131	SER	5.5
1	A	5	GLU	5.4
4	P	1	ALA	5.3
2	J	131	SER	5.1
1	I	386	GLY	4.9
3	C	64	GLU	4.7
1	A	211	THR	4.5
1	I	208	THR	4.4
4	P	130	ASP	4.4
1	A	208	THR	4.3
1	E	9	GLN	4.3
1	A	209	GLU	4.3
3	O	64	GLU	4.3
1	M	208	THR	4.2
4	P	2	PRO	4.2
1	M	5	GLU	4.1
1	I	9	GLN	4.0
4	P	127	ASP	3.9
3	G	1	ASP	3.9
4	H	140	ALA	3.9
3	O	18	ASP	3.9
3	K	1	ASP	3.9
4	P	3	GLN	3.8
3	O	1	ASP	3.8
3	C	1	ASP	3.8
4	H	137	GLU	3.6
4	D	129	LYS	3.6
1	M	9	GLN	3.5
4	H	135	THR	3.5
3	K	64	GLU	3.4
4	H	136	ASP	3.3
3	C	8	GLU	3.2
4	H	127	ASP	3.2
3	G	64	GLU	3.1
1	I	211	THR	3.1
3	C	60	GLY	3.0
1	M	207	GLY	3.0
1	M	209	GLU	3.0
1	E	207	GLY	2.9
4	L	128	PRO	2.9
4	L	140	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	9	GLN	2.8
4	L	24	ASP	2.8
4	H	24	ASP	2.8
3	C	6	PRO	2.8
4	L	1	ALA	2.8
1	I	209	GLU	2.8
1	A	210	GLY	2.7
1	M	386	GLY	2.7
3	C	63	GLY	2.7
3	O	60	GLY	2.7
4	L	127	ASP	2.7
1	E	209	GLU	2.7
1	A	386	GLY	2.7
4	H	128	PRO	2.6
4	P	140	ALA	2.6
4	P	128	PRO	2.6
1	E	211	THR	2.6
1	I	12	GLU	2.6
3	O	3	ALA	2.6
4	L	143	THR	2.6
4	D	24	ASP	2.6
1	E	6	ALA	2.6
3	C	18	ASP	2.5
1	A	207	GLY	2.5
1	I	5	GLU	2.5
1	A	319	LYS	2.5
4	P	138	GLN	2.4
4	L	20	GLU	2.4
3	C	65	ALA	2.3
3	O	8	GLU	2.3
3	G	61	VAL	2.2
1	I	207	GLY	2.2
1	I	20	ARG	2.2
4	L	45	ILE	2.1
4	H	146	GLN	2.1
4	H	142	PHE	2.1
4	L	146	GLN	2.0
1	M	211	THR	2.0
4	L	129	LYS	2.0
4	H	1	ALA	2.0
4	H	129	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	TRQ	B	57	16/17	0.96	0.11	14,16,19,23	0
2	TRQ	F	57	16/17	0.97	0.11	9,13,16,17	0
2	TRQ	J	57	16/17	0.97	0.10	10,13,15,18	0
2	TRQ	N	57	16/17	0.98	0.09	13,14,18,19	0

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, 95^{th} 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
5	PO4	M	407	5/5	0.73	0.35	76,76,79,81	0
5	PO4	A	408	5/5	0.76	0.25	51,54,57,58	0
5	PO4	N	404	5/5	0.81	0.28	78,78,81,81	0
5	PO4	J	403	5/5	0.88	0.22	63,64,66,66	0
5	PO4	E	406	5/5	0.88	0.24	69,70,72,73	0
5	PO4	I	405	5/5	0.88	0.23	65,68,69,70	0
5	PO4	F	401	5/5	0.93	0.22	66,67,68,68	0
5	PO4	B	402	5/5	0.97	0.15	51,52,53,54	0
7	NA	H	603	1/1	0.97	0.15	14,14,14,14	0
8	HEC	H	200	43/43	0.97	0.12	12,19,23,29	0
8	HEC	L	200	43/43	0.97	0.12	15,18,22,27	0
8	HEC	P	200	43/43	0.97	0.13	16,25,29,32	0
8	HEC	D	200	43/43	0.98	0.12	6,14,19,25	0
7	NA	L	601	1/1	0.99	0.14	13,13,13,13	0
7	NA	P	602	1/1	0.99	0.10	8,8,8,8	0
7	NA	D	604	1/1	0.99	0.09	22,22,22,22	0
6	CU	C	107	1/1	1.00	0.05	26,26,26,26	0
6	CU	G	107	1/1	1.00	0.07	19,19,19,19	0

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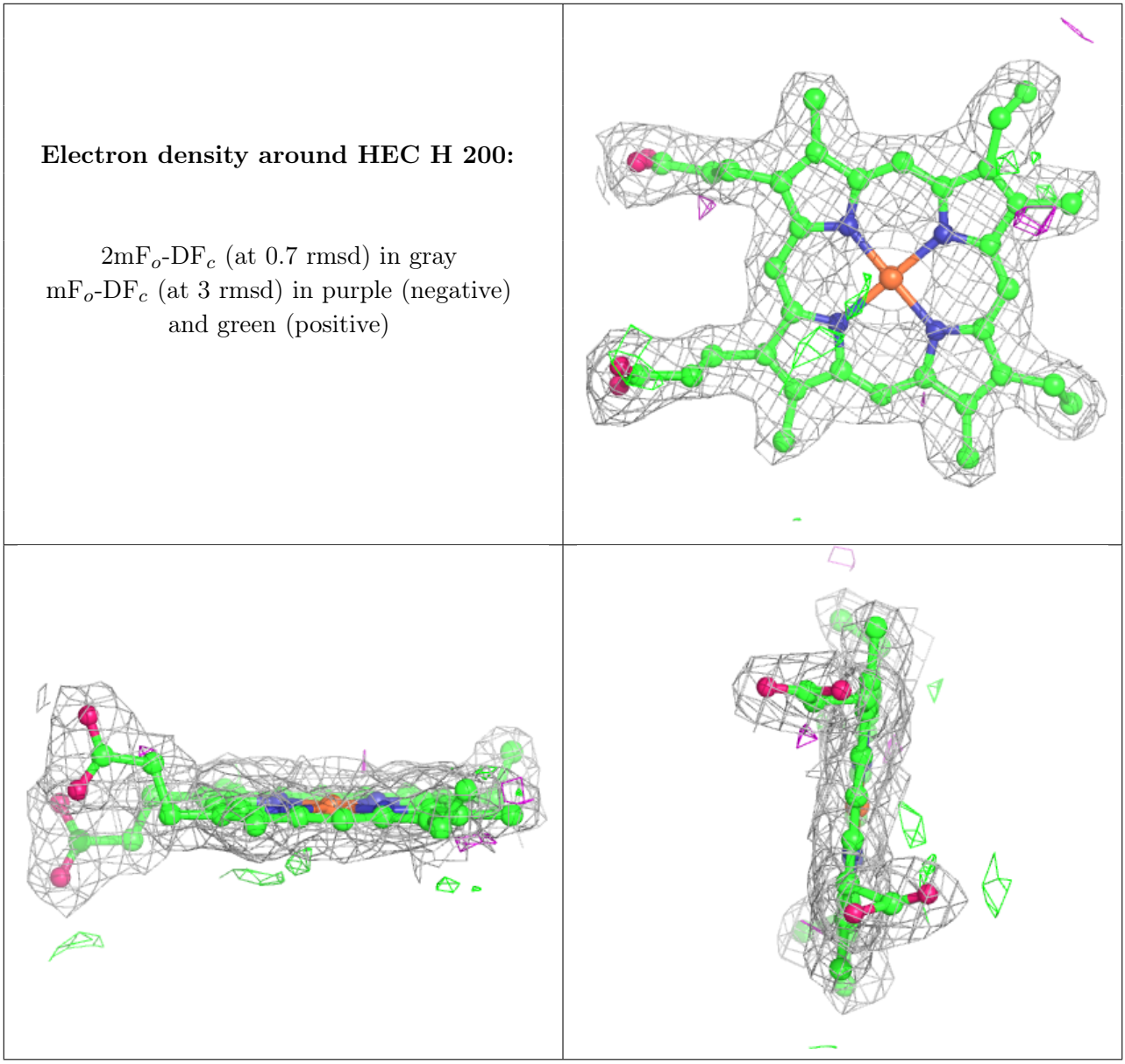
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	CU	K	107	1/1	1.00	0.09	18,18,18,18	0
6	CU	O	107	1/1	1.00	0.06	29,29,29,29	0

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.

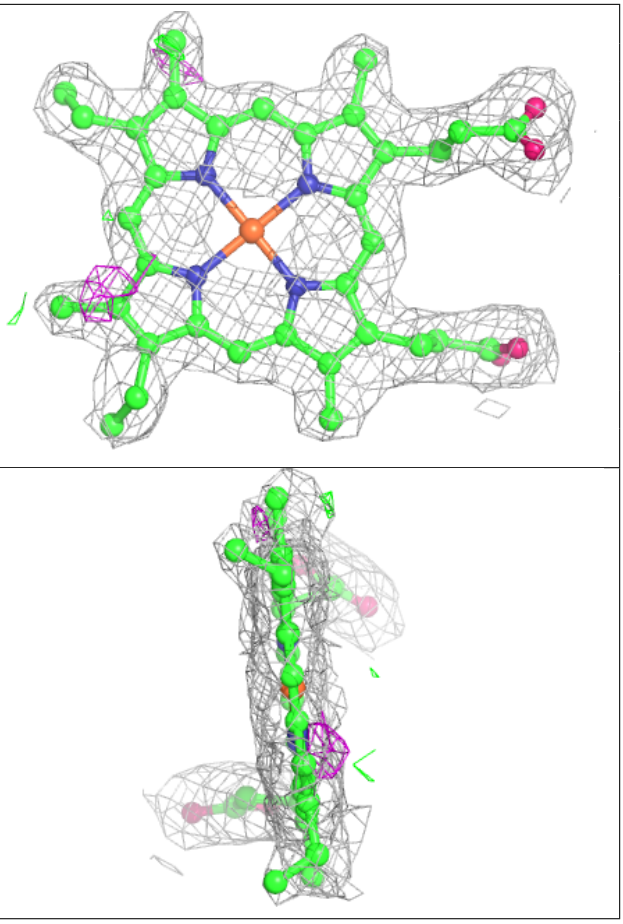
Electron density around HEC H 200:

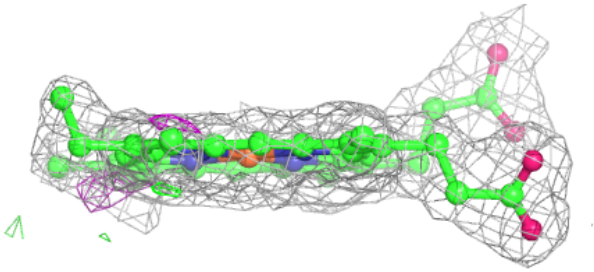
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around HEC L 200:

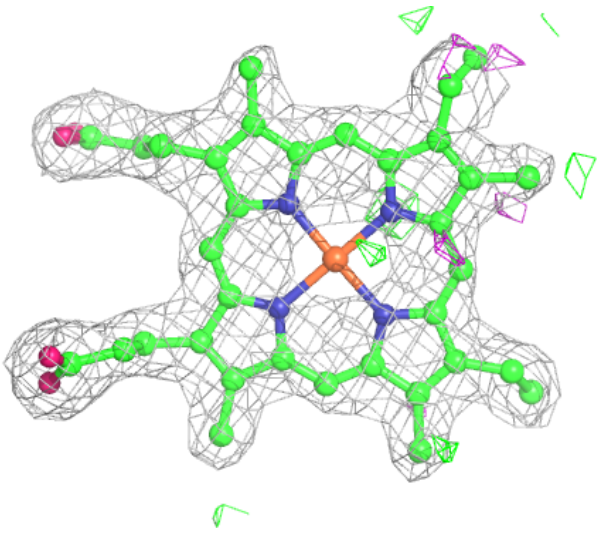
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

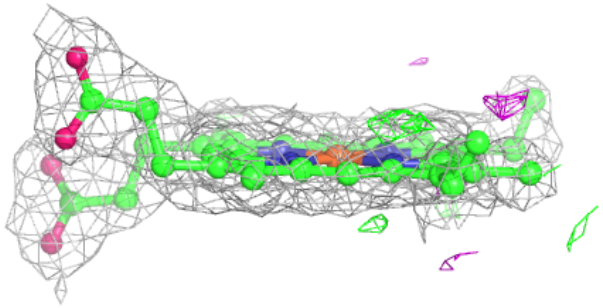




Electron density around HEC P 200:

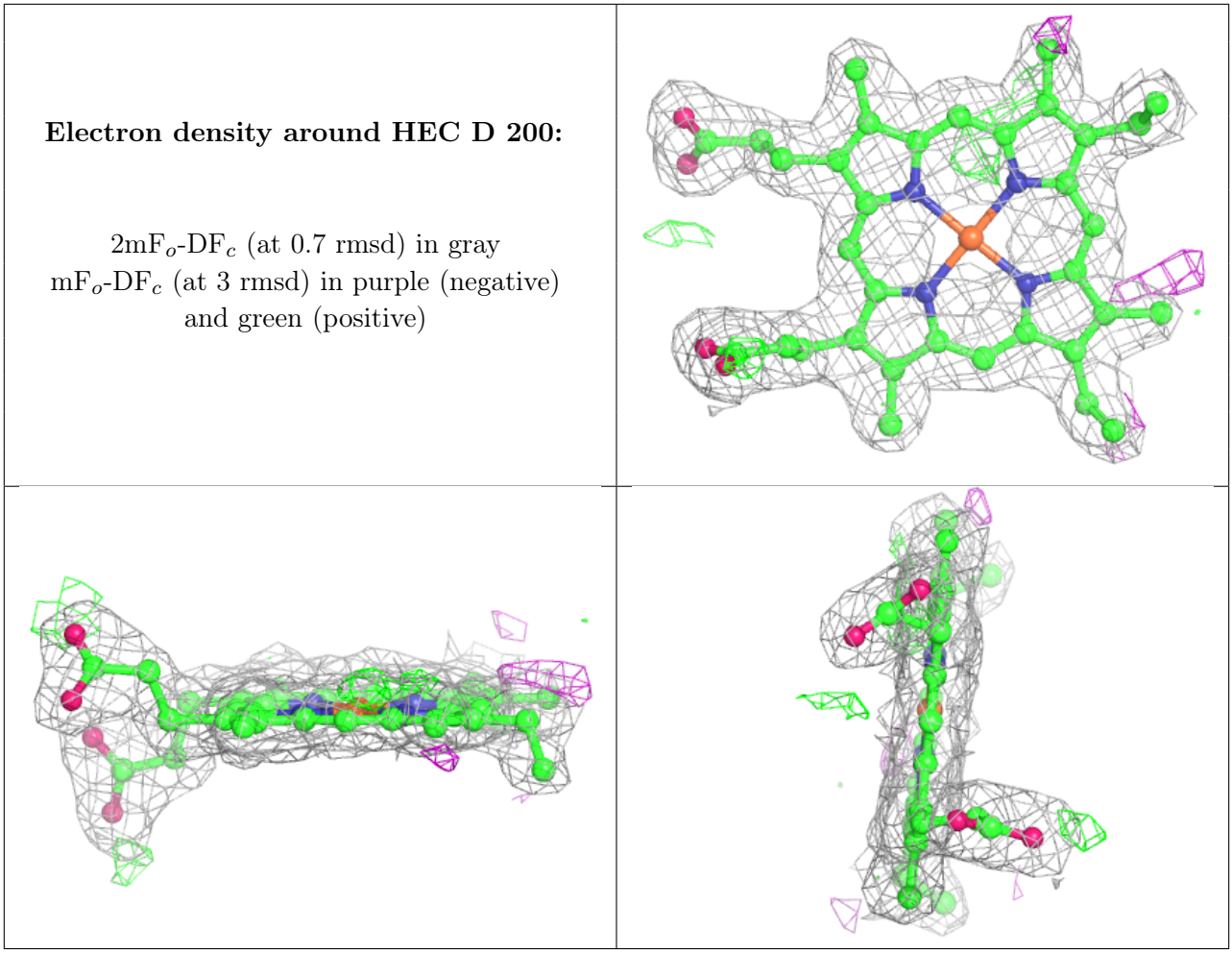
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





Electron density around HEC D 200:

$2mF_o$-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

There are no such residues in this entry.