



Full wwPDB NMR Structure Validation Report ⓘ

Mar 14, 2026 – 11:18 PM UTC

PDB ID : 1LM2 / pdb_00001lm2
Title : NMR structural characterization of the reduction of chromium(VI) to chromium(III) by cytochrome c7
Authors : Assfalg, M.; Bertini, I.; Bruschi, M.; Michel, C.; Turano, P.
Deposited on : 2002-04-30

This is a Full wwPDB NMR 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/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

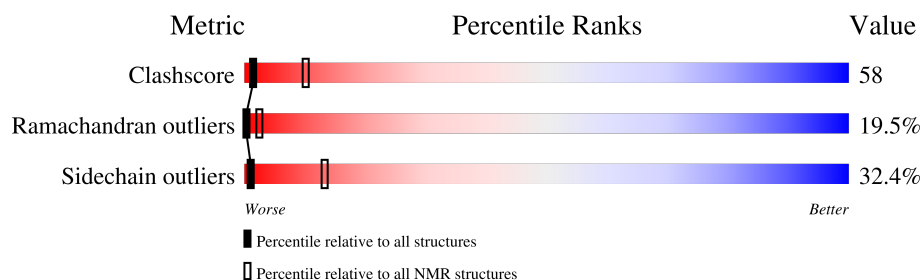
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

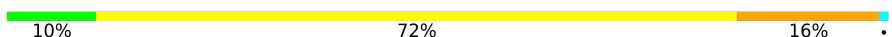
The overall completeness of chemical shifts assignment was not calculated.

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)	NMR archive (#Entries)
Clashscore	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	68	

2 Ensemble composition and analysis

This entry contains 35 models. Model 32 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:2-A:68 (67)	1.25	32

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 5 clusters and 2 single-model clusters were found.

Cluster number	Models
1	4, 5, 6, 7, 11, 13, 14, 15, 20, 29, 33, 35
2	12, 17, 19, 21, 24, 25, 32, 34
3	9, 10, 16, 26, 27
4	18, 22, 28, 31
5	1, 2, 3, 8
Single-model clusters	23; 30

- Molecule 1 is a protein called cytochrome c7.

Mol	Chain	Residues	Atoms						Trace
1	A	68	Total	C	H	N	O	S	0
			994	306	490	96	96	6	

- | Mol | Chain | Residues | Atoms | |
|-----|-------|----------|------------|---------|
| 2 | A | 1 | Total
1 | Cr
1 |

-
- The chemical structure of HEC (Hydroxyethylchlorin) is shown. It features a central iron atom (Fe) coordinated by four nitrogen atoms (N) in a porphyrin-like ring. The structure includes various side chains and a central hydroxyl group (OH). The atoms are labeled with green and red text, and the bonds are colored green and red.

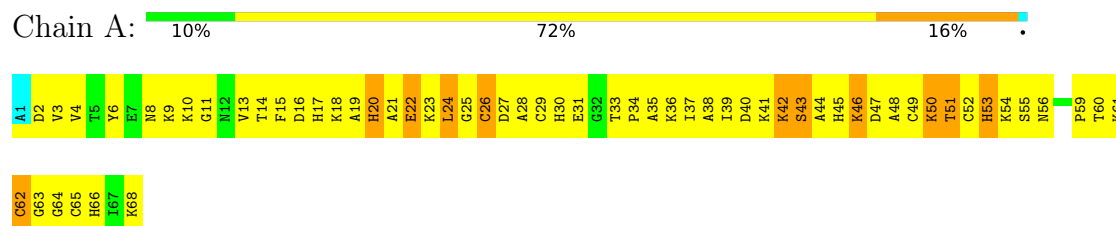
Mol	Chain	Residues	Atoms					
3	A	1	Total 75	C 34	Fe 1	H 32	N 4	O 4
3	A	1	Total 75	C 34	Fe 1	H 32	N 4	O 4
3	A	1	Total 75	C 34	Fe 1	H 32	N 4	O 4

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: cytochrome c7

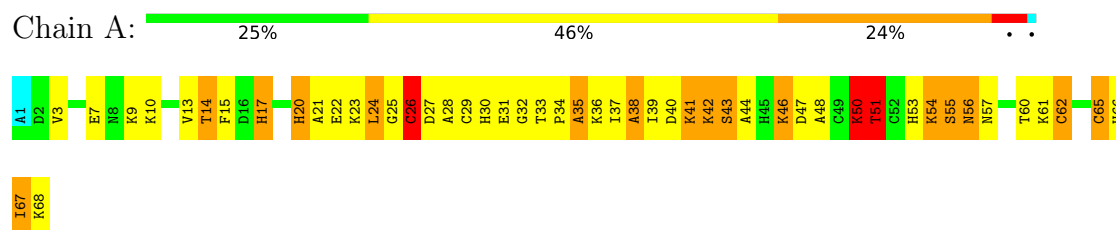


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

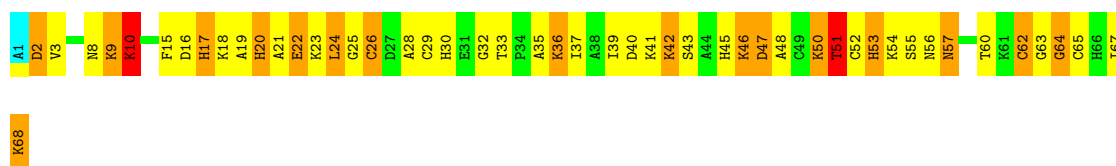
- Molecule 1: cytochrome c7



4.2.2 Score per residue for model 2

- Molecule 1: cytochrome c7





4.2.3 Score per residue for model 3

- Molecule 1: cytochrome c7

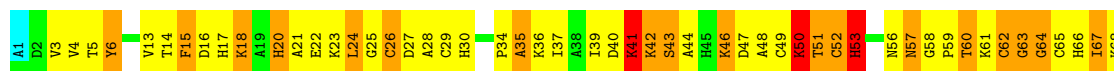
Chain A: 32% 40% 22% . .



4.2.4 Score per residue for model 4

- Molecule 1: cytochrome c7

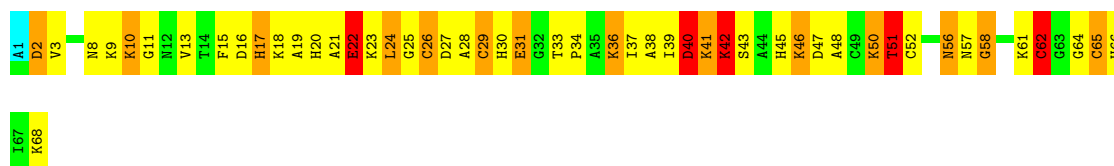
Chain A: 22% 46% 26% . .



4.2.5 Score per residue for model 5

- Molecule 1: cytochrome c7

Chain A: 25% 46% 21% 7% .



4.2.6 Score per residue for model 6

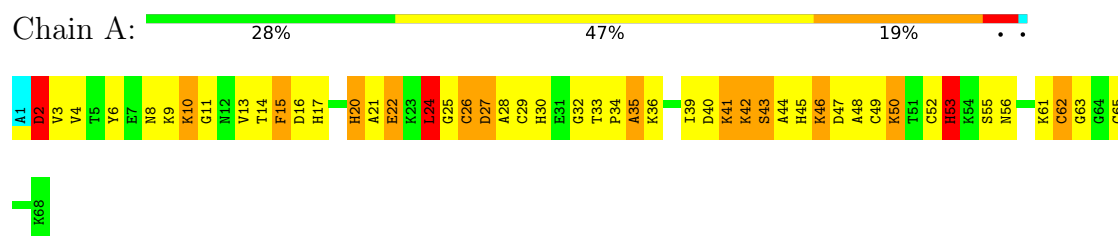
- Molecule 1: cytochrome c7

Chain A: 37% 40% 19% . .



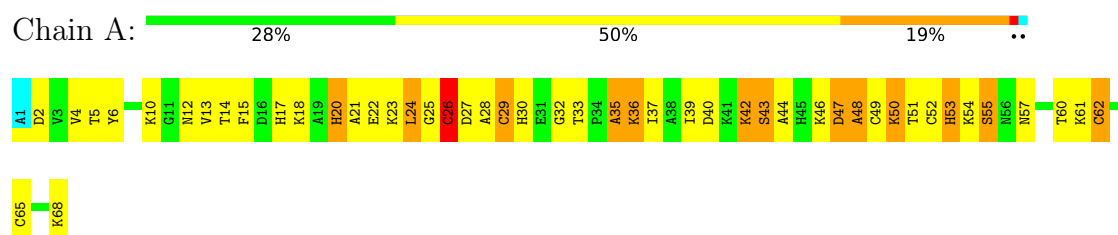
4.2.7 Score per residue for model 7

- Molecule 1: cytochrome c7



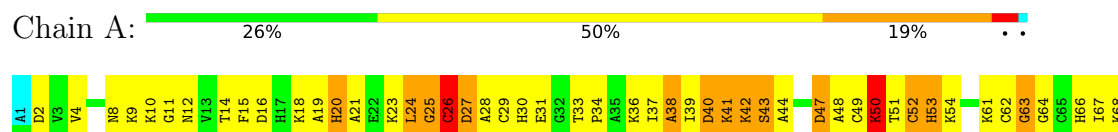
4.2.8 Score per residue for model 8

- Molecule 1: cytochrome c7



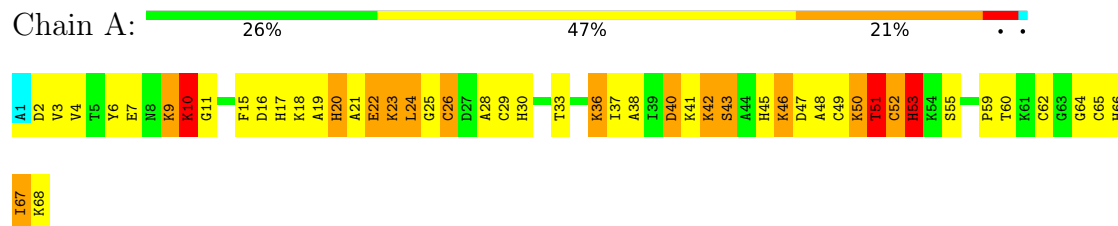
4.2.9 Score per residue for model 9

- Molecule 1: cytochrome c7



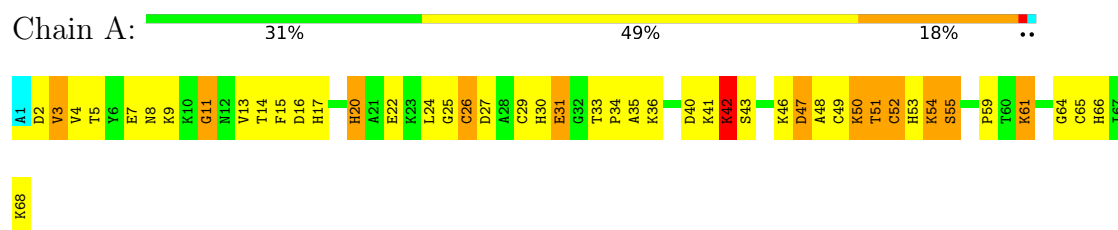
4.2.10 Score per residue for model 10

- Molecule 1: cytochrome c7



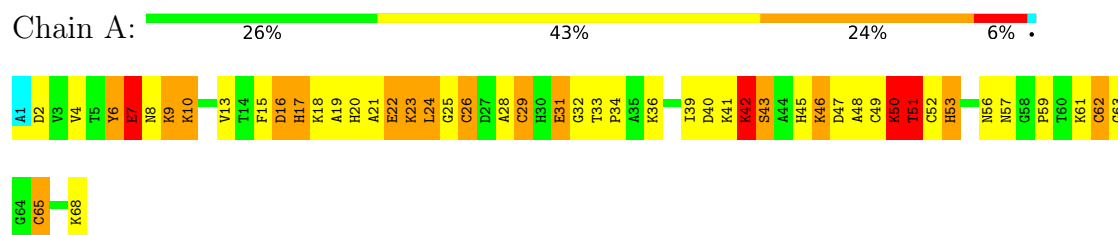
4.2.11 Score per residue for model 11

- Molecule 1: cytochrome c7



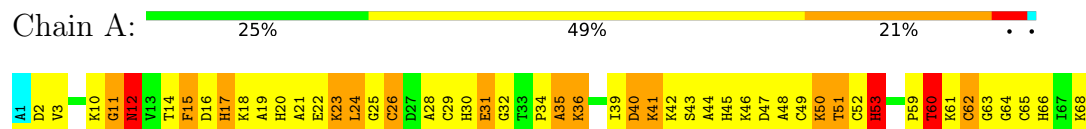
4.2.12 Score per residue for model 12

- Molecule 1: cytochrome c7



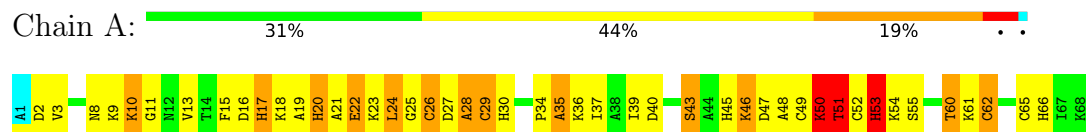
4.2.13 Score per residue for model 13

- Molecule 1: cytochrome c7



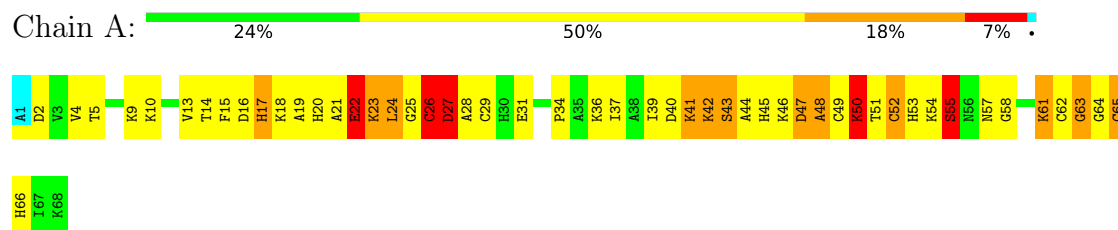
4.2.14 Score per residue for model 14

- Molecule 1: cytochrome c7



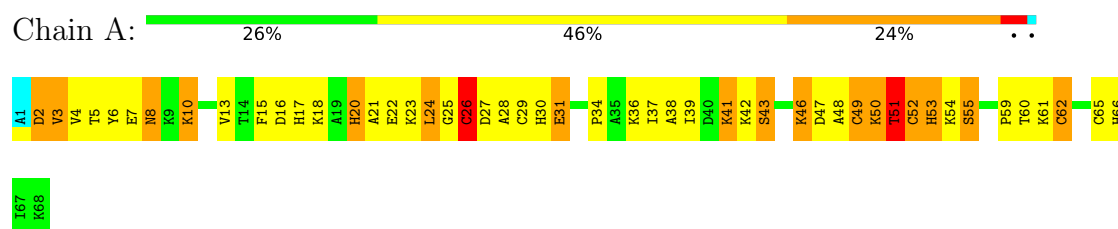
4.2.15 Score per residue for model 15

- Molecule 1: cytochrome c7



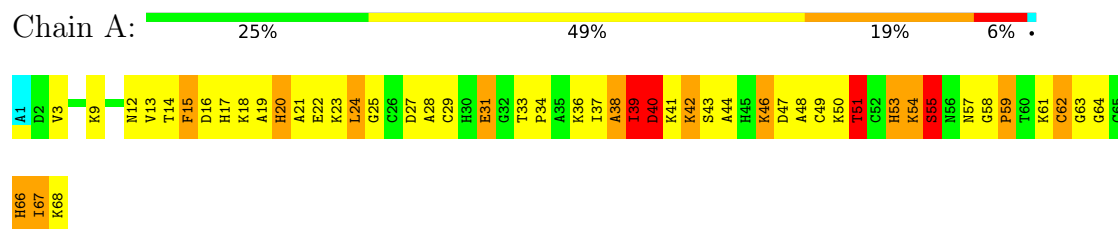
4.2.16 Score per residue for model 16

- Molecule 1: cytochrome c7



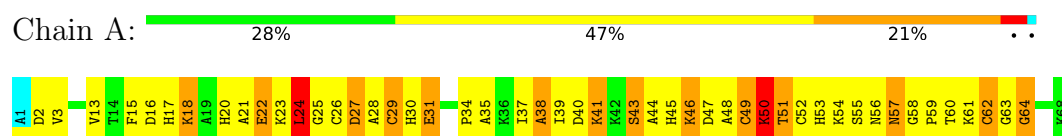
4.2.17 Score per residue for model 17

- Molecule 1: cytochrome c7



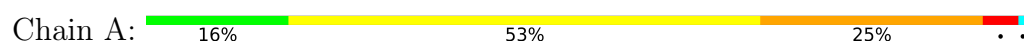
4.2.18 Score per residue for model 18

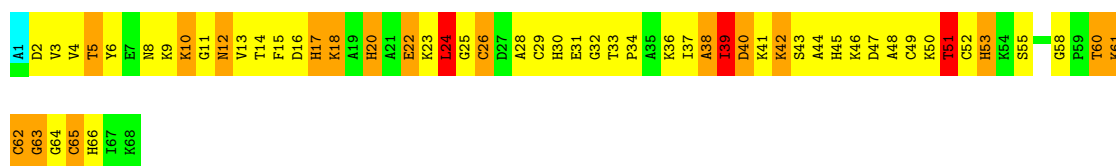
- Molecule 1: cytochrome c7



4.2.19 Score per residue for model 19

- Molecule 1: cytochrome c7

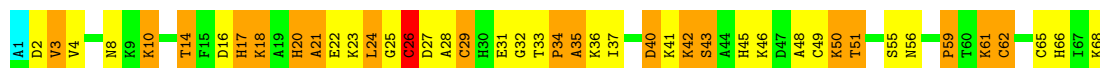




4.2.20 Score per residue for model 20

- Molecule 1: cytochrome c7

Chain A: 34% 35% 28% ..



4.2.21 Score per residue for model 21

- Molecule 1: cytochrome c7

Chain A: 32% 35% 25% 6% .



4.2.22 Score per residue for model 22

- Molecule 1: cytochrome c7

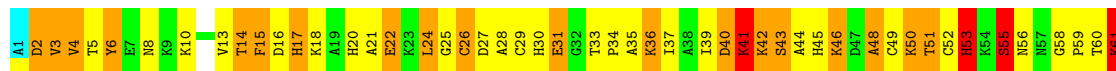
Chain A: 31% 37% 24% 7% .



4.2.23 Score per residue for model 23

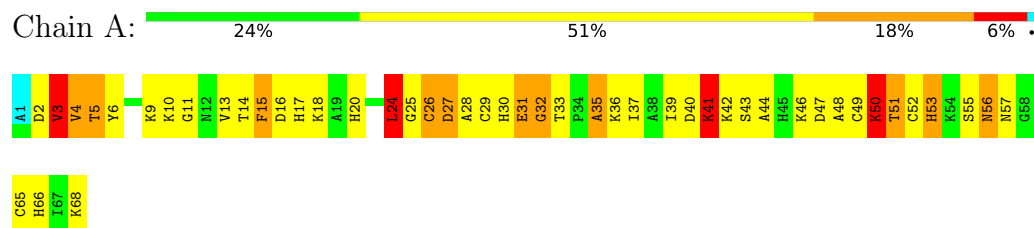
- Molecule 1: cytochrome c7

Chain A: 19% 44% 28% 7% .



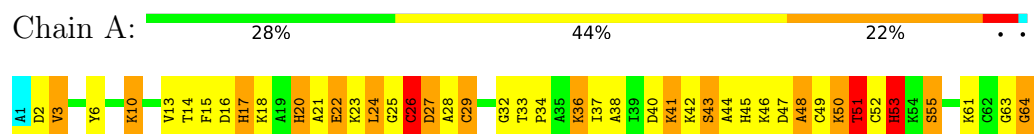
4.2.24 Score per residue for model 24

- Molecule 1: cytochrome c7



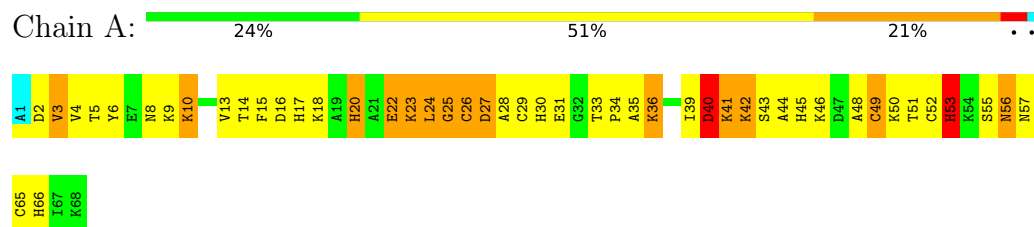
4.2.25 Score per residue for model 25

- Molecule 1: cytochrome c7



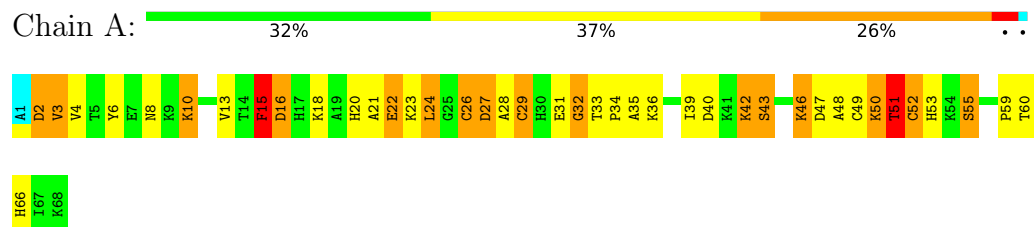
4.2.26 Score per residue for model 26

- Molecule 1: cytochrome c7



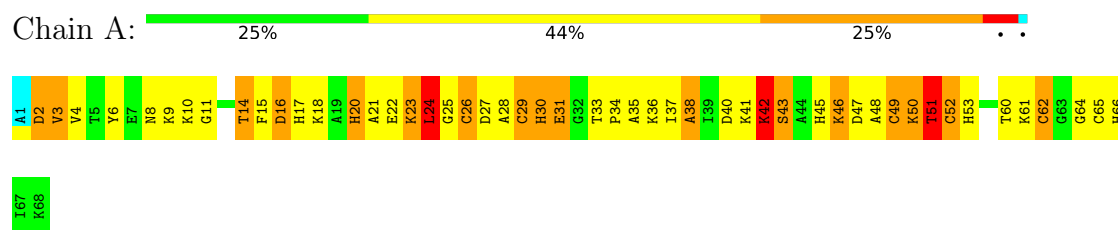
4.2.27 Score per residue for model 27

- Molecule 1: cytochrome c7



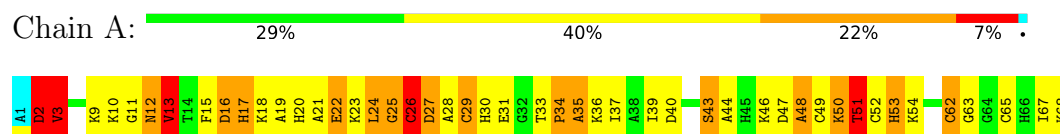
4.2.28 Score per residue for model 28

- Molecule 1: cytochrome c7



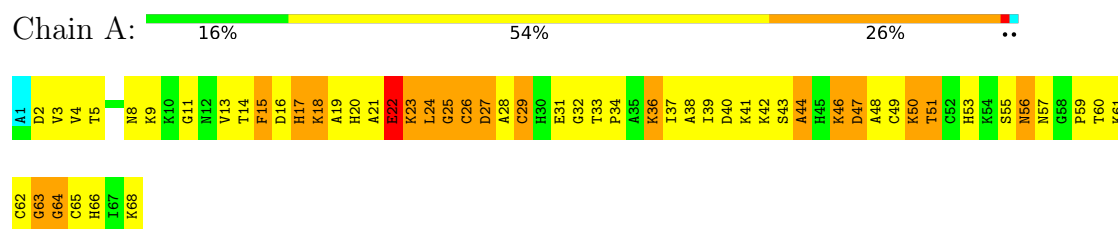
4.2.29 Score per residue for model 29

- Molecule 1: cytochrome c7



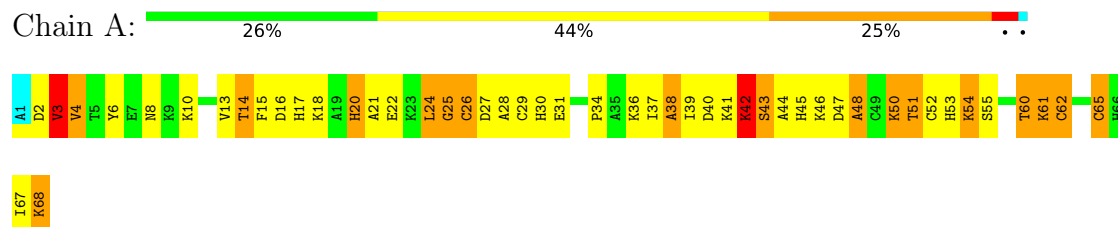
4.2.30 Score per residue for model 30

- Molecule 1: cytochrome c7



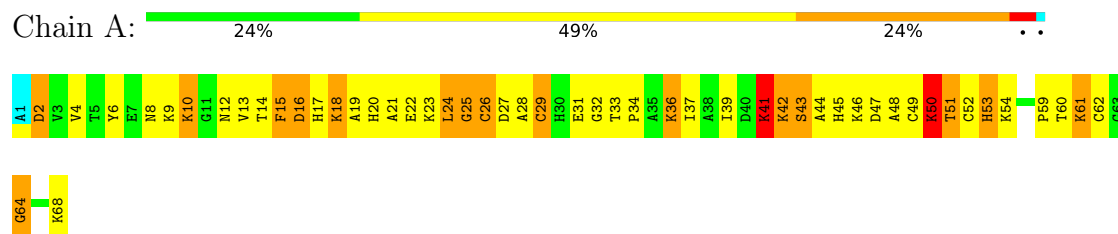
4.2.31 Score per residue for model 31

- Molecule 1: cytochrome c7



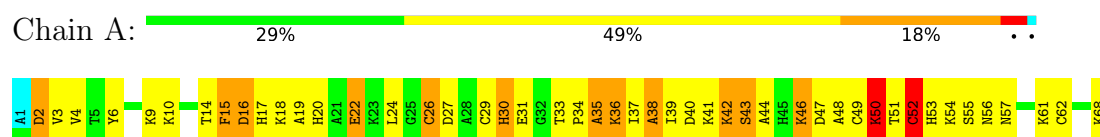
4.2.32 Score per residue for model 32 (medoid)

- Molecule 1: cytochrome c7



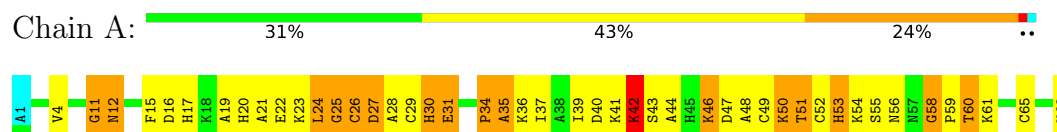
4.2.33 Score per residue for model 33

- Molecule 1: cytochrome c7



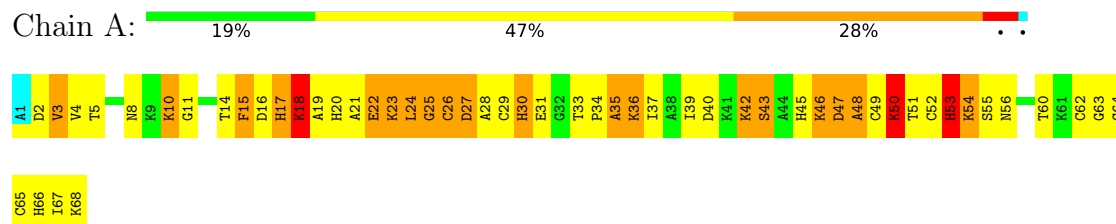
4.2.34 Score per residue for model 34

- Molecule 1: cytochrome c7



4.2.35 Score per residue for model 35

- Molecule 1: cytochrome c7



5 Refinement protocol and experimental data overview ⓘ

The models were refined using the following method: *simulated annealing in torsion angle space*.

Of the 500 calculated structures, 35 were deposited, based on the following criterion: *structures with best target function*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
DYANA	structure solution	1.5
DYANA	refinement	1.5

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

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

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	499	485	488	66±10
3	A	129	96	93	35±7
All	All	22015	20335	20356	2476

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 58.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:62:CYS:SG	3:A:158:HEC:HAB	1.78	1.17	9	27
1:A:49:CYS:SG	3:A:128:HEC:HAB	1.77	1.16	23	14
1:A:65:CYS:SG	3:A:158:HEC:HAC	1.64	1.32	15	20
1:A:26:CYS:SG	3:A:98:HEC:HAB	1.64	1.28	12	11
1:A:29:CYS:SG	3:A:98:HEC:HAC	1.60	1.34	17	25
1:A:52:CYS:SG	3:A:128:HEC:HAC	1.55	1.37	2	7
1:A:29:CYS:SG	3:A:98:HEC:CAC	1.39	2.11	2	35
1:A:49:CYS:SG	3:A:128:HEC:C3B	1.16	2.33	17	8
1:A:29:CYS:SG	3:A:98:HEC:C3C	1.14	2.35	27	35
1:A:65:CYS:SG	3:A:158:HEC:C3C	1.13	2.36	5	18
1:A:26:CYS:CB	3:A:98:HEC:HAB	1.07	1.79	12	9

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:15:PHE:CE1	3:A:128:HEC:HBB2	1.07	1.84	17	4
3:A:98:HEC:HBC3	3:A:98:HEC:HHD	1.06	1.26	20	6
1:A:29:CYS:SG	3:A:98:HEC:CBC	1.02	2.47	35	11
3:A:128:HEC:HMB2	3:A:158:HEC:HAC	0.99	1.33	8	5
1:A:37:ILE:HD12	3:A:98:HEC:C1D	0.96	1.91	28	18
1:A:52:CYS:SG	3:A:128:HEC:CBC	0.96	2.54	24	8
1:A:28:ALA:HB1	3:A:128:HEC:HBC2	0.95	1.38	27	14
1:A:26:CYS:CA	3:A:98:HEC:HAB	0.94	1.92	21	8
1:A:43:SER:O	1:A:48:ALA:HB3	0.94	1.63	23	29
1:A:62:CYS:HG	3:A:158:HEC:HAB	0.93	1.17	12	18
1:A:24:LEU:HD23	1:A:28:ALA:CB	0.93	1.92	27	7
1:A:49:CYS:HG	3:A:128:HEC:HAB	0.92	1.22	32	5
1:A:52:CYS:CB	3:A:128:HEC:CAC	0.92	2.48	3	5
1:A:62:CYS:SG	3:A:158:HEC:CBB	0.91	2.58	35	16
1:A:26:CYS:CB	3:A:98:HEC:CAB	0.91	2.47	21	9
3:A:158:HEC:HBB2	3:A:158:HEC:HHC	0.91	1.43	19	26
1:A:15:PHE:CZ	3:A:128:HEC:HBB3	0.91	2.01	8	6
1:A:24:LEU:HD22	3:A:98:HEC:HMC1	0.89	1.44	22	1
1:A:24:LEU:HD11	3:A:128:HEC:CHD	0.89	1.96	19	4
1:A:39:ILE:HG23	1:A:44:ALA:HB2	0.88	1.43	1	14
1:A:39:ILE:HD12	1:A:44:ALA:HB2	0.88	1.43	7	5
1:A:24:LEU:HD22	3:A:98:HEC:HMC3	0.87	1.45	2	19
1:A:44:ALA:HB1	3:A:158:HEC:CMD	0.87	1.97	23	6
1:A:29:CYS:SG	3:A:98:HEC:HBC2	0.86	2.09	20	6
1:A:16:ASP:O	3:A:98:HEC:HBC3	0.86	1.70	26	5
1:A:29:CYS:SG	3:A:98:HEC:HBC3	0.86	2.10	32	5
1:A:26:CYS:N	3:A:98:HEC:HAB	0.85	1.87	18	8
1:A:62:CYS:SG	3:A:158:HEC:C3B	0.85	2.64	17	6
1:A:65:CYS:SG	3:A:158:HEC:CBC	0.84	2.65	3	8
1:A:24:LEU:HD23	1:A:28:ALA:HB3	0.84	1.45	15	3
1:A:52:CYS:HG	3:A:128:HEC:HAC	0.83	1.29	24	3
1:A:15:PHE:CE1	3:A:128:HEC:HBB3	0.83	2.07	3	8
1:A:29:CYS:CB	3:A:98:HEC:HBC2	0.83	2.02	20	4
1:A:26:CYS:SG	3:A:98:HEC:CBB	0.82	2.67	27	8
1:A:37:ILE:HD12	3:A:98:HEC:C2D	0.82	2.05	35	18
1:A:44:ALA:HB1	3:A:158:HEC:HMD1	0.80	1.52	23	2
1:A:44:ALA:HB1	3:A:158:HEC:HMD2	0.80	1.52	30	3
1:A:24:LEU:HD23	1:A:28:ALA:HB1	0.79	1.54	27	3
1:A:39:ILE:CD1	3:A:128:HEC:HBB1	0.79	2.07	17	1
1:A:62:CYS:SG	3:A:158:HEC:HBB1	0.78	2.18	13	8
1:A:28:ALA:HB1	3:A:128:HEC:CBC	0.78	2.09	8	17

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:16:ASP:HB3	1:A:19:ALA:HB3	0.78	1.55	5	13
1:A:24:LEU:N	1:A:24:LEU:HD23	0.77	1.93	34	3
1:A:13:VAL:HG21	3:A:158:HEC:C2D	0.77	2.09	29	2
1:A:29:CYS:SG	3:A:98:HEC:HHD	0.76	2.20	35	2
1:A:49:CYS:SG	3:A:128:HEC:CBB	0.76	2.74	32	4
3:A:98:HEC:HHD	3:A:98:HEC:CBC	0.76	2.06	20	6
1:A:20:HIS:HB3	1:A:24:LEU:HD13	0.75	1.56	7	7
1:A:2:ASP:C	1:A:3:VAL:HG13	0.75	2.06	29	1
1:A:13:VAL:HG23	1:A:65:CYS:HB2	0.75	1.55	31	1
3:A:98:HEC:HBC1	3:A:128:HEC:C1C	0.75	2.11	19	2
1:A:24:LEU:CD2	3:A:98:HEC:HMC1	0.74	2.12	22	1
1:A:24:LEU:HD22	3:A:98:HEC:CMC	0.74	2.13	7	18
1:A:29:CYS:HG	3:A:98:HEC:HAC	0.74	0.90	5	2
3:A:98:HEC:HBC1	3:A:128:HEC:HHC	0.73	1.58	25	7
1:A:21:ALA:HB1	3:A:98:HEC:HBB2	0.73	1.58	27	4
1:A:2:ASP:O	1:A:3:VAL:HG23	0.73	1.84	13	2
1:A:43:SER:C	1:A:48:ALA:HB3	0.73	2.09	23	6
1:A:44:ALA:HA	1:A:48:ALA:HB3	0.73	1.61	26	3
3:A:98:HEC:HBC1	3:A:128:HEC:CHC	0.73	2.13	25	5
1:A:6:TYR:CD2	1:A:15:PHE:CE2	0.73	2.76	19	1
1:A:26:CYS:SG	3:A:98:HEC:C3B	0.72	2.77	34	5
1:A:20:HIS:CB	1:A:24:LEU:HD13	0.72	2.15	22	11
1:A:29:CYS:SG	3:A:98:HEC:C2C	0.72	2.76	31	15
1:A:3:VAL:HG12	1:A:3:VAL:O	0.72	1.84	28	6
1:A:15:PHE:CE2	3:A:128:HEC:HBB3	0.72	2.19	11	6
1:A:26:CYS:O	1:A:28:ALA:N	0.72	2.23	35	20
1:A:3:VAL:HG13	1:A:15:PHE:O	0.72	1.84	4	4
1:A:49:CYS:CB	3:A:128:HEC:HAB	0.71	2.14	8	3
1:A:54:LYS:HA	1:A:60:THR:HG21	0.71	1.62	8	1
1:A:49:CYS:HG	3:A:128:HEC:CAB	0.71	1.72	16	2
1:A:54:LYS:HG3	1:A:60:THR:HG21	0.71	1.62	1	1
1:A:29:CYS:HB3	3:A:98:HEC:HBC2	0.71	1.59	20	3
1:A:61:LYS:HA	3:A:158:HEC:HMC3	0.71	1.61	27	1
1:A:13:VAL:HG23	1:A:65:CYS:CB	0.71	2.15	31	1
1:A:24:LEU:CD1	3:A:128:HEC:HBC2	0.71	2.15	34	2
1:A:24:LEU:CD2	3:A:128:HEC:HBC2	0.71	2.15	12	13
1:A:4:VAL:HG11	3:A:98:HEC:CGD	0.71	2.15	15	1
1:A:15:PHE:CZ	3:A:128:HEC:CBB	0.70	2.75	3	4
1:A:3:VAL:HG23	1:A:15:PHE:O	0.70	1.86	21	5
1:A:15:PHE:CE1	3:A:128:HEC:CBB	0.70	2.75	32	5
1:A:29:CYS:SG	3:A:98:HEC:C4C	0.69	2.80	32	10

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:24:LEU:HD23	3:A:128:HEC:HBC2	0.69	1.65	14	13
1:A:34:PRO:O	1:A:35:ALA:HB3	0.69	1.86	29	2
1:A:39:ILE:CD1	1:A:44:ALA:HB2	0.68	2.18	7	4
1:A:14:THR:HG23	1:A:14:THR:O	0.68	1.87	4	2
1:A:17:HIS:CE1	3:A:98:HEC:C4B	0.68	2.76	18	5
1:A:24:LEU:N	1:A:24:LEU:CD2	0.68	2.56	34	2
1:A:66:HIS:CE1	3:A:158:HEC:C1B	0.67	2.77	3	3
1:A:13:VAL:HG11	3:A:158:HEC:O1D	0.67	1.89	17	1
1:A:4:VAL:CG1	1:A:6:TYR:CE1	0.67	2.77	28	1
1:A:39:ILE:HD12	3:A:128:HEC:HBB1	0.67	1.66	17	1
1:A:17:HIS:CE1	3:A:98:HEC:NB	0.67	2.63	18	9
1:A:6:TYR:CD1	1:A:15:PHE:CE1	0.67	2.83	16	2
1:A:20:HIS:HB3	3:A:98:HEC:HMC3	0.67	1.64	26	5
1:A:2:ASP:C	1:A:3:VAL:HG23	0.66	2.15	20	1
1:A:15:PHE:CZ	1:A:39:ILE:HG21	0.66	2.25	31	5
1:A:6:TYR:CD1	3:A:158:HEC:CGD	0.66	2.79	4	1
1:A:24:LEU:HB3	1:A:28:ALA:HB3	0.66	1.66	23	12
1:A:2:ASP:O	1:A:3:VAL:HG22	0.66	1.89	29	1
1:A:17:HIS:CE1	3:A:98:HEC:CHC	0.66	2.79	26	3
3:A:98:HEC:HBC1	3:A:128:HEC:HMC1	0.66	1.66	5	3
1:A:13:VAL:HG21	3:A:158:HEC:HMD2	0.66	1.67	1	6
1:A:15:PHE:CD1	3:A:128:HEC:HBB3	0.66	2.26	14	5
1:A:24:LEU:CD2	3:A:98:HEC:HBC2	0.66	2.21	32	2
3:A:98:HEC:HBC1	3:A:128:HEC:CMC	0.65	2.20	30	5
1:A:15:PHE:CZ	3:A:128:HEC:HBB2	0.65	2.25	17	3
1:A:16:ASP:CG	1:A:19:ALA:HB3	0.65	2.15	13	2
1:A:13:VAL:HG22	1:A:13:VAL:O	0.65	1.92	29	4
1:A:4:VAL:O	1:A:14:THR:HG23	0.65	1.90	26	2
1:A:20:HIS:CE1	3:A:128:HEC:C4D	0.65	2.80	15	21
1:A:16:ASP:CB	1:A:19:ALA:HB3	0.65	2.22	13	4
1:A:26:CYS:CA	3:A:98:HEC:CAB	0.65	2.74	18	6
1:A:37:ILE:HD12	3:A:98:HEC:CHD	0.65	2.21	28	2
1:A:49:CYS:O	1:A:50:LYS:C	0.64	2.39	24	19
1:A:13:VAL:HG21	3:A:158:HEC:CMD	0.64	2.22	29	1
1:A:24:LEU:HD21	3:A:128:HEC:CAC	0.64	2.22	21	5
1:A:24:LEU:HD22	1:A:28:ALA:HB1	0.64	1.69	18	2
1:A:66:HIS:CE1	3:A:158:HEC:NA	0.63	2.66	9	11
1:A:29:CYS:SG	3:A:98:HEC:CHD	0.63	2.85	35	3
1:A:51:THR:HG22	1:A:52:CYS:N	0.63	2.06	28	6
1:A:52:CYS:SG	3:A:128:HEC:HBC1	0.63	2.33	4	6
1:A:2:ASP:HB3	1:A:17:HIS:CB	0.63	2.24	35	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:14:THR:O	1:A:15:PHE:CD2	0.62	2.52	31	1
1:A:56:ASN:CG	3:A:128:HEC:HMD3	0.62	2.19	34	1
3:A:158:HEC:HHC	3:A:158:HEC:CBB	0.62	2.23	30	12
1:A:60:THR:HG22	1:A:60:THR:O	0.62	1.93	24	1
1:A:67:ILE:HG23	1:A:68:LYS:N	0.62	2.09	23	1
1:A:39:ILE:HG23	1:A:44:ALA:CB	0.62	2.24	33	5
1:A:65:CYS:HG	3:A:158:HEC:CAC	0.62	2.08	12	1
1:A:2:ASP:CB	1:A:18:LYS:N	0.62	2.63	35	1
1:A:45:HIS:CE1	3:A:158:HEC:NB	0.62	2.68	13	8
3:A:128:HEC:HBB3	3:A:158:HEC:CMD	0.62	2.25	9	1
1:A:52:CYS:O	1:A:53:HIS:CD2	0.62	2.53	8	8
1:A:13:VAL:CG2	3:A:158:HEC:HMD2	0.61	2.25	29	2
1:A:21:ALA:HB1	3:A:98:HEC:CBB	0.61	2.25	31	6
3:A:98:HEC:HBC3	3:A:98:HEC:CHD	0.61	2.15	29	6
1:A:47:ASP:O	1:A:48:ALA:C	0.61	2.42	35	30
1:A:2:ASP:HB3	1:A:18:LYS:N	0.61	2.10	35	1
1:A:13:VAL:O	1:A:13:VAL:HG13	0.61	1.93	30	3
1:A:16:ASP:CB	1:A:20:HIS:CG	0.61	2.84	16	5
1:A:50:LYS:O	1:A:51:THR:C	0.61	2.44	25	13
1:A:66:HIS:CE1	3:A:158:HEC:CHB	0.60	2.83	3	2
1:A:26:CYS:CB	3:A:98:HEC:C3B	0.60	2.79	28	8
1:A:23:LYS:C	1:A:24:LEU:HD23	0.60	2.20	34	2
1:A:4:VAL:O	1:A:4:VAL:HG12	0.60	1.97	23	7
1:A:16:ASP:OD1	1:A:20:HIS:CE1	0.60	2.54	22	3
1:A:15:PHE:CE2	1:A:39:ILE:HG21	0.60	2.32	18	3
1:A:15:PHE:CE2	3:A:128:HEC:CBB	0.60	2.84	6	3
1:A:13:VAL:CG2	3:A:128:HEC:CMB	0.60	2.79	19	7
1:A:15:PHE:CE2	3:A:98:HEC:O2D	0.60	2.54	19	1
1:A:39:ILE:HG22	3:A:158:HEC:O2D	0.60	1.97	8	1
1:A:44:ALA:HB1	3:A:158:HEC:C2D	0.60	2.27	19	1
1:A:62:CYS:HG	3:A:158:HEC:CAB	0.60	2.07	26	5
1:A:15:PHE:CE1	3:A:128:HEC:HMB3	0.59	2.31	22	1
1:A:62:CYS:O	1:A:63:GLY:C	0.59	2.44	19	2
3:A:98:HEC:CBC	3:A:98:HEC:CHD	0.59	2.77	20	6
1:A:3:VAL:HG22	1:A:16:ASP:OD1	0.59	1.97	13	1
1:A:24:LEU:HG	3:A:128:HEC:HBC2	0.59	1.73	2	5
1:A:24:LEU:HD22	3:A:128:HEC:HBC2	0.59	1.75	21	3
1:A:24:LEU:CD1	3:A:128:HEC:CBC	0.59	2.81	34	1
1:A:34:PRO:O	1:A:35:ALA:CB	0.59	2.50	29	4
1:A:34:PRO:O	1:A:35:ALA:HB2	0.59	1.98	13	11
3:A:128:HEC:CMB	3:A:158:HEC:HAC	0.59	2.21	8	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:61:LYS:O	1:A:63:GLY:N	0.58	2.36	19	6
1:A:5:THR:OG1	1:A:14:THR:HG23	0.58	1.97	15	2
1:A:60:THR:O	1:A:61:LYS:O	0.58	2.20	27	2
1:A:49:CYS:O	1:A:51:THR:N	0.58	2.36	15	14
1:A:15:PHE:CZ	3:A:98:HEC:HMD2	0.58	2.33	11	1
3:A:128:HEC:HMB2	3:A:158:HEC:CAC	0.58	2.21	8	2
1:A:16:ASP:O	1:A:20:HIS:CG	0.58	2.56	35	1
1:A:3:VAL:O	1:A:4:VAL:HG23	0.58	1.98	23	1
1:A:65:CYS:HG	3:A:158:HEC:HAC	0.58	1.52	12	4
1:A:24:LEU:HD12	1:A:24:LEU:N	0.58	2.13	35	6
1:A:53:HIS:CE1	3:A:128:HEC:C1B	0.58	2.87	16	10
1:A:26:CYS:SG	3:A:98:HEC:CMB	0.58	2.92	28	5
1:A:26:CYS:O	1:A:29:CYS:N	0.58	2.36	31	12
1:A:24:LEU:HD22	3:A:98:HEC:HBC2	0.58	1.73	32	3
1:A:43:SER:HA	1:A:48:ALA:HB2	0.58	1.75	30	1
1:A:37:ILE:O	1:A:38:ALA:C	0.57	2.45	18	3
1:A:15:PHE:CD2	3:A:128:HEC:HBB2	0.57	2.34	9	1
1:A:13:VAL:O	1:A:13:VAL:HG23	0.57	1.99	4	1
1:A:66:HIS:CE1	3:A:158:HEC:C1D	0.57	2.88	17	1
1:A:43:SER:C	1:A:48:ALA:CB	0.57	2.78	30	2
1:A:2:ASP:O	1:A:3:VAL:HG12	0.57	1.99	24	1
1:A:14:THR:O	1:A:14:THR:HG22	0.57	2.00	9	5
1:A:38:ALA:O	1:A:39:ILE:HB	0.57	1.99	19	1
1:A:60:THR:O	1:A:61:LYS:CG	0.57	2.52	27	1
1:A:24:LEU:CD2	3:A:128:HEC:CBC	0.57	2.82	11	3
1:A:10:LYS:O	1:A:66:HIS:CE1	0.57	2.57	3	1
1:A:34:PRO:O	3:A:98:HEC:C3A	0.57	2.53	3	1
1:A:4:VAL:HG11	1:A:6:TYR:CE1	0.57	2.34	28	4
1:A:16:ASP:OD2	1:A:20:HIS:CE1	0.57	2.58	32	2
1:A:46:LYS:O	1:A:47:ASP:C	0.57	2.48	35	16
1:A:30:HIS:CE1	3:A:98:HEC:NA	0.57	2.72	2	2
1:A:20:HIS:CE1	3:A:128:HEC:CHA	0.57	2.88	13	8
1:A:26:CYS:O	1:A:27:ASP:C	0.57	2.48	22	18
1:A:13:VAL:CG2	3:A:128:HEC:HMB3	0.57	2.29	19	1
1:A:49:CYS:O	1:A:51:THR:HG23	0.57	2.00	35	1
1:A:6:TYR:CD1	3:A:158:HEC:O1D	0.56	2.58	12	3
1:A:24:LEU:HD12	3:A:98:HEC:CBC	0.56	2.30	34	1
1:A:53:HIS:CE1	3:A:128:HEC:NB	0.56	2.74	15	3
1:A:17:HIS:O	1:A:21:ALA:HB2	0.56	2.00	6	4
1:A:17:HIS:CD2	3:A:98:HEC:NC	0.56	2.73	6	2
1:A:30:HIS:CG	1:A:34:PRO:HB3	0.56	2.35	34	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:2:ASP:C	1:A:3:VAL:CG1	0.56	2.76	29	1
1:A:25:GLY:O	1:A:27:ASP:N	0.56	2.38	9	17
1:A:40:ASP:O	1:A:41:LYS:C	0.56	2.48	15	7
1:A:25:GLY:O	3:A:98:HEC:HMC2	0.56	2.00	28	2
1:A:17:HIS:O	1:A:21:ALA:CB	0.56	2.54	35	6
1:A:20:HIS:O	1:A:24:LEU:HD13	0.56	2.01	10	1
1:A:24:LEU:HD11	3:A:128:HEC:C3C	0.56	2.31	24	2
1:A:44:ALA:N	1:A:48:ALA:HB3	0.56	2.16	30	1
3:A:158:HEC:HBC3	3:A:158:HEC:HMC1	0.56	1.78	29	6
1:A:10:LYS:HD2	3:A:158:HEC:HMA1	0.55	1.78	1	1
1:A:65:CYS:SG	3:A:158:HEC:C4C	0.55	2.94	28	6
1:A:20:HIS:CE1	3:A:128:HEC:ND	0.55	2.74	15	9
1:A:59:PRO:O	1:A:60:THR:C	0.55	2.49	10	4
1:A:20:HIS:HD1	3:A:98:HEC:HBC3	0.55	1.61	11	1
1:A:24:LEU:HD21	3:A:128:HEC:C3C	0.55	2.31	8	15
1:A:6:TYR:CD2	3:A:158:HEC:CGD	0.55	2.89	16	1
1:A:2:ASP:O	1:A:3:VAL:CB	0.55	2.55	24	2
1:A:37:ILE:HG22	1:A:37:ILE:O	0.55	2.02	1	1
1:A:16:ASP:CB	1:A:20:HIS:ND1	0.55	2.70	20	5
1:A:37:ILE:CD1	3:A:98:HEC:C1D	0.55	2.85	24	3
1:A:24:LEU:CD2	3:A:128:HEC:CAC	0.55	2.84	11	1
1:A:39:ILE:HG13	3:A:98:HEC:HMD1	0.55	1.78	12	3
1:A:20:HIS:CD2	3:A:128:HEC:ND	0.55	2.74	34	3
1:A:14:THR:O	1:A:14:THR:CG2	0.55	2.54	4	2
3:A:128:HEC:HMC3	3:A:128:HEC:HBC3	0.55	1.79	14	29
1:A:34:PRO:O	3:A:98:HEC:C4A	0.55	2.55	3	1
1:A:43:SER:O	1:A:46:LYS:N	0.55	2.37	31	4
1:A:16:ASP:OD1	3:A:128:HEC:C4A	0.55	2.55	18	1
1:A:6:TYR:CD2	1:A:15:PHE:CZ	0.55	2.94	26	1
1:A:66:HIS:CE1	3:A:158:HEC:ND	0.55	2.74	17	1
1:A:51:THR:O	1:A:52:CYS:C	0.54	2.50	8	3
1:A:45:HIS:CD2	3:A:158:HEC:NC	0.54	2.75	23	2
1:A:24:LEU:CD1	3:A:128:HEC:CAC	0.54	2.85	34	1
1:A:62:CYS:O	1:A:64:GLY:N	0.54	2.40	19	6
1:A:16:ASP:CB	1:A:20:HIS:CE1	0.54	2.91	18	3
1:A:24:LEU:HD12	3:A:98:HEC:HBC2	0.54	1.77	34	1
1:A:41:LYS:O	1:A:42:LYS:CB	0.54	2.54	15	6
1:A:67:ILE:O	1:A:67:ILE:HG23	0.54	2.01	17	3
1:A:21:ALA:CB	3:A:98:HEC:HBB2	0.54	2.31	31	3
1:A:15:PHE:CE1	3:A:98:HEC:HBC2	0.54	2.37	11	1
1:A:15:PHE:CE1	3:A:158:HEC:HMD2	0.54	2.37	28	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:52:CYS:O	1:A:53:HIS:CB	0.54	2.56	9	11
1:A:38:ALA:O	1:A:39:ILE:CB	0.54	2.56	19	1
1:A:17:HIS:CE1	3:A:98:HEC:C4C	0.54	2.91	35	1
1:A:20:HIS:O	1:A:24:LEU:N	0.54	2.41	16	10
1:A:3:VAL:O	1:A:3:VAL:CG1	0.54	2.55	28	3
3:A:158:HEC:HBC2	3:A:158:HEC:HMC3	0.54	1.79	1	1
1:A:34:PRO:HB2	3:A:98:HEC:CHB	0.54	2.32	3	16
1:A:65:CYS:SG	3:A:158:HEC:C2C	0.54	2.96	28	6
1:A:39:ILE:HD13	1:A:43:SER:O	0.53	2.03	30	1
1:A:65:CYS:SG	3:A:128:HEC:HMB2	0.53	2.43	25	2
1:A:40:ASP:O	1:A:42:LYS:N	0.53	2.39	19	10
1:A:16:ASP:HB2	1:A:20:HIS:CE1	0.53	2.38	26	8
1:A:65:CYS:SG	3:A:128:HEC:HMB3	0.53	2.43	7	1
1:A:20:HIS:O	1:A:21:ALA:C	0.53	2.52	32	23
1:A:15:PHE:CZ	3:A:98:HEC:HBC2	0.53	2.38	11	3
1:A:15:PHE:HE1	3:A:128:HEC:HMB3	0.53	1.63	22	1
1:A:25:GLY:O	1:A:26:CYS:CB	0.53	2.55	14	4
1:A:19:ALA:O	1:A:22:GLU:CG	0.53	2.57	30	5
1:A:53:HIS:CD2	3:A:128:HEC:NC	0.53	2.77	19	2
1:A:37:ILE:HG23	1:A:38:ALA:N	0.53	2.17	21	1
1:A:25:GLY:O	1:A:26:CYS:SG	0.52	2.67	14	3
1:A:59:PRO:O	1:A:60:THR:CB	0.52	2.57	30	2
1:A:62:CYS:O	3:A:158:HEC:HMC2	0.52	2.04	7	2
1:A:29:CYS:CB	1:A:37:ILE:CD1	0.52	2.87	33	1
1:A:26:CYS:C	1:A:28:ALA:N	0.52	2.65	25	21
1:A:28:ALA:HB1	3:A:128:HEC:HBC1	0.52	1.81	15	3
1:A:16:ASP:HB2	1:A:20:HIS:CG	0.52	2.39	16	16
3:A:158:HEC:HMC3	3:A:158:HEC:CBC	0.52	2.35	23	2
1:A:39:ILE:O	1:A:40:ASP:CB	0.52	2.58	19	4
3:A:98:HEC:HBC1	3:A:128:HEC:C2C	0.52	2.34	34	3
1:A:16:ASP:HB3	1:A:20:HIS:CG	0.52	2.40	16	2
1:A:13:VAL:HG21	3:A:158:HEC:CHD	0.52	2.35	26	1
1:A:21:ALA:O	1:A:22:GLU:C	0.52	2.53	13	11
1:A:30:HIS:CE1	3:A:98:HEC:ND	0.52	2.78	3	2
1:A:53:HIS:CB	1:A:60:THR:HG23	0.52	2.34	1	1
1:A:24:LEU:HD11	3:A:128:HEC:CAC	0.52	2.35	34	2
1:A:16:ASP:O	1:A:17:HIS:C	0.52	2.52	22	1
1:A:17:HIS:CE1	3:A:98:HEC:CHD	0.52	2.93	35	1
1:A:23:LYS:O	1:A:24:LEU:C	0.52	2.52	16	5
1:A:35:ALA:O	3:A:98:HEC:CAA	0.52	2.57	29	5
1:A:20:HIS:CD2	3:A:98:HEC:HBC3	0.52	2.39	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:25:GLY:O	3:A:98:HEC:CMC	0.52	2.58	28	2
1:A:17:HIS:O	1:A:21:ALA:N	0.52	2.40	35	1
3:A:158:HEC:O1D	3:A:158:HEC:C3D	0.52	2.58	2	2
1:A:36:LYS:CD	1:A:36:LYS:O	0.52	2.58	25	5
1:A:15:PHE:CZ	3:A:158:HEC:HMD2	0.51	2.40	1	2
1:A:15:PHE:CD2	3:A:128:HEC:HBB3	0.51	2.40	25	4
1:A:24:LEU:CD2	3:A:98:HEC:CAC	0.51	2.88	2	2
1:A:43:SER:O	1:A:48:ALA:CB	0.51	2.59	10	23
3:A:128:HEC:HMC3	3:A:128:HEC:CBC	0.51	2.35	15	6
1:A:19:ALA:HB1	3:A:128:HEC:O2D	0.51	2.06	35	1
1:A:30:HIS:CD2	1:A:34:PRO:HB3	0.51	2.40	34	5
1:A:6:TYR:CE2	1:A:15:PHE:CE2	0.51	2.98	19	2
1:A:60:THR:C	1:A:61:LYS:CG	0.51	2.83	23	1
1:A:25:GLY:C	1:A:26:CYS:SG	0.51	2.94	35	18
1:A:4:VAL:CG1	1:A:6:TYR:CE2	0.51	2.93	33	2
1:A:15:PHE:CZ	3:A:158:HEC:CMD	0.51	2.93	16	1
1:A:26:CYS:HB3	3:A:98:HEC:C3B	0.51	2.36	15	5
1:A:13:VAL:HG11	3:A:158:HEC:HBD2	0.51	1.82	23	4
1:A:39:ILE:HD13	1:A:44:ALA:HB2	0.51	1.82	4	1
1:A:28:ALA:O	3:A:128:HEC:CBC	0.51	2.59	23	2
1:A:49:CYS:SG	3:A:128:HEC:HBB1	0.51	2.44	32	1
1:A:56:ASN:O	1:A:58:GLY:N	0.51	2.44	34	1
1:A:65:CYS:CB	3:A:158:HEC:CAC	0.51	2.89	19	3
1:A:39:ILE:C	1:A:40:ASP:CG	0.51	2.79	21	1
1:A:63:GLY:O	1:A:64:GLY:C	0.51	2.53	30	7
1:A:4:VAL:CG1	1:A:5:THR:N	0.51	2.74	26	3
1:A:20:HIS:O	1:A:23:LYS:N	0.51	2.43	16	10
1:A:11:GLY:O	1:A:12:ASN:CB	0.51	2.59	13	1
1:A:6:TYR:OH	3:A:98:HEC:CGD	0.50	2.59	6	2
1:A:4:VAL:HG11	1:A:6:TYR:CE2	0.50	2.41	27	2
3:A:158:HEC:HBA2	3:A:158:HEC:HMA3	0.50	1.82	34	2
1:A:51:THR:CG2	1:A:52:CYS:N	0.50	2.74	15	5
1:A:5:THR:HG23	1:A:14:THR:OG1	0.50	2.06	26	1
1:A:24:LEU:HD21	3:A:128:HEC:C2C	0.50	2.37	8	3
1:A:52:CYS:O	1:A:53:HIS:CG	0.50	2.64	12	7
1:A:59:PRO:CG	1:A:65:CYS:SG	0.50	2.99	4	1
1:A:20:HIS:CE1	3:A:128:HEC:C1A	0.50	2.93	9	4
1:A:43:SER:O	1:A:46:LYS:O	0.50	2.29	23	2
1:A:39:ILE:HG22	3:A:158:HEC:CGD	0.50	2.36	8	1
1:A:63:GLY:O	1:A:65:CYS:N	0.50	2.41	15	4
1:A:15:PHE:CD2	3:A:128:HEC:CBB	0.50	2.94	25	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:18:LYS:O	1:A:22:GLU:CG	0.50	2.60	29	11
3:A:128:HEC:CBC	3:A:128:HEC:HMC3	0.50	2.36	3	5
1:A:49:CYS:SG	3:A:128:HEC:C2B	0.50	2.94	17	1
1:A:28:ALA:HB3	3:A:98:HEC:HBC3	0.50	1.84	30	1
1:A:61:LYS:O	1:A:62:CYS:CB	0.49	2.59	5	4
1:A:13:VAL:O	1:A:15:PHE:CE1	0.49	2.65	16	1
1:A:62:CYS:CB	3:A:158:HEC:HBB1	0.49	2.37	35	2
1:A:64:GLY:O	1:A:65:CYS:CB	0.49	2.60	22	1
1:A:61:LYS:CA	3:A:158:HEC:HMC3	0.49	2.34	27	1
1:A:3:VAL:CG2	1:A:16:ASP:OD1	0.49	2.60	13	1
1:A:24:LEU:HD22	1:A:28:ALA:CB	0.49	2.37	18	2
1:A:14:THR:HG22	1:A:15:PHE:H	0.49	1.66	31	1
1:A:20:HIS:C	1:A:22:GLU:N	0.49	2.69	29	17
1:A:57:ASN:CG	1:A:58:GLY:N	0.49	2.70	15	2
1:A:49:CYS:C	1:A:51:THR:N	0.49	2.71	35	2
1:A:53:HIS:CE1	1:A:59:PRO:HD2	0.49	2.42	11	1
1:A:16:ASP:CG	1:A:20:HIS:CE1	0.49	2.90	21	1
1:A:36:LYS:O	1:A:36:LYS:CG	0.49	2.61	23	6
1:A:41:LYS:O	1:A:42:LYS:C	0.49	2.55	2	2
1:A:2:ASP:O	1:A:17:HIS:CB	0.49	2.61	3	1
1:A:6:TYR:O	1:A:12:ASN:CB	0.49	2.60	6	1
1:A:13:VAL:HG23	3:A:128:HEC:HMB2	0.49	1.82	5	1
1:A:3:VAL:CG1	1:A:4:VAL:N	0.49	2.75	33	1
1:A:21:ALA:C	1:A:23:LYS:N	0.49	2.70	5	11
1:A:2:ASP:O	1:A:3:VAL:HG13	0.49	2.07	29	1
1:A:46:LYS:C	1:A:48:ALA:N	0.49	2.68	18	21
1:A:4:VAL:HG11	1:A:6:TYR:CZ	0.49	2.43	22	2
1:A:16:ASP:HB2	1:A:20:HIS:CD2	0.49	2.43	18	3
1:A:11:GLY:O	1:A:66:HIS:CE1	0.49	2.66	30	1
1:A:60:THR:O	1:A:61:LYS:C	0.49	2.55	31	1
1:A:53:HIS:O	1:A:55:SER:N	0.49	2.46	15	7
1:A:20:HIS:CD2	1:A:24:LEU:CD1	0.49	2.96	18	1
1:A:13:VAL:O	1:A:13:VAL:CG1	0.49	2.60	30	1
1:A:41:LYS:O	1:A:41:LYS:CG	0.48	2.61	24	2
1:A:37:ILE:HG22	1:A:38:ALA:N	0.48	2.23	25	5
1:A:6:TYR:CD2	1:A:15:PHE:CE1	0.48	3.01	12	1
1:A:20:HIS:O	1:A:22:GLU:N	0.48	2.47	22	10
1:A:26:CYS:O	1:A:30:HIS:N	0.48	2.44	31	9
1:A:30:HIS:CE1	1:A:37:ILE:HD11	0.48	2.43	23	4
1:A:67:ILE:CG2	1:A:68:LYS:N	0.48	2.75	23	1
1:A:39:ILE:CG1	3:A:98:HEC:HMD1	0.48	2.39	33	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:62:CYS:C	1:A:64:GLY:N	0.48	2.71	17	6
1:A:41:LYS:C	1:A:43:SER:N	0.48	2.70	17	1
1:A:27:ASP:C	1:A:29:CYS:N	0.48	2.69	20	2
1:A:2:ASP:O	1:A:3:VAL:CG1	0.48	2.61	24	1
1:A:47:ASP:O	1:A:48:ALA:HB2	0.48	2.08	25	1
1:A:24:LEU:HD12	3:A:128:HEC:HBC2	0.48	1.84	34	1
1:A:26:CYS:HB3	3:A:98:HEC:C2B	0.48	2.39	33	3
1:A:18:LYS:O	1:A:19:ALA:C	0.48	2.56	35	2
1:A:25:GLY:O	1:A:26:CYS:C	0.48	2.56	25	1
1:A:4:VAL:HG12	1:A:5:THR:N	0.48	2.24	11	2
1:A:67:ILE:HG22	1:A:67:ILE:O	0.48	2.09	25	1
3:A:158:HEC:CBC	3:A:158:HEC:HMC3	0.48	2.37	7	1
1:A:13:VAL:O	1:A:15:PHE:CD1	0.48	2.66	16	1
1:A:15:PHE:HE1	3:A:158:HEC:HMD2	0.48	1.67	28	1
1:A:4:VAL:O	1:A:5:THR:C	0.48	2.57	35	3
1:A:2:ASP:N	1:A:17:HIS:HB3	0.48	2.24	22	4
1:A:16:ASP:N	1:A:16:ASP:OD1	0.47	2.47	12	1
1:A:13:VAL:O	1:A:13:VAL:CG2	0.47	2.62	4	3
1:A:45:HIS:C	1:A:46:LYS:CG	0.47	2.87	20	1
1:A:3:VAL:O	1:A:4:VAL:CG2	0.47	2.62	23	1
1:A:24:LEU:HD12	1:A:28:ALA:CB	0.47	2.40	5	1
1:A:61:LYS:O	1:A:62:CYS:C	0.47	2.57	27	5
1:A:11:GLY:C	1:A:12:ASN:CG	0.47	2.81	13	1
1:A:2:ASP:O	1:A:3:VAL:C	0.47	2.55	35	1
1:A:52:CYS:HB3	3:A:128:HEC:CAC	0.47	2.38	32	2
3:A:98:HEC:C3D	3:A:98:HEC:O1D	0.47	2.63	4	1
1:A:21:ALA:CB	3:A:98:HEC:CBB	0.47	2.92	34	2
3:A:128:HEC:HMB1	3:A:158:HEC:HAC	0.47	1.85	5	1
1:A:43:SER:C	1:A:45:HIS:N	0.47	2.72	23	12
1:A:52:CYS:O	1:A:53:HIS:C	0.47	2.57	32	3
1:A:25:GLY:O	1:A:26:CYS:O	0.47	2.32	15	1
1:A:39:ILE:CD1	1:A:43:SER:O	0.47	2.63	30	1
1:A:37:ILE:CD1	3:A:98:HEC:C2D	0.47	2.88	35	2
1:A:50:LYS:O	1:A:51:THR:CB	0.47	2.63	5	6
1:A:24:LEU:CD2	3:A:98:HEC:HMC3	0.47	2.34	16	2
1:A:59:PRO:C	1:A:60:THR:HG22	0.47	2.35	13	1
1:A:37:ILE:O	1:A:38:ALA:HB3	0.47	2.10	16	1
1:A:37:ILE:O	1:A:37:ILE:CG2	0.47	2.62	1	2
1:A:62:CYS:O	3:A:158:HEC:CMC	0.47	2.63	7	1
1:A:39:ILE:CG1	3:A:98:HEC:O2D	0.47	2.62	35	1
1:A:60:THR:O	1:A:60:THR:CG2	0.47	2.61	24	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:34:PRO:HB2	3:A:98:HEC:HBB	0.47	1.86	15	2
1:A:15:PHE:CD1	1:A:15:PHE:N	0.47	2.79	18	4
1:A:44:ALA:CA	1:A:48:ALA:HB3	0.47	2.38	26	1
1:A:60:THR:C	1:A:61:LYS:O	0.47	2.58	27	1
1:A:20:HIS:CA	1:A:24:LEU:HD13	0.47	2.39	22	4
1:A:39:ILE:HG22	3:A:158:HEC:HAD2	0.47	1.86	30	1
1:A:16:ASP:OD1	3:A:128:HEC:CHB	0.46	2.63	18	1
1:A:6:TYR:O	1:A:13:VAL:HG12	0.46	2.10	19	1
1:A:42:LYS:O	1:A:46:LYS:CB	0.46	2.63	26	1
1:A:27:ASP:O	1:A:30:HIS:O	0.46	2.34	16	13
3:A:128:HEC:HMB1	3:A:158:HEC:HHD	0.46	1.86	7	2
1:A:51:THR:O	1:A:53:HIS:N	0.46	2.48	10	2
1:A:8:ASN:ND2	1:A:11:GLY:O	0.46	2.48	11	1
1:A:50:LYS:O	1:A:52:CYS:O	0.46	2.34	15	1
3:A:158:HEC:CGD	3:A:158:HEC:HHA	0.46	2.40	31	3
1:A:21:ALA:O	1:A:23:LYS:N	0.46	2.48	30	8
1:A:42:LYS:O	1:A:46:LYS:N	0.46	2.49	2	3
1:A:37:ILE:CG2	1:A:38:ALA:N	0.46	2.79	21	4
1:A:35:ALA:O	1:A:36:LYS:C	0.46	2.58	26	1
1:A:50:LYS:CD	1:A:50:LYS:C	0.46	2.88	31	1
1:A:46:LYS:O	1:A:48:ALA:N	0.46	2.49	14	8
3:A:158:HEC:HMC3	3:A:158:HEC:HBC2	0.46	1.86	7	1
1:A:5:THR:O	1:A:6:TYR:CD2	0.46	2.68	19	1
1:A:45:HIS:O	1:A:50:LYS:CD	0.46	2.63	35	1
1:A:36:LYS:C	1:A:37:ILE:CG1	0.46	2.89	35	2
1:A:8:ASN:O	1:A:9:LYS:CB	0.46	2.63	30	1
1:A:27:ASP:O	1:A:28:ALA:C	0.46	2.58	8	9
1:A:26:CYS:HB3	3:A:98:HEC:CAB	0.46	2.41	12	2
1:A:13:VAL:O	1:A:15:PHE:N	0.46	2.48	23	1
1:A:16:ASP:OD1	1:A:16:ASP:N	0.46	2.48	29	1
1:A:17:HIS:CE1	3:A:98:HEC:NC	0.46	2.84	35	1
1:A:56:ASN:O	1:A:57:ASN:CB	0.46	2.64	1	2
1:A:8:ASN:OD1	1:A:10:LYS:C	0.46	2.59	27	6
1:A:13:VAL:O	1:A:14:THR:C	0.46	2.58	11	2
1:A:61:LYS:CD	3:A:158:HEC:HBB1	0.46	2.41	27	1
1:A:37:ILE:HG13	3:A:98:HEC:C3D	0.46	2.41	33	1
1:A:54:LYS:HB3	1:A:60:THR:HG21	0.45	1.88	2	2
1:A:10:LYS:O	1:A:66:HIS:ND1	0.45	2.49	3	2
1:A:57:ASN:ND2	3:A:128:HEC:CGD	0.45	2.79	12	1
1:A:64:GLY:C	1:A:65:CYS:SG	0.45	3.00	22	1
1:A:45:HIS:CE1	3:A:158:HEC:C4B	0.45	2.98	13	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:8:ASN:OD1	1:A:11:GLY:N	0.45	2.49	35	4
1:A:49:CYS:O	1:A:52:CYS:N	0.45	2.49	24	1
1:A:36:LYS:O	1:A:37:ILE:CG1	0.45	2.64	8	3
1:A:31:GLU:CG	1:A:32:GLY:N	0.45	2.79	24	2
1:A:3:VAL:CG2	1:A:15:PHE:O	0.45	2.64	21	1
1:A:6:TYR:HB2	1:A:13:VAL:HG13	0.45	1.89	24	2
1:A:57:ASN:O	1:A:58:GLY:C	0.45	2.60	5	1
1:A:2:ASP:C	1:A:3:VAL:CG2	0.45	2.83	20	1
1:A:61:LYS:HB2	3:A:158:HEC:HBB1	0.45	1.88	23	1
1:A:23:LYS:C	1:A:24:LEU:CD2	0.45	2.87	34	1
1:A:9:LYS:O	1:A:10:LYS:C	0.45	2.60	2	3
1:A:8:ASN:OD1	1:A:11:GLY:C	0.45	2.60	14	6
1:A:2:ASP:O	1:A:17:HIS:N	0.45	2.49	5	2
1:A:23:LYS:CG	1:A:24:LEU:N	0.45	2.79	12	1
3:A:98:HEC:HBC1	3:A:128:HEC:HMC2	0.45	1.87	34	2
1:A:67:ILE:O	1:A:68:LYS:C	0.45	2.60	31	3
1:A:53:HIS:O	1:A:54:LYS:C	0.45	2.59	8	1
1:A:24:LEU:HD12	3:A:98:HEC:CMC	0.45	2.42	9	1
1:A:24:LEU:N	1:A:24:LEU:CD1	0.45	2.78	35	3
1:A:17:HIS:CE1	3:A:98:HEC:C1D	0.45	3.00	35	1
1:A:65:CYS:O	1:A:67:ILE:N	0.45	2.50	1	1
1:A:53:HIS:C	1:A:55:SER:N	0.45	2.73	34	3
1:A:12:ASN:OD1	1:A:12:ASN:N	0.45	2.49	13	1
1:A:30:HIS:CE1	3:A:98:HEC:C4B	0.45	3.00	33	3
3:A:158:HEC:HHA	3:A:158:HEC:O1D	0.45	2.11	29	1
1:A:35:ALA:O	1:A:36:LYS:HB3	0.45	2.12	35	3
1:A:53:HIS:CE1	1:A:59:PRO:HG2	0.45	2.46	12	2
1:A:15:PHE:HE1	3:A:128:HEC:HBB2	0.45	1.72	13	1
1:A:39:ILE:O	1:A:40:ASP:CG	0.45	2.60	13	1
1:A:13:VAL:O	1:A:13:VAL:HG22	0.45	2.10	11	1
1:A:13:VAL:HG11	3:A:158:HEC:C2D	0.45	2.42	21	2
1:A:67:ILE:CG2	1:A:67:ILE:O	0.45	2.64	29	1
1:A:15:PHE:HZ	3:A:98:HEC:HAC	0.45	1.71	32	1
1:A:3:VAL:HG12	1:A:16:ASP:OD1	0.45	2.12	35	1
1:A:4:VAL:O	1:A:15:PHE:N	0.44	2.50	4	2
1:A:4:VAL:CG1	1:A:6:TYR:CZ	0.44	3.00	8	2
1:A:16:ASP:OD2	1:A:20:HIS:ND1	0.44	2.50	9	1
1:A:67:ILE:O	1:A:67:ILE:CG2	0.44	2.65	4	3
1:A:25:GLY:C	3:A:98:HEC:HAB	0.44	2.36	11	2
1:A:34:PRO:CB	3:A:98:HEC:CHB	0.44	2.95	31	2
1:A:29:CYS:SG	3:A:98:HEC:CMC	0.44	3.05	23	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:2:ASP:O	1:A:3:VAL:HB	0.44	2.12	24	3
1:A:36:LYS:CE	1:A:37:ILE:O	0.44	2.66	32	1
1:A:23:LYS:HG3	1:A:24:LEU:HD12	0.44	1.89	12	1
1:A:13:VAL:HG11	3:A:158:HEC:CGD	0.44	2.42	17	1
1:A:53:HIS:CD2	3:A:128:HEC:C4C	0.44	3.00	19	1
1:A:43:SER:O	1:A:47:ASP:N	0.44	2.51	25	1
1:A:56:ASN:O	1:A:57:ASN:C	0.44	2.60	2	4
1:A:4:VAL:HG12	1:A:6:TYR:CZ	0.44	2.47	7	1
1:A:27:ASP:O	1:A:29:CYS:N	0.44	2.50	20	1
1:A:29:CYS:HB2	1:A:37:ILE:CD1	0.44	2.43	33	1
1:A:24:LEU:HD22	3:A:98:HEC:CAC	0.44	2.43	1	1
1:A:2:ASP:O	1:A:3:VAL:CG2	0.44	2.65	29	2
1:A:41:LYS:O	1:A:43:SER:N	0.44	2.49	18	3
1:A:6:TYR:O	1:A:8:ASN:ND2	0.44	2.51	23	1
1:A:24:LEU:N	1:A:24:LEU:HD12	0.44	2.28	27	2
1:A:8:ASN:O	3:A:158:HEC:CBA	0.44	2.65	30	1
1:A:15:PHE:HZ	1:A:39:ILE:HG21	0.44	1.69	31	1
1:A:24:LEU:CG	3:A:128:HEC:HBC2	0.44	2.42	4	2
1:A:24:LEU:HB3	1:A:28:ALA:CB	0.44	2.43	16	5
3:A:158:HEC:CBB	3:A:158:HEC:CHC	0.44	2.96	19	2
1:A:37:ILE:O	1:A:38:ALA:O	0.44	2.36	31	6
1:A:22:GLU:C	1:A:22:GLU:OE1	0.44	2.60	10	2
1:A:66:HIS:CD2	3:A:158:HEC:C4B	0.44	3.00	24	1
1:A:52:CYS:HB2	3:A:128:HEC:CAC	0.44	2.38	3	1
1:A:59:PRO:O	1:A:61:LYS:N	0.44	2.48	17	2
1:A:53:HIS:CE1	3:A:128:HEC:CHB	0.44	3.01	33	1
1:A:24:LEU:HD23	1:A:29:CYS:SG	0.43	2.52	2	1
1:A:13:VAL:HG22	1:A:14:THR:N	0.43	2.27	19	1
3:A:158:HEC:HBB2	3:A:158:HEC:CHC	0.43	2.31	30	2
1:A:40:ASP:O	1:A:44:ALA:N	0.43	2.48	18	1
3:A:128:HEC:HMA2	3:A:128:HEC:HBA1	0.43	1.90	23	1
1:A:20:HIS:NE2	3:A:128:HEC:C4D	0.43	2.82	24	2
1:A:35:ALA:O	3:A:98:HEC:HAA1	0.43	2.11	33	3
3:A:158:HEC:O1D	3:A:158:HEC:C4D	0.43	2.67	2	1
1:A:59:PRO:HA	1:A:64:GLY:CA	0.43	2.42	23	2
1:A:29:CYS:HB3	1:A:37:ILE:CD1	0.43	2.42	33	2
1:A:24:LEU:HD11	3:A:128:HEC:HHD	0.43	1.86	19	1
1:A:50:LYS:O	1:A:52:CYS:N	0.43	2.51	25	2
1:A:39:ILE:CG2	3:A:158:HEC:HMD3	0.43	2.44	29	1
1:A:29:CYS:HG	3:A:98:HEC:CAC	0.43	2.20	34	1
3:A:158:HEC:CBC	3:A:158:HEC:CMC	0.43	2.97	7	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:16:ASP:O	3:A:98:HEC:CBC	0.43	2.66	16	1
1:A:44:ALA:CB	3:A:158:HEC:C2D	0.43	2.96	19	1
1:A:44:ALA:N	1:A:48:ALA:CB	0.43	2.81	30	1
1:A:20:HIS:O	1:A:24:LEU:HD12	0.43	2.14	33	1
3:A:98:HEC:HBC2	3:A:98:HEC:HMC3	0.43	1.90	33	1
1:A:11:GLY:O	1:A:12:ASN:C	0.43	2.61	34	1
1:A:15:PHE:CE2	3:A:98:HEC:HMD2	0.43	2.49	35	2
1:A:54:LYS:CG	1:A:60:THR:CG2	0.43	2.96	35	1
1:A:4:VAL:HG23	1:A:15:PHE:HB2	0.43	1.90	30	1
1:A:53:HIS:HB3	1:A:60:THR:HG23	0.43	1.90	1	1
1:A:17:HIS:CD2	3:A:98:HEC:NB	0.43	2.86	2	1
1:A:6:TYR:CE1	3:A:158:HEC:CGD	0.43	3.01	4	1
1:A:6:TYR:O	1:A:7:GLU:C	0.43	2.62	12	1
1:A:51:THR:HG23	1:A:52:CYS:N	0.43	2.28	26	3
3:A:158:HEC:HMC3	3:A:158:HEC:HBC3	0.43	1.90	26	1
1:A:15:PHE:HE2	1:A:39:ILE:HG21	0.43	1.73	29	1
1:A:24:LEU:HD13	3:A:128:HEC:CBC	0.43	2.43	34	1
1:A:31:GLU:C	1:A:33:THR:N	0.43	2.76	29	2
1:A:8:ASN:O	1:A:9:LYS:C	0.43	2.60	26	1
1:A:6:TYR:CE1	3:A:158:HEC:HBD1	0.43	2.49	3	1
1:A:20:HIS:CD2	3:A:128:HEC:C4D	0.43	3.02	32	1
1:A:6:TYR:CE1	3:A:158:HEC:O2D	0.42	2.72	4	1
1:A:4:VAL:HB	1:A:15:PHE:CD1	0.42	2.49	9	1
1:A:30:HIS:O	1:A:31:GLU:CB	0.42	2.67	21	1
1:A:62:CYS:HA	3:A:158:HEC:CBB	0.42	2.44	22	1
1:A:41:LYS:HE3	3:A:158:HEC:HMA2	0.42	1.90	32	1
1:A:20:HIS:O	1:A:24:LEU:CD1	0.42	2.66	33	2
1:A:4:VAL:O	1:A:4:VAL:CG1	0.42	2.67	24	3
1:A:5:THR:CG2	1:A:6:TYR:N	0.42	2.81	19	1
1:A:37:ILE:HB	3:A:98:HEC:C3D	0.42	2.44	19	1
1:A:2:ASP:HB2	1:A:18:LYS:CA	0.42	2.44	35	1
1:A:24:LEU:HD12	1:A:28:ALA:HB1	0.42	1.91	5	1
1:A:58:GLY:N	1:A:59:PRO:CD	0.42	2.82	18	1
1:A:62:CYS:O	1:A:65:CYS:N	0.42	2.48	19	1
1:A:61:LYS:C	1:A:62:CYS:O	0.42	2.62	20	1
1:A:61:LYS:O	1:A:62:CYS:O	0.42	2.37	27	2
1:A:13:VAL:O	1:A:14:THR:O	0.42	2.38	31	1
1:A:26:CYS:O	1:A:30:HIS:ND1	0.42	2.46	35	1
1:A:39:ILE:HG13	3:A:98:HEC:HMD3	0.42	1.91	5	1
1:A:23:LYS:CG	1:A:24:LEU:HD12	0.42	2.44	12	1
1:A:23:LYS:O	1:A:24:LEU:O	0.42	2.38	26	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:59:PRO:CB	1:A:64:GLY:HA3	0.42	2.44	27	1
1:A:63:GLY:C	1:A:65:CYS:N	0.42	2.76	30	1
1:A:52:CYS:C	1:A:54:LYS:N	0.42	2.75	34	1
1:A:34:PRO:HG3	3:A:98:HEC:HMB2	0.42	1.90	6	2
1:A:15:PHE:CZ	3:A:98:HEC:CMD	0.42	3.02	11	1
1:A:50:LYS:O	1:A:50:LYS:HG3	0.42	2.15	31	1
1:A:23:LYS:HE3	3:A:128:HEC:C2D	0.42	2.45	12	1
1:A:40:ASP:O	1:A:41:LYS:CB	0.42	2.67	13	1
1:A:13:VAL:HG22	3:A:128:HEC:CMB	0.42	2.45	16	1
1:A:45:HIS:C	1:A:46:LYS:CD	0.42	2.92	23	1
1:A:51:THR:O	1:A:54:LYS:N	0.42	2.52	32	1
1:A:24:LEU:CD2	3:A:98:HEC:HAC	0.42	2.44	1	1
1:A:47:ASP:HA	1:A:51:THR:CB	0.42	2.45	12	3
1:A:37:ILE:O	1:A:37:ILE:HG22	0.42	2.14	28	2
1:A:4:VAL:HG13	1:A:6:TYR:CE2	0.42	2.50	33	1
1:A:20:HIS:CD2	1:A:24:LEU:HD11	0.42	2.50	8	1
1:A:15:PHE:CD1	1:A:16:ASP:N	0.42	2.88	9	1
1:A:66:HIS:O	1:A:68:LYS:N	0.42	2.53	9	2
1:A:66:HIS:CE1	3:A:158:HEC:CHD	0.42	3.02	17	1
1:A:61:LYS:CB	3:A:158:HEC:HBB1	0.42	2.45	23	1
1:A:50:LYS:HB2	1:A:54:LYS:CD	0.42	2.44	18	1
1:A:13:VAL:HG21	3:A:158:HEC:C1D	0.42	2.44	26	1
1:A:62:CYS:O	1:A:66:HIS:N	0.42	2.53	26	1
1:A:15:PHE:CG	1:A:16:ASP:N	0.41	2.88	7	1
3:A:128:HEC:HBA1	3:A:128:HEC:CMA	0.41	2.45	29	2
1:A:56:ASN:CG	1:A:57:ASN:N	0.41	2.76	26	1
1:A:2:ASP:O	1:A:18:LYS:N	0.41	2.46	30	1
1:A:61:LYS:CG	1:A:62:CYS:N	0.41	2.82	31	2
1:A:30:HIS:CE1	3:A:98:HEC:C1A	0.41	3.03	9	1
1:A:20:HIS:CD2	3:A:128:HEC:NC	0.41	2.87	15	1
1:A:8:ASN:ND2	1:A:13:VAL:HG12	0.41	2.31	23	1
1:A:24:LEU:HD12	1:A:29:CYS:SG	0.41	2.55	24	1
3:A:158:HEC:CBB	3:A:158:HEC:HHC	0.41	2.35	35	1
1:A:60:THR:O	1:A:61:LYS:HG3	0.41	2.15	27	1
1:A:14:THR:O	1:A:15:PHE:O	0.41	2.38	33	2
3:A:128:HEC:O1D	3:A:128:HEC:C3D	0.41	2.68	1	1
1:A:6:TYR:CZ	3:A:98:HEC:O1D	0.41	2.73	8	1
1:A:16:ASP:O	1:A:20:HIS:ND1	0.41	2.53	24	1
1:A:41:LYS:HA	1:A:45:HIS:CE1	0.41	2.51	7	1
1:A:46:LYS:O	1:A:49:CYS:O	0.41	2.39	8	2
1:A:2:ASP:N	1:A:17:HIS:CB	0.41	2.83	22	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:59:PRO:O	1:A:60:THR:HB	0.41	2.15	24	1
1:A:29:CYS:HB2	1:A:37:ILE:HD11	0.41	1.91	28	1
1:A:26:CYS:HA	3:A:98:HEC:CAB	0.41	2.44	18	2
1:A:44:ALA:HB1	3:A:158:HEC:HMD3	0.41	1.87	23	1
1:A:36:LYS:N	1:A:36:LYS:HE3	0.41	2.31	26	1
1:A:40:ASP:O	1:A:41:LYS:O	0.41	2.38	26	1
1:A:31:GLU:O	1:A:32:GLY:O	0.41	2.38	27	1
1:A:52:CYS:CB	3:A:128:HEC:C2C	0.41	2.99	31	1
1:A:53:HIS:CE1	3:A:128:HEC:C4A	0.41	3.04	33	1
1:A:8:ASN:OD1	1:A:11:GLY:O	0.41	2.39	11	1
1:A:63:GLY:O	1:A:66:HIS:O	0.41	2.37	19	1
1:A:6:TYR:HD2	1:A:13:VAL:HG13	0.41	1.76	22	1
1:A:59:PRO:HG2	3:A:158:HEC:HBC3	0.41	1.92	34	1
1:A:39:ILE:CG2	3:A:158:HEC:HAD2	0.41	2.45	3	1
1:A:14:THR:O	1:A:16:ASP:OD1	0.41	2.39	9	1
1:A:11:GLY:C	1:A:12:ASN:OD1	0.41	2.63	13	1
1:A:7:GLU:O	1:A:8:ASN:O	0.41	2.39	16	1
1:A:3:VAL:C	1:A:4:VAL:HG23	0.41	2.40	24	2
1:A:5:THR:O	1:A:5:THR:HG23	0.41	2.16	30	1
1:A:26:CYS:HA	3:A:98:HEC:CHC	0.41	2.46	35	1
1:A:36:LYS:O	1:A:36:LYS:CD	0.41	2.68	10	1
1:A:26:CYS:O	1:A:27:ASP:CB	0.41	2.69	15	1
1:A:50:LYS:O	1:A:50:LYS:CG	0.41	2.68	22	1
1:A:44:ALA:O	1:A:49:CYS:SG	0.41	2.79	23	1
1:A:61:LYS:CB	3:A:158:HEC:HMC3	0.41	2.45	27	1
1:A:4:VAL:HG12	1:A:5:THR:H	0.41	1.75	19	1
1:A:30:HIS:HE1	3:A:98:HEC:C4B	0.41	2.29	28	1
3:A:158:HEC:HBA2	3:A:158:HEC:CMA	0.41	2.46	34	1
1:A:29:CYS:CB	3:A:98:HEC:CHD	0.41	2.98	35	1
1:A:41:LYS:HG3	3:A:158:HEC:C2A	0.40	2.46	4	1
1:A:6:TYR:HB2	1:A:13:VAL:CG1	0.40	2.46	19	1
1:A:14:THR:HG22	1:A:14:THR:O	0.40	2.16	20	1
1:A:44:ALA:CB	3:A:158:HEC:CMD	0.40	2.86	23	1
1:A:6:TYR:CE2	1:A:15:PHE:CZ	0.40	3.09	26	1
1:A:53:HIS:CG	1:A:59:PRO:HD2	0.40	2.51	12	1
1:A:59:PRO:HB3	1:A:64:GLY:CA	0.40	2.46	13	1
1:A:56:ASN:O	1:A:57:ASN:O	0.40	2.40	18	1
1:A:3:VAL:HG13	1:A:3:VAL:O	0.40	2.17	21	1
1:A:11:GLY:O	1:A:12:ASN:O	0.40	2.39	29	1
1:A:25:GLY:C	1:A:27:ASP:N	0.40	2.80	35	1
1:A:24:LEU:CD2	1:A:29:CYS:SG	0.40	3.10	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:23:LYS:CE	3:A:128:HEC:HAD2	0.40	2.46	10	1
1:A:8:ASN:O	3:A:158:HEC:O1A	0.40	2.40	30	1
1:A:59:PRO:C	1:A:60:THR:OG1	0.40	2.63	30	1
1:A:66:HIS:CE1	3:A:158:HEC:C4A	0.40	3.04	5	1
1:A:30:HIS:C	1:A:31:GLU:CG	0.40	2.94	18	1
1:A:39:ILE:O	1:A:40:ASP:OD2	0.40	2.38	19	1
1:A:14:THR:O	1:A:15:PHE:C	0.40	2.64	33	1
1:A:52:CYS:SG	3:A:128:HEC:HHD	0.40	2.56	8	1
1:A:6:TYR:OH	3:A:98:HEC:O1D	0.40	2.40	12	1
1:A:24:LEU:HD21	3:A:128:HEC:CBC	0.40	2.47	18	1
1:A:45:HIS:C	1:A:46:LYS:HG3	0.40	2.41	20	1
1:A:65:CYS:SG	3:A:128:HEC:CMB	0.40	3.09	25	1
1:A:39:ILE:HG13	3:A:98:HEC:CMD	0.40	2.47	29	1

6.3 Torsion angles

6.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. 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	66/68 (97%)	31±3 (47±5%)	22±3 (33±5%)	13±3 (20±4%)	0	2
All	All	2310/2380 (97%)	1092 (47%)	767 (33%)	451 (20%)	0	2

All 54 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	24	LEU	31
1	A	50	LYS	27
1	A	51	THR	26
1	A	42	LYS	23
1	A	33	THR	22
1	A	3	VAL	20
1	A	31	GLU	19
1	A	40	ASP	18
1	A	35	ALA	17

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Mol	Chain	Res	Type	Models (Total)
1	A	41	LYS	15
1	A	32	GLY	13
1	A	55	SER	13
1	A	53	HIS	13
1	A	26	CYS	12
1	A	15	PHE	12
1	A	62	CYS	12
1	A	27	ASP	11
1	A	64	GLY	10
1	A	38	ALA	9
1	A	2	ASP	9
1	A	25	GLY	9
1	A	10	LYS	8
1	A	60	THR	8
1	A	67	ILE	7
1	A	48	ALA	7
1	A	22	GLU	6
1	A	11	GLY	6
1	A	58	GLY	6
1	A	12	ASN	6
1	A	63	GLY	5
1	A	61	LYS	5
1	A	14	THR	4
1	A	54	LYS	4
1	A	52	CYS	4
1	A	56	ASN	3
1	A	39	ILE	3
1	A	59	PRO	3
1	A	34	PRO	3
1	A	57	ASN	2
1	A	5	THR	2
1	A	8	ASN	2
1	A	21	ALA	2
1	A	18	LYS	2
1	A	4	VAL	2
1	A	66	HIS	1
1	A	30	HIS	1
1	A	7	GLU	1
1	A	28	ALA	1
1	A	36	LYS	1
1	A	65	CYS	1
1	A	46	LYS	1

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Mol	Chain	Res	Type	Models (Total)
1	A	13	VAL	1
1	A	44	ALA	1
1	A	47	ASP	1

6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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	54/54 (100%)	37±3 (68±5%)	17±3 (32±5%)	1	13
All	All	1890/1890 (100%)	1278 (68%)	612 (32%)	1	13

All 51 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	36	LYS	34
1	A	26	CYS	30
1	A	18	LYS	27
1	A	50	LYS	26
1	A	10	LYS	25
1	A	17	HIS	24
1	A	43	SER	24
1	A	46	LYS	24
1	A	51	THR	21
1	A	20	HIS	20
1	A	42	LYS	20
1	A	22	GLU	20
1	A	68	LYS	19
1	A	53	HIS	19
1	A	9	LYS	18
1	A	41	LYS	18
1	A	23	LYS	16
1	A	31	GLU	15
1	A	61	LYS	15
1	A	2	ASP	15
1	A	29	CYS	14
1	A	55	SER	14

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Mol	Chain	Res	Type	Models (Total)
1	A	40	ASP	12
1	A	56	ASN	10
1	A	62	CYS	9
1	A	65	CYS	9
1	A	52	CYS	9
1	A	54	LYS	9
1	A	49	CYS	8
1	A	24	LEU	8
1	A	27	ASP	8
1	A	16	ASP	8
1	A	47	ASP	7
1	A	14	THR	6
1	A	60	THR	6
1	A	7	GLU	5
1	A	12	ASN	5
1	A	57	ASN	4
1	A	3	VAL	4
1	A	30	HIS	4
1	A	8	ASN	3
1	A	6	TYR	3
1	A	13	VAL	3
1	A	15	PHE	2
1	A	5	THR	2
1	A	33	THR	2
1	A	39	ILE	2
1	A	66	HIS	2
1	A	4	VAL	2
1	A	37	ILE	1
1	A	67	ILE	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.6 Ligand geometry

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds 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 is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Counts	Bond lengths	
						RMSZ	#Z>2
3	HEC	A	158	1	46,50,50	2.20±0.00	12±1 (25±1%)
3	HEC	A	98	1	46,50,50	2.20±0.00	12±0 (25±1%)
3	HEC	A	128	1	46,50,50	2.20±0.00	12±1 (26±1%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of 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 angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Counts	Bond angles	
						RMSZ	#Z>2
3	HEC	A	158	1	58,82,82	2.26±0.00	19±0 (32±0%)
3	HEC	A	98	1	58,82,82	2.26±0.00	19±0 (32±0%)
3	HEC	A	128	1	58,82,82	2.26±0.00	19±0 (32±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
3	HEC	A	128	1	-	0±0,14,54,54	-
3	HEC	A	158	1	-	0±0,14,54,54	-
3	HEC	A	98	1	-	0±0,14,54,54	-

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
3	A	128	HEC	CAC-C3C	6.65	1.56	1.35	15	35
3	A	98	HEC	CAC-C3C	6.65	1.56	1.35	13	35
3	A	158	HEC	CAC-C3C	6.64	1.56	1.35	12	35
3	A	158	HEC	CAB-C3B	4.99	1.51	1.35	4	35
3	A	128	HEC	CAB-C3B	4.99	1.51	1.35	10	35
3	A	98	HEC	CAB-C3B	4.98	1.51	1.35	24	35
3	A	98	HEC	C4A-NA	4.85	1.48	1.39	4	35
3	A	158	HEC	C4A-NA	4.84	1.48	1.39	18	35
3	A	128	HEC	C4A-NA	4.83	1.48	1.39	9	35
3	A	158	HEC	CMD-C2D	4.63	1.60	1.50	5	35
3	A	128	HEC	CMD-C2D	4.63	1.60	1.50	17	35
3	A	98	HEC	CMD-C2D	4.61	1.60	1.50	15	35
3	A	158	HEC	CMA-C3A	3.63	1.58	1.50	25	35
3	A	98	HEC	CMA-C3A	3.62	1.58	1.50	19	35
3	A	128	HEC	CMA-C3A	3.62	1.58	1.50	20	35
3	A	128	HEC	CMB-C2B	3.44	1.57	1.50	23	35
3	A	98	HEC	CMB-C2B	3.43	1.57	1.50	4	35
3	A	158	HEC	CMB-C2B	3.41	1.57	1.50	20	35
3	A	158	HEC	CHC-C1C	3.25	1.46	1.39	11	35
3	A	98	HEC	CHC-C1C	3.23	1.46	1.39	11	35
3	A	128	HEC	CHC-C1C	3.23	1.46	1.39	5	35
3	A	98	HEC	C4A-C3A	2.75	1.39	1.45	19	35
3	A	158	HEC	C4A-C3A	2.75	1.39	1.45	20	35
3	A	128	HEC	C4A-C3A	2.75	1.39	1.45	3	35
3	A	128	HEC	C1A-NA	2.70	1.34	1.39	8	35
3	A	158	HEC	C1A-NA	2.70	1.34	1.39	34	35
3	A	98	HEC	C1A-NA	2.69	1.34	1.39	19	35
3	A	128	HEC	C4B-NB	2.64	1.34	1.39	26	35
3	A	98	HEC	C4B-NB	2.62	1.34	1.39	16	35
3	A	158	HEC	C4B-NB	2.62	1.34	1.39	32	35
3	A	158	HEC	CHB-C4A	2.16	1.34	1.38	6	35
3	A	128	HEC	CHB-C4A	2.16	1.34	1.38	9	35
3	A	98	HEC	CHB-C4A	2.15	1.34	1.38	9	35
3	A	98	HEC	C1A-C2A	2.08	1.48	1.45	16	20
3	A	158	HEC	C1A-C2A	2.08	1.48	1.45	9	21
3	A	128	HEC	C1A-C2A	2.08	1.48	1.45	9	21
3	A	128	HEC	CHD-C1D	2.05	1.34	1.39	20	14
3	A	158	HEC	CHD-C1D	2.04	1.34	1.39	12	11
3	A	98	HEC	CHD-C1D	2.03	1.34	1.39	17	6

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
3	A	128	HEC	CBC-CAC-C3C	7.85	111.74	127.43	13	35
3	A	98	HEC	CBC-CAC-C3C	7.85	111.75	127.43	29	35
3	A	158	HEC	CBC-CAC-C3C	7.84	111.76	127.43	31	35
3	A	158	HEC	CBB-CAB-C3B	6.67	114.11	127.43	22	35
3	A	128	HEC	CBB-CAB-C3B	6.67	114.11	127.43	20	35
3	A	98	HEC	CBB-CAB-C3B	6.65	114.14	127.43	29	35
3	A	128	HEC	CHD-C4C-NC	5.68	118.27	124.45	18	35
3	A	158	HEC	CHD-C4C-NC	5.66	118.29	124.45	12	35
3	A	98	HEC	CHD-C4C-NC	5.66	118.29	124.45	4	35
3	A	98	HEC	C2C-C1C-NC	4.71	117.69	110.14	10	35
3	A	128	HEC	C2C-C1C-NC	4.70	117.68	110.14	4	35
3	A	158	HEC	C2C-C1C-NC	4.69	117.65	110.14	24	35
3	A	128	HEC	CHD-C4C-C3C	3.62	131.31	125.21	18	35
3	A	98	HEC	CHD-C4C-C3C	3.61	131.30	125.21	28	35
3	A	158	HEC	CHD-C4C-C3C	3.60	131.28	125.21	35	35
3	A	98	HEC	O1A-CGA-CBA	2.99	113.62	123.09	30	35
3	A	158	HEC	O1A-CGA-CBA	2.98	113.64	123.09	23	35
3	A	128	HEC	O1A-CGA-CBA	2.98	113.64	123.09	32	35
3	A	128	HEC	C2B-C1B-NB	2.93	105.45	110.14	8	35
3	A	98	HEC	C2B-C1B-NB	2.92	105.46	110.14	5	35
3	A	158	HEC	C2B-C1B-NB	2.91	105.48	110.14	6	35
3	A	128	HEC	C1D-CHD-C4C	2.87	133.51	124.66	16	35
3	A	98	HEC	C1D-CHD-C4C	2.87	133.51	124.66	4	35
3	A	158	HEC	C1D-CHD-C4C	2.86	133.48	124.66	30	35
3	A	128	HEC	CMB-C2B-C1B	2.80	121.16	125.42	31	35
3	A	158	HEC	CMB-C2B-C1B	2.78	121.18	125.42	4	35
3	A	98	HEC	CMB-C2B-C1B	2.77	121.19	125.42	25	35
3	A	158	HEC	C4C-NC-C1C	2.77	101.31	105.82	32	35
3	A	98	HEC	C4C-NC-C1C	2.77	101.31	105.82	21	35
3	A	128	HEC	C4C-NC-C1C	2.76	101.32	105.82	18	35
3	A	158	HEC	CMC-C2C-C1C	2.70	129.53	125.42	20	35
3	A	98	HEC	CMC-C2C-C1C	2.69	129.52	125.42	29	35
3	A	128	HEC	CMC-C2C-C1C	2.69	129.51	125.42	4	35
3	A	158	HEC	CAA-C2A-C3A	2.35	132.27	127.87	33	35
3	A	98	HEC	CAA-C2A-C3A	2.35	132.26	127.87	3	35
3	A	128	HEC	CAA-C2A-C3A	2.33	132.24	127.87	16	35
3	A	158	HEC	CHB-C4A-NA	2.34	121.91	124.45	11	35
3	A	128	HEC	CHB-C4A-NA	2.30	121.95	124.45	34	35
3	A	158	HEC	C3D-C4D-ND	2.28	107.62	110.15	26	35
3	A	128	HEC	C3D-C4D-ND	2.27	107.63	110.15	19	35
3	A	98	HEC	C2A-C1A-NA	2.27	112.51	110.32	33	35
3	A	98	HEC	CHB-C4A-NA	2.27	121.98	124.45	30	35

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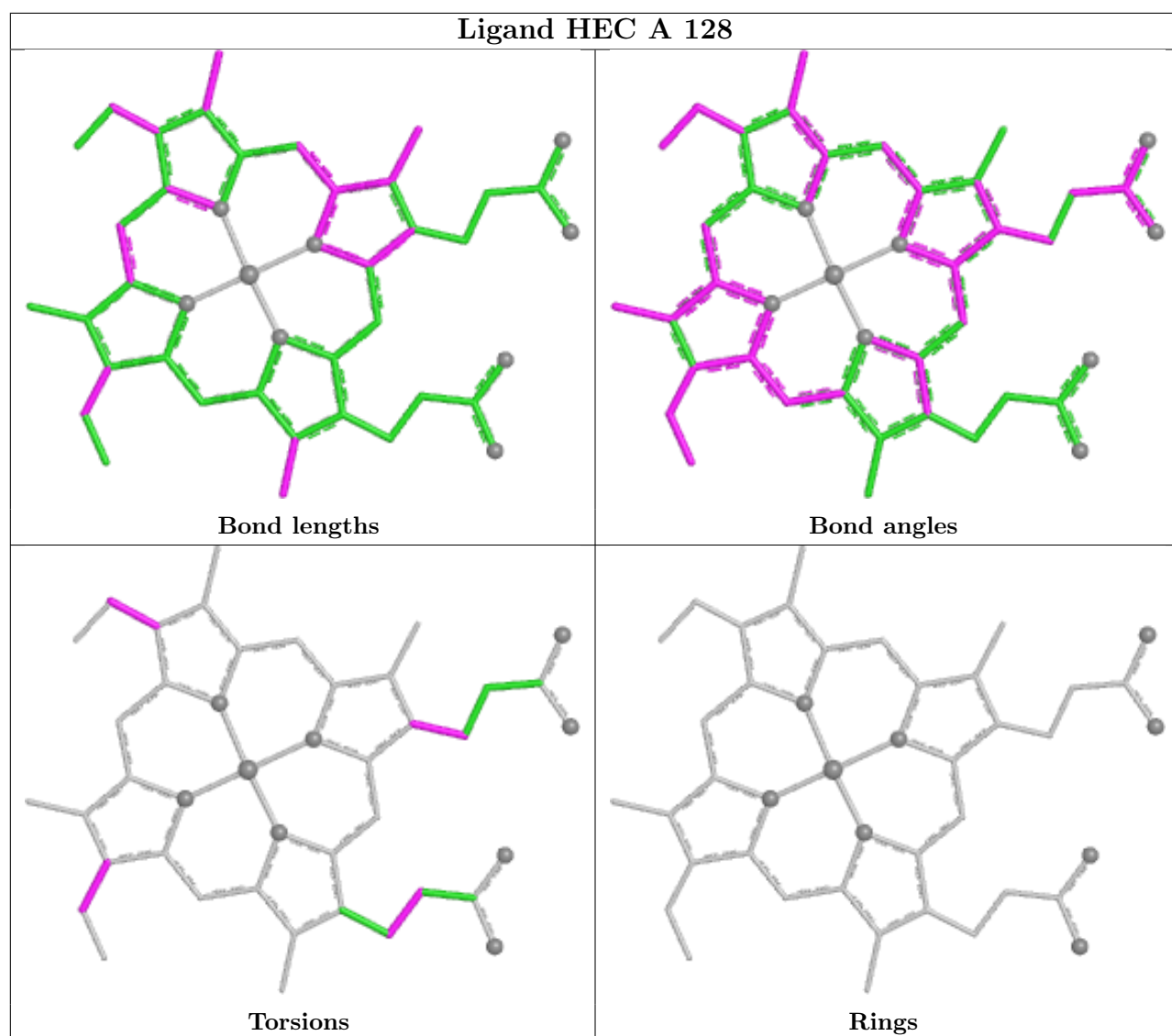
Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
3	A	98	HEC	C3D-C4D-ND	2.27	107.64	110.15	10	35
3	A	158	HEC	C2A-C1A-NA	2.25	112.49	110.32	34	35
3	A	128	HEC	C2A-C1A-NA	2.24	112.48	110.32	17	35
3	A	128	HEC	C4A-NA-C1A	2.22	102.20	105.82	17	35
3	A	98	HEC	C4A-NA-C1A	2.21	102.22	105.82	28	35
3	A	158	HEC	C4A-NA-C1A	2.20	102.23	105.82	9	35
3	A	128	HEC	CHA-C1A-NA	2.19	122.06	124.45	3	35
3	A	158	HEC	CHA-C1A-NA	2.19	122.07	124.45	7	35
3	A	98	HEC	CHA-C1A-NA	2.16	122.10	124.45	22	35
3	A	158	HEC	CHC-C1C-NC	2.16	119.94	123.86	10	35
3	A	98	HEC	CHC-C1C-NC	2.16	119.95	123.86	10	35
3	A	128	HEC	CHC-C1C-NC	2.16	119.95	123.86	18	35
3	A	158	HEC	O2A-CGA-CBA	2.11	120.66	114.00	17	35
3	A	98	HEC	O2A-CGA-CBA	2.10	120.63	114.00	16	35
3	A	128	HEC	O2A-CGA-CBA	2.10	120.64	114.00	17	35

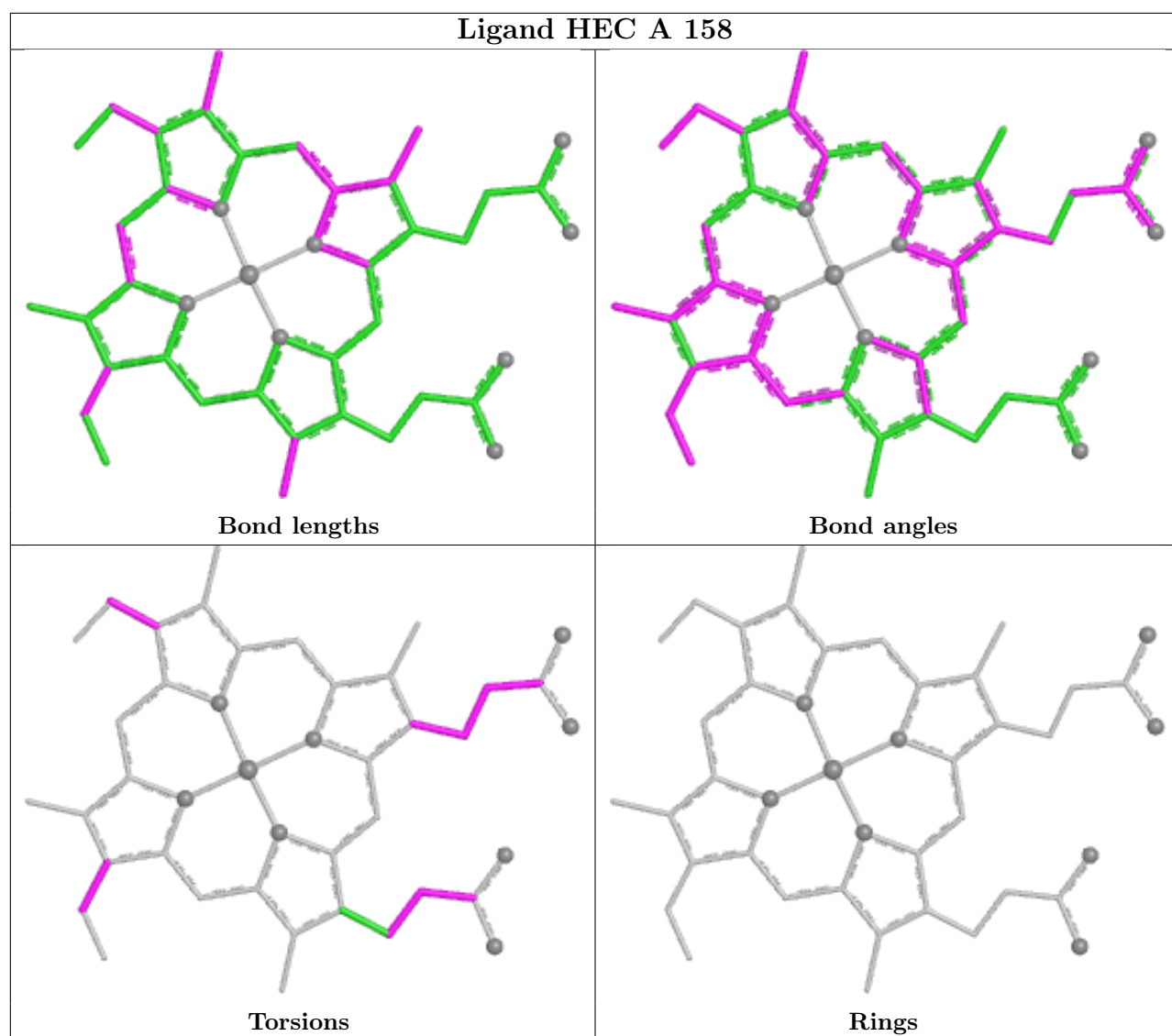
There are no chirality outliers.

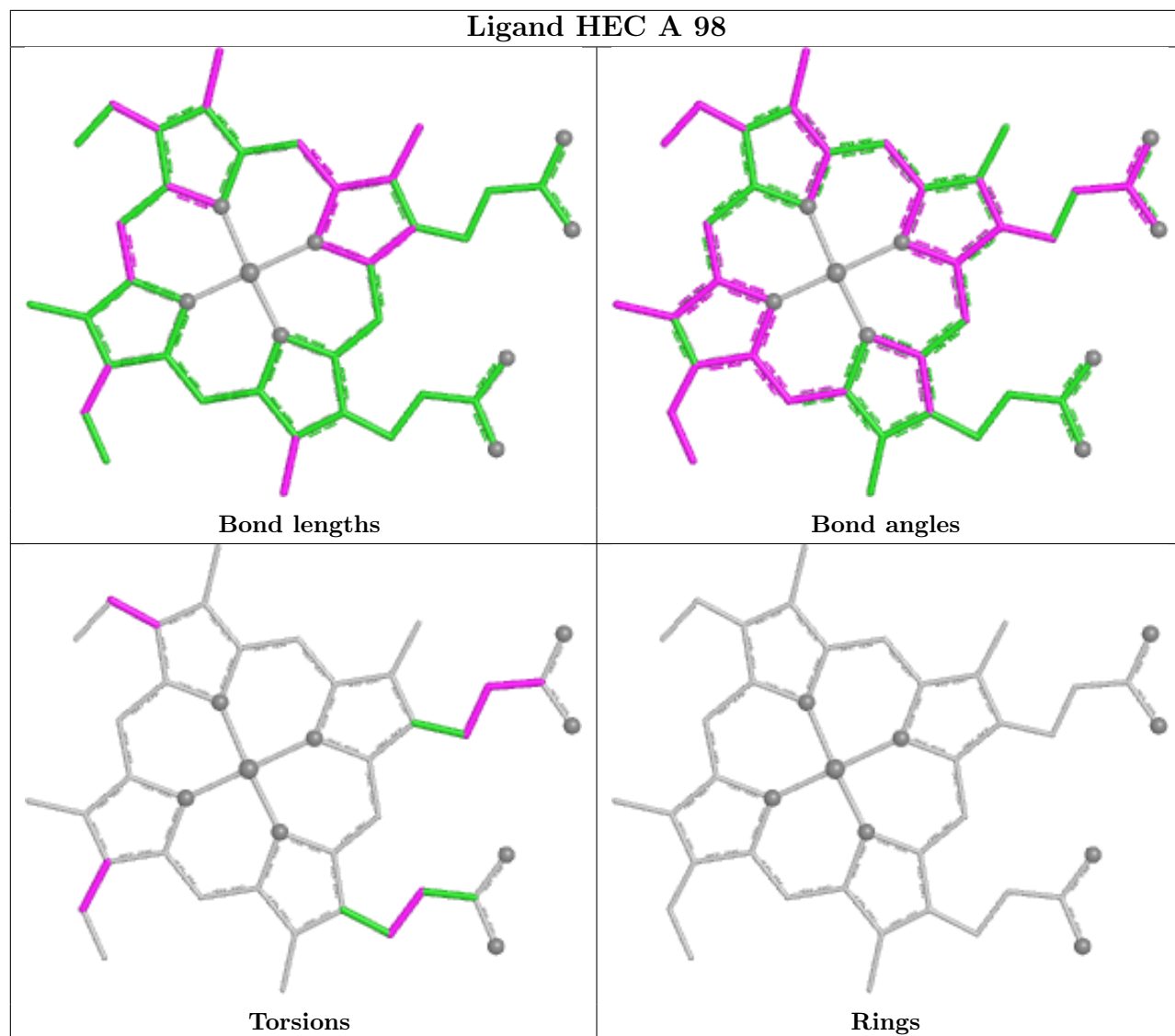
There are no torsion outliers.

There are no ring outliers.

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 than 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.







6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided