

Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	2KSU
Title	:	Redox linked conformational changes in cytochrome C3 from Desulfovibrio
		desulfuricans ATCC 27774
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Deposited on	:	2010-01-13

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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

Cyrange NmrClust MolProbity Mogul buster-report Percentile statistics RCI PANAV ShiftChecker Ideal geometry (proteins) Ideal geometry (DNA, RNA)	: : : : : : : : : : : : : : : : : : : :	Kirchner and Güntert (2011) Kelley et al. (1996) 4.02b-467 1.8.5 (274361), CSD as541be (2020) 1.1.7 (2018) 20191225.v01 (using entries in the PDB archive December 25th 2019) v_1n_11_5_13_A (Berjanski et al., 2005) Wang et al. (2010) 2.11 Engh & Huber (2001) Parkinson et al. (1996)
Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)	:	Parkinson et al. (1996) 2.11
	•	

1 Overall quality at a glance (i)

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.

Metri	С	Percentile Rank	S	Value
Clashscore				33
Ramachandran outliers				3.8%
Sidechain outliers				27.3%
	Worse		Better	-
	Percentile	e relative to all structures		
	Percentile	e relative to all NMR structures		
		TT7 1 1 1 •		· · · · · · · · · · · · · · · · · · ·
Ramachandran outliers Sidechain outliers	Worse Percentile Percentile	e relative to all structures e relative to all NMR structures	Better	3.8% 27.3%

Metric	Whole archive (#Entries)	NMR archive $(\#\operatorname{Entries})$
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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 <=5%

Mol	Chain	Length		Quality of chain		
1	A	107	36%	51%	•	8%



2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 19 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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

	Well-defined (core) p	protein residues	
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:3-A:88, A:96-A:107 (98)	0.23	19

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 3 clusters and 1 single-model cluster was found.

Cluster number	Models
1	1, 2, 3, 4, 5, 8, 9, 11, 12, 13, 14, 17, 19
2	6, 10, 16, 18
3	7, 15
Single-model clusters	20



3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1775 atoms, of which 796 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called Cytochrome c3.

Mol	Chain	Residues			Aton	ıs			Trace
1	Λ	107	Total	С	Η	Ν	Ο	\mathbf{S}	0
L	A	107	1603	503	796	145	150	9	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	71	ARG	LYS	SEE REMARK 999	UNP Q9L915

• Molecule 2 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



Mol	Chain	Residues		At	\mathbf{oms}		
0	Λ	1	Total	С	Fe	Ν	Ο
	A	L	43	34	1	4	4
0	Λ	1	Total	С	Fe	Ν	Ο
	A	L	43	34	1	4	4
0	Λ	1	Total	С	Fe	Ν	Ο
	A	L	43	34	1	4	4
0	Λ	1	Total	С	Fe	Ν	Ο
	A		43	34	1	4	4



4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA 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 c3



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 c3



4.2.2 Score per residue for model 2





4.2.3 Score per residue for model 3

• Molecule 1: Cytochrome c3



4.2.4 Score per residue for model 4

• Molecule 1: Cytochrome c3



4.2.5 Score per residue for model 5

• Molecule 1: Cytochrome c3



4.2.6 Score per residue for model 6





4.2.7 Score per residue for model 7

• Molecule 1: Cytochrome c3



4.2.8 Score per residue for model 8

• Molecule 1: Cytochrome c3

Cł	ıa	in	1 /	4:						30	%	_														49	9%										12	2%		·	8	3%	_				
A1 23	R3		<mark>8</mark> 8	<mark>⊻ 8</mark>	6A	E10 V11	K12	G13	S14	d Th	2	M19	F20	P21	H22 A02	624 P24	H25	E26	K27	V28	R CE	V31	T32	C33	H34	н <u>3</u> 5 	136 V37	D38	639 7700	D#40	542 S42	Y43	A44 VAE	C46	G47	DE A	104 155	T56	A57	K58	E61	K62	S63	L64	V68	69H	A70
R7 1	L74	K75	H76	S78	C79	L80 A81	C82	H83	S84	VR6	V87	A88	E89	K90	P91 F07	193	K94	K95	D96	L97	IA8	K102	S103	K104	C105	H106	P107																				

4.2.9 Score per residue for model 9





4.2.10 Score per residue for model 10

• Molecule 1: Cytochrome c3



4.2.11 Score per residue for model 11

• Molecule 1: Cytochrome c3



4.2.12 Score per residue for model 12

• Molecule 1: Cytochrome c3



4.2.13 Score per residue for model 13



4.2.14 Score per residue for model 14

• Molecule 1: Cytochrome c3



4.2.15 Score per residue for model 15

• Molecule 1: Cytochrome c3



4.2.16 Score per residue for model 16



4.2.17 Score per residue for model 17

• Molecule 1: Cytochrome c3



4.2.18 Score per residue for model 18

• Molecule 1: Cytochrome c3



4.2.19 Score per residue for model 19 (medoid)

• Molecule 1: Cytochrome c3



4.2.20 Score per residue for model 20





5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: torsion angle dynamics, simulated annealing.

Of the 500 calculated structures, 20 were deposited, based on the following criterion: target function.

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

Software name	Classification	Version
PARADYANA	structure solution	
PARADYANA	refinement	

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.



6 Model quality (i)

6.1 Standard geometry (i)

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

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 (i)

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	А	735	716	722	45 ± 5
2	А	172	0	120	25 ± 4
All	All	18140	14320	16840	1162

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 33.

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

Atom 1	Atom-2	$\mathrm{Clash}(\mathrm{\AA})$	Distance(Å)	Models	
Atom-1				Worst	Total
2:A:251:HEC:CGD	2:A:251:HEC:HMD1	1.02	1.83	11	3
2:A:251:HEC:HMD1	2:A:251:HEC:CGD	1.01	1.84	8	6
1:A:70:ALA:CB	1:A:74:LEU:HD11	0.98	1.89	2	20
1:A:83:HIS:O	1:A:87:VAL:HG23	0.90	1.66	18	6
2:A:282:HEC:HBC3	2:A:282:HEC:HMC1	0.87	1.47	3	10
1:A:68:VAL:HG21	2:A:305:HEC:CGD	0.87	2.00	5	3
1:A:68:VAL:HG21	2:A:305:HEC:O2D	0.86	1.71	5	4
1:A:11:VAL:HG22	2:A:233:HEC:CGD	0.86	2.01	14	8
1:A:11:VAL:HG13	2:A:233:HEC:O2D	0.86	1.71	2	3
2:A:251:HEC:HMB1	2:A:251:HEC:HBB3	0.85	1.48	9	13
2:A:282:HEC:HMC1	2:A:282:HEC:HBC3	0.85	1.47	19	10



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			D1 (8)	Models		
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total	
2:A:305:HEC:HBC3	2:A:305:HEC:HMC1	0.84	1.49	9	11	
1:A:70:ALA:HB3	1:A:74:LEU:HD11	0.84	1.49	8	20	
2:A:305:HEC:HMC1	2:A:305:HEC:HBC3	0.84	1.49	8	9	
1:A:23:ALA:HB3	1:A:24:PRO:HD3	0.81	1.51	16	20	
1:A:104:LYS:CD	2:A:282:HEC:HMA3	0.80	2.07	17	2	
2:A:233:HEC:HBD2	2:A:233:HEC:HMD1	0.80	1.51	14	6	
2:A:233:HEC:HMD1	2:A:233:HEC:HBD2	0.79	1.51	7	3	
2:A:233:HEC:HBD1	2:A:233:HEC:HMD1	0.79	1.51	2	2	
1:A:68:VAL:HG21	2:A:305:HEC:O1D	0.79	1.77	1	3	
2:A:305:HEC:HMC1	2:A:305:HEC:CBC	0.78	2.08	19	11	
1:A:70:ALA:HB1	1:A:74:LEU:HD11	0.78	1.55	18	20	
1:A:11:VAL:HG13	2:A:233:HEC:O1D	0.78	1.78	7	2	
2:A:305:HEC:CBC	2:A:305:HEC:HMC1	0.78	2.07	13	9	
1:A:74:LEU:HD12	1:A:78:SER:OG	0.78	1.78	14	20	
2:A:233:HEC:CBD	2:A:233:HEC:HMD1	0.77	2.10	14	5	
2:A:233:HEC:HMD1	2:A:233:HEC:CBD	0.76	2.10	3	6	
2:A:251:HEC:CBB	2:A:251:HEC:HMB1	0.76	2.11	9	1	
1:A:46:CYS:SG	2:A:251:HEC:C3B	0.76	2.74	9	1	
1:A:20:PHE:CE2	2:A:233:HEC:CHD	0.75	2.70	7	20	
1:A:87:VAL:HG21	1:A:98:THR:HG21	0.74	1.60	7	9	
1:A:45:LYS:O	2:A:251:HEC:HMC3	0.71	1.84	19	7	
1:A:78:SER:O	1:A:81:ALA:HB3	0.71	1.85	6	20	
1:A:11:VAL:HG22	2:A:233:HEC:O1D	0.71	1.86	6	2	
1:A:69:HIS:O	1:A:70:ALA:C	0.70	2.29	13	20	
1:A:20:PHE:CZ	2:A:233:HEC:CHD	0.69	2.75	5	17	
2:A:282:HEC:HMB1	2:A:282:HEC:HBB3	0.69	1.65	12	9	
1:A:36:LEU:N	1:A:36:LEU:HD23	0.69	2.03	12	3	
1:A:21:PRO:CG	1:A:24:PRO:HG2	0.69	2.18	9	19	
2:A:282:HEC:HBB3	2:A:282:HEC:HMB1	0.69	1.65	2	11	
1:A:35:HIS:CD2	1:A:76:HIS:CD2	0.68	2.82	3	4	
1:A:96:ASP:C	1:A:97:LEU:HD23	0.68	2.08	20	4	
1:A:100:CYS:SG	2:A:305:HEC:HMB1	0.67	2.29	20	7	
1:A:86:VAL:HG11	1:A:97:LEU:CD1	0.65	2.21	2	9	
1:A:28:VAL:HG11	2:A:282:HEC:HBC2	0.65	1.68	18	20	
1:A:55:LEU:HD21	1:A:64:LEU:HB3	0.65	1.69	10	1	
1:A:87:VAL:HG21	1:A:98:THR:CG2	0.64	2.23	8	6	
1:A:104:LYS:HD2	2:A:282:HEC:HMA3	0.64	1.69	17	1	
2:A:251:HEC:HBB3	2:A:251:HEC:HMB1	0.64	1.70	8	5	
2:A:282:HEC:HMC1	2:A:282:HEC:CBC	0.64	2.22	3	12	
2:A:282:HEC:CBC	2:A:282:HEC:HMC1	0.64	2.22	14	8	
2:A:251:HEC:O1D	2:A:251:HEC:HMD1	0.63	1.93	11	2	



		(9)	^ 0 、	Mo	dels
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:A:9:VAL:HG23	2:A:233:HEC:O1D	0.63	1.94	6	1
2:A:251:HEC:HMD1	2:A:251:HEC:CBD	0.63	2.24	15	7
1:A:21:PRO:HG2	1:A:24:PRO:HG2	0.63	1.69	5	19
1:A:46:CYS:SG	2:A:251:HEC:CBB	0.62	2.87	9	1
1:A:64:LEU:HD23	2:A:305:HEC:O1D	0.62	1.94	4	3
1:A:66:TYR:CD2	1:A:66:TYR:O	0.62	2.52	13	1
2:A:251:HEC:CBD	2:A:251:HEC:HMD1	0.61	2.25	14	2
1:A:20:PHE:CD2	1:A:20:PHE:O	0.61	2.54	16	1
1:A:104:LYS:HZ3	1:A:105:CYS:CB	0.61	2.09	10	1
1:A:42:SER:O	1:A:43:TYR:CD1	0.60	2.54	2	7
1:A:104:LYS:HD3	2:A:282:HEC:HMA3	0.60	1.71	10	2
2:A:251:HEC:HMD1	2:A:251:HEC:O2D	0.60	1.95	8	1
1:A:104:LYS:NZ	2:A:282:HEC:C2A	0.60	2.65	17	1
1:A:86:VAL:CG1	1:A:97:LEU:CD1	0.59	2.80	4	6
1:A:5:PRO:HG2	1:A:22:HIS:ND1	0.59	2.12	11	2
1:A:104:LYS:CE	2:A:282:HEC:C3A	0.59	2.80	17	1
1:A:104:LYS:HZ1	2:A:282:HEC:C1A	0.59	2.10	17	1
2:A:233:HEC:HBC3	2:A:233:HEC:HMC1	0.59	1.73	9	2
1:A:86:VAL:CG1	1:A:97:LEU:HD12	0.58	2.29	2	5
1:A:58:LYS:O	1:A:65:TYR:CD2	0.57	2.57	10	6
2:A:233:HEC:CGD	2:A:233:HEC:HMD1	0.57	2.30	12	2
1:A:31:VAL:HG22	1:A:36:LEU:HD21	0.57	1.76	12	1
1:A:86:VAL:HG11	1:A:97:LEU:HD12	0.57	1.77	7	5
1:A:44:ALA:HB1	1:A:48:SER:CB	0.56	2.30	3	4
1:A:26:GLU:O	1:A:26:GLU:CG	0.56	2.51	9	6
2:A:233:HEC:HMC1	2:A:233:HEC:HBC3	0.56	1.75	12	12
1:A:87:VAL:CG2	1:A:98:THR:HG21	0.56	2.29	7	3
1:A:64:LEU:HD23	2:A:305:HEC:CGD	0.56	2.31	11	3
1:A:8:PRO:HG3	1:A:21:PRO:HA	0.56	1.77	14	7
2:A:251:HEC:HMD1	2:A:251:HEC:HBD2	0.56	1.78	15	4
1:A:25:HIS:CD2	2:A:233:HEC:HBC2	0.56	2.35	4	18
1:A:106:HIS:N	1:A:107:PRO:CD	0.56	2.68	10	4
1:A:64:LEU:HD23	2:A:305:HEC:O2D	0.56	2.00	9	1
1:A:23:ALA:CB	1:A:24:PRO:HD3	0.56	2.29	5	18
1:A:11:VAL:HG22	2:A:233:HEC:O2D	0.55	2.01	9	2
1:A:104:LYS:NZ	2:A:282:HEC:C1A	0.55	2.69	17	1
1:A:57:ALA:O	1:A:58:LYS:CB	0.55	2.55	9	13
1:A:85:LYS:O	1:A:88:ALA:HB3	0.55	2.01	1	6
1:A:31:VAL:HG23	1:A:36:LEU:CD2	0.55	2.32	9	1
1:A:31:VAL:HG23	1:A:36:LEU:HD21	0.55	1.76	9	1
2:A:305:HEC:C3D	2:A:305:HEC:O2D	0.54	2.55	12	1



	A 4 0			Models	
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:A:87:VAL:CG2	1:A:98:THR:CG2	0.54	2.85	7	5
1:A:42:SER:C	1:A:43:TYR:CD1	0.54	2.80	18	11
2:A:251:HEC:HBD2	2:A:251:HEC:HMD1	0.54	1.80	19	1
1:A:26:GLU:CG	1:A:26:GLU:O	0.53	2.55	18	1
1:A:14:SER:CB	1:A:55:LEU:HD22	0.53	2.33	18	1
1:A:23:ALA:N	1:A:24:PRO:CD	0.53	2.71	5	20
2:A:305:HEC:O2A	2:A:305:HEC:C2A	0.53	2.55	14	1
1:A:68:VAL:HG11	2:A:305:HEC:O2D	0.53	2.04	12	1
1:A:20:PHE:CE2	2:A:233:HEC:C1D	0.53	2.92	5	2
1:A:97:LEU:N	1:A:97:LEU:HD23	0.52	2.19	20	1
1:A:14:SER:N	1:A:55:LEU:CD2	0.52	2.72	3	1
2:A:305:HEC:CGD	2:A:305:HEC:CHA	0.52	2.88	12	1
1:A:65:TYR:CD1	2:A:305:HEC:O1A	0.52	2.62	9	1
1:A:100:CYS:SG	2:A:305:HEC:CMB	0.52	2.98	4	3
1:A:31:VAL:CG2	1:A:36:LEU:HD21	0.51	2.36	9	2
1:A:37:VAL:HG12	1:A:38:ASP:OD1	0.51	2.06	16	1
2:A:251:HEC:HMD1	2:A:251:HEC:HBD1	0.51	1.80	2	1
2:A:305:HEC:CMC	2:A:305:HEC:CBC	0.51	2.87	9	2
2:A:233:HEC:HMD1	2:A:233:HEC:HBD1	0.51	1.80	1	1
1:A:58:LYS:O	1:A:65:TYR:CE2	0.50	2.64	10	3
1:A:30:CYS:O	1:A:34:HIS:N	0.50	2.42	5	9
1:A:58:LYS:O	1:A:59:LYS:CG	0.50	2.60	18	1
2:A:251:HEC:HBD1	2:A:251:HEC:HMD1	0.50	1.81	18	1
1:A:64:LEU:O	2:A:305:HEC:CGD	0.50	2.60	1	6
1:A:96:ASP:OD2	1:A:104:LYS:CG	0.50	2.60	5	1
1:A:33:CYS:HB2	2:A:233:HEC:C2C	0.50	2.37	11	20
1:A:54:ASP:CB	1:A:62:LYS:O	0.50	2.60	6	9
1:A:97:LEU:C	1:A:98:THR:CG2	0.50	2.80	15	2
1:A:31:VAL:O	1:A:33:CYS:N	0.49	2.46	5	11
1:A:14:SER:N	1:A:55:LEU:HD22	0.49	2.21	8	1
1:A:11:VAL:O	1:A:13:GLY:N	0.49	2.46	1	4
1:A:25:HIS:CD2	2:A:233:HEC:CBC	0.49	2.96	15	12
1:A:4:VAL:HG11	1:A:26:GLU:OE2	0.48	2.08	15	1
1:A:66:TYR:CG	1:A:66:TYR:O	0.48	2.66	13	1
1:A:81:ALA:O	1:A:84:SER:CB	0.48	2.61	8	15
1:A:29:GLU:OE1	1:A:31:VAL:HG12	0.48	2.07	6	1
1:A:36:LEU:N	1:A:36:LEU:CD2	0.48	2.74	12	2
1:A:104:LYS:HE3	2:A:282:HEC:C3A	0.48	2.38	17	1
1:A:71:ARG:CG	1:A:71:ARG:O	0.48	2.61	18	2
2:A:233:HEC:O1A	2:A:233:HEC:HMA3	0.48	2.07	10	1
1:A:68:VAL:CG2	2:A:305:HEC:O1D	0.48	2.60	5	2



			^ 0 、	Mo	dels
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:A:57:ALA:C	1:A:58:LYS:CG	0.48	2.81	7	1
1:A:82:CYS:O	1:A:85:LYS:N	0.48	2.46	9	15
1:A:31:VAL:HG22	1:A:36:LEU:CD2	0.48	2.38	12	1
1:A:35:HIS:HB2	1:A:76:HIS:CD2	0.48	2.43	2	3
2:A:233:HEC:HHA	2:A:233:HEC:CBD	0.48	2.38	6	2
2:A:233:HEC:HMD1	2:A:233:HEC:O2D	0.48	2.08	17	1
1:A:20:PHE:CE1	1:A:25:HIS:CE1	0.48	3.02	9	10
1:A:35:HIS:CG	1:A:76:HIS:CE1	0.48	3.01	11	5
1:A:68:VAL:HG11	2:A:305:HEC:O1D	0.48	2.09	1	1
1:A:104:LYS:HZ3	1:A:105:CYS:HB2	0.47	1.68	10	1
1:A:14:SER:CB	2:A:305:HEC:O2A	0.47	2.63	11	1
2:A:233:HEC:HBC1	2:A:282:HEC:CHC	0.47	2.39	9	11
1:A:16:LYS:HD2	1:A:106:HIS:CE1	0.47	2.44	6	1
1:A:28:VAL:CG1	1:A:32:THR:HG21	0.47	2.40	8	1
1:A:68:VAL:CG2	2:A:305:HEC:O2D	0.47	2.62	2	1
1:A:35:HIS:CG	1:A:76:HIS:CD2	0.47	3.02	3	2
1:A:11:VAL:HG22	2:A:233:HEC:CBD	0.47	2.39	7	2
2:A:233:HEC:HBA2	2:A:233:HEC:HMA3	0.47	1.86	4	1
2:A:233:HEC:CBD	2:A:233:HEC:CMD	0.47	2.88	15	3
1:A:35:HIS:HB3	1:A:76:HIS:CD2	0.46	2.45	8	2
2:A:305:HEC:CGD	2:A:305:HEC:C4D	0.46	2.92	12	2
2:A:233:HEC:O1D	2:A:233:HEC:HMD1	0.46	2.09	16	1
2:A:305:HEC:C4D	2:A:305:HEC:O2D	0.46	2.63	12	1
1:A:64:LEU:CD2	2:A:305:HEC:CGD	0.46	2.93	15	3
1:A:20:PHE:CE1	1:A:25:HIS:ND1	0.46	2.83	8	8
1:A:55:LEU:HD22	2:A:305:HEC:O1A	0.46	2.09	4	1
1:A:71:ARG:O	1:A:71:ARG:CG	0.46	2.64	15	1
1:A:104:LYS:CD	2:A:282:HEC:CMA	0.46	2.87	17	1
1:A:82:CYS:O	1:A:84:SER:N	0.46	2.48	17	9
2:A:233:HEC:HMD1	2:A:233:HEC:O1D	0.46	2.10	10	1
1:A:11:VAL:CG2	2:A:233:HEC:CGD	0.46	2.94	16	2
1:A:70:ALA:HB3	1:A:74:LEU:CD1	0.46	2.34	9	8
1:A:9:VAL:HG21	2:A:233:HEC:HBD1	0.46	1.86	5	1
1:A:102:LYS:N	1:A:106:HIS:O	0.46	2.49	15	3
1:A:21:PRO:HB2	1:A:24:PRO:CD	0.45	2.40	9	20
1:A:35:HIS:CD2	1:A:76:HIS:CE1	0.45	3.04	11	2
2:A:233:HEC:CGD	2:A:233:HEC:CHA	0.45	2.95	13	1
1:A:4:VAL:HG13	1:A:4:VAL:O	0.45	2.11	4	2
1:A:31:VAL:O	1:A:32:THR:C	0.45	2.55	15	19
1:A:16:LYS:HG2	1:A:106:HIS:CE1	0.45	2.46	19	1
1:A:30:CYS:O	1:A:33:CYS:N	0.45	2.44	20	4



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			(9)	Models	
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
2:A:251:HEC:CMD	2:A:251:HEC:HBD2	0.45	2.40	15	3
1:A:104:LYS:NZ	1:A:105:CYS:SG	0.45	2.88	10	1
1:A:48:SER:OG	2:A:251:HEC:CMC	0.45	2.65	6	1
1:A:31:VAL:C	1:A:33:CYS:N	0.45	2.70	5	10
1:A:66:TYR:CD2	2:A:251:HEC:O1A	0.45	2.70	10	1
1:A:28:VAL:CG1	2:A:282:HEC:HBC2	0.45	2.41	9	2
1:A:57:ALA:O	1:A:58:LYS:CG	0.45	2.65	7	1
1:A:14:SER:OG	1:A:15:GLN:N	0.45	2.49	3	6
1:A:52:HIS:ND1	1:A:61:GLU:O	0.45	2.49	20	1
1:A:104:LYS:HZ1	2:A:282:HEC:C4A	0.45	2.25	17	1
2:A:251:HEC:CMD	2:A:251:HEC:HBD1	0.45	2.42	2	1
1:A:5:PRO:HG3	2:A:233:HEC:CGA	0.45	2.42	18	1
1:A:11:VAL:HG12	2:A:305:HEC:CGD	0.45	2.42	10	1
1:A:87:VAL:CG2	1:A:98:THR:HG23	0.45	2.40	3	1
1:A:30:CYS:O	1:A:31:VAL:C	0.45	2.55	3	11
2:A:233:HEC:CMD	2:A:233:HEC:CBD	0.44	2.89	1	1
1:A:105:CYS:C	1:A:107:PRO:CD	0.44	2.85	14	3
1:A:104:LYS:NZ	2:A:305:HEC:HBC3	0.44	2.27	10	1
1:A:68:VAL:CB	2:A:305:HEC:O1D	0.44	2.66	5	1
1:A:55:LEU:CD2	2:A:305:HEC:CGA	0.44	2.95	15	1
1:A:36:LEU:CD2	1:A:36:LEU:N	0.44	2.79	9	1
2:A:251:HEC:HBD2	2:A:251:HEC:CMD	0.44	2.43	7	2
1:A:31:VAL:HG13	1:A:32:THR:N	0.44	2.27	16	4
1:A:82:CYS:O	1:A:85:LYS:CG	0.44	2.66	10	1
1:A:66:TYR:CD2	2:A:251:HEC:O2A	0.44	2.69	2	1
1:A:66:TYR:CE2	2:A:251:HEC:O1A	0.44	2.71	10	1
1:A:74:LEU:C	1:A:76:HIS:N	0.44	2.70	15	2
2:A:305:HEC:CBC	2:A:305:HEC:CMC	0.44	2.86	15	2
2:A:233:HEC:HMD1	2:A:233:HEC:CGD	0.44	2.43	17	2
1:A:29:GLU:O	1:A:32:THR:CB	0.44	2.66	8	3
1:A:25:HIS:CG	2:A:233:HEC:HBC2	0.44	2.48	11	7
2:A:233:HEC:HMB1	2:A:233:HEC:HBB3	0.44	1.90	10	6
1:A:69:HIS:O	1:A:70:ALA:O	0.44	2.35	13	7
1:A:33:CYS:HB2	2:A:233:HEC:CMC	0.44	2.43	20	2
1:A:16:LYS:CB	2:A:305:HEC:O1D	0.44	2.65	20	1
1:A:75:LYS:CD	2:A:251:HEC:O1D	0.44	2.66	3	1
1:A:55:LEU:HD11	2:A:305:HEC:O2D	0.43	2.12	19	1
2:A:251:HEC:O2D	2:A:251:HEC:HMD1	0.43	2.13	16	1
2:A:233:HEC:CMD	2:A:282:HEC:HBB2	0.43	2.42	5	1
1:A:66:TYR:O	1:A:66:TYR:CD2	0.43	2.71	5	2
1:A:104:LYS:NZ	2:A:282:HEC:C3A	0.43	2.81	17	1



				Models	
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
2:A:251:HEC:HBD1	2:A:251:HEC:CMD	0.43	2.43	18	1
1:A:9:VAL:CG2	2:A:233:HEC:HBD2	0.43	2.44	8	1
1:A:71:ARG:NE	1:A:84:SER:OG	0.43	2.50	15	2
1:A:20:PHE:CZ	2:A:233:HEC:C4C	0.43	3.01	16	1
1:A:61:GLU:OE2	1:A:61:GLU:N	0.43	2.51	7	1
1:A:16:LYS:O	2:A:305:HEC:CBD	0.43	2.66	20	1
2:A:233:HEC:HBB3	2:A:233:HEC:HMB1	0.43	1.91	6	1
1:A:74:LEU:O	1:A:76:HIS:N	0.43	2.52	15	1
1:A:103:SER:OG	1:A:104:LYS:N	0.43	2.51	9	1
1:A:11:VAL:HG12	2:A:305:HEC:O2D	0.43	2.14	15	1
1:A:31:VAL:HG13	1:A:32:THR:H	0.42	1.74	5	1
1:A:82:CYS:C	1:A:84:SER:N	0.42	2.72	10	7
1:A:56:THR:O	1:A:57:ALA:C	0.42	2.56	15	4
1:A:101:ALA:C	1:A:103:SER:N	0.42	2.72	17	1
1:A:11:VAL:HG22	2:A:233:HEC:HBD1	0.42	1.91	7	1
2:A:233:HEC:CBD	2:A:233:HEC:HHA	0.42	2.44	4	1
1:A:74:LEU:HD22	2:A:251:HEC:O1A	0.42	2.14	4	1
1:A:33:CYS:CB	2:A:233:HEC:C2C	0.42	2.97	20	1
1:A:56:THR:O	1:A:56:THR:CG2	0.42	2.67	1	1
1:A:9:VAL:HG23	2:A:233:HEC:HBD2	0.42	1.90	8	1
2:A:233:HEC:C4D	2:A:233:HEC:CGD	0.42	2.98	13	1
2:A:305:HEC:CHA	2:A:305:HEC:CGD	0.42	2.97	2	1
1:A:29:GLU:OE1	1:A:31:VAL:CG1	0.42	2.68	6	1
2:A:251:HEC:CMD	2:A:251:HEC:CBD	0.42	2.98	18	1
1:A:79:CYS:C	1:A:81:ALA:N	0.42	2.71	5	15
2:A:251:HEC:CBD	2:A:251:HEC:HHA	0.42	2.45	4	4
1:A:21:PRO:HG3	2:A:282:HEC:CBA	0.42	2.45	10	1
2:A:282:HEC:HHA	2:A:282:HEC:CBA	0.42	2.45	11	1
2:A:233:HEC:HBD2	2:A:233:HEC:CMD	0.41	2.45	12	3
1:A:42:SER:O	1:A:43:TYR:CG	0.41	2.73	17	2
2:A:282:HEC:CMC	2:A:282:HEC:CBC	0.41	2.96	3	2
1:A:101:ALA:O	1:A:102:LYS:CG	0.41	2.68	10	1
1:A:45:LYS:C	1:A:47:GLY:N	0.41	2.72	8	3
2:A:251:HEC:HHA	2:A:251:HEC:CBD	0.41	2.45	9	4
1:A:11:VAL:N	1:A:18:VAL:O	0.41	2.50	12	3
1:A:104:LYS:HZ2	2:A:282:HEC:C2A	0.41	2.27	17	1
1:A:46:CYS:SG	1:A:64:LEU:HD11	0.41	2.55	5	2
1:A:49:SER:O	1:A:51:CYS:SG	0.41	2.79	16	3
1:A:11:VAL:O	1:A:12:LYS:C	0.41	2.58	6	1
1:A:6:ASP:C	1:A:6:ASP:OD1	0.41	2.59	8	1
1:A:74:LEU:O	1:A:75:LYS:C	0.41	2.59	8	1



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A 4 1	A 4 0		\mathbf{D}	Models	
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:A:21:PRO:HG3	2:A:282:HEC:HBA1	0.41	1.92	10	1
1:A:54:ASP:O	1:A:62:LYS:O	0.41	2.39	13	1
1:A:57:ALA:O	1:A:58:LYS:HB2	0.41	2.16	7	1
1:A:64:LEU:CD2	2:A:305:HEC:O1D	0.41	2.66	4	1
1:A:25:HIS:CE1	2:A:282:HEC:NA	0.41	2.89	14	5
1:A:44:ALA:O	1:A:45:LYS:C	0.41	2.59	13	4
1:A:55:LEU:HD12	1:A:55:LEU:N	0.41	2.31	13	1
2:A:233:HEC:HBC1	2:A:282:HEC:C1C	0.41	2.45	16	1
1:A:50:GLY:C	1:A:51:CYS:SG	0.41	2.99	9	1
1:A:97:LEU:O	1:A:98:THR:HG22	0.41	2.16	15	1
1:A:104:LYS:O	2:A:282:HEC:HMA3	0.41	2.16	8	1
2:A:282:HEC:CBC	2:A:282:HEC:CMC	0.40	2.97	10	1
1:A:48:SER:O	1:A:49:SER:C	0.40	2.60	13	1
1:A:14:SER:HA	1:A:55:LEU:HD13	0.40	1.93	2	1
1:A:14:SER:N	2:A:305:HEC:O2A	0.40	2.49	15	1
1:A:106:HIS:O	1:A:107:PRO:O	0.40	2.39	2	1
1:A:100:CYS:O	1:A:106:HIS:CB	0.40	2.70	1	1
1:A:53:ASP:CG	1:A:53:ASP:O	0.40	2.60	12	1
1:A:13:GLY:HA3	2:A:305:HEC:CBD	0.40	2.46	1	1
1:A:10:GLU:OE2	1:A:10:GLU:O	0.40	2.40	14	1

6.3 Torsion angles (i)

6.3.1 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 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	А	97/107~(91%)	68 ± 3 (70±3%)	25 ± 3 (26 $\pm3\%$)	$4\pm2~(4\pm2\%)$	5	33	
All	All	1940/2140~(91%)	1366~(70%)	500 (26%)	74 (4%)	5	33	

All 12 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	А	70	ALA	20
1	А	58	LYS	10



Mol	Chain	Res	Type	Models (Total)
1	А	32	THR	10
1	А	12	LYS	8
1	А	83	HIS	8
1	А	13	GLY	7
1	А	35	HIS	4
1	А	99	GLY	3
1	А	8	PRO	1
1	А	46	CYS	1
1	А	51	CYS	1
1	А	41	GLU	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	А	83/91~(91%)	60 ± 3 (73 $\pm3\%$)	23 ± 3 (27 $\pm3\%$)	2 21
All	All	1660/1820~(91%)	1206~(73%)	454 (27%)	2 21

All 41 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	\mathbf{Res}	Type	Models (Total)
1	А	14	SER	20
1	А	78	SER	20
1	А	54	ASP	19
1	А	71	ARG	19
1	А	105	CYS	18
1	А	46	CYS	17
1	А	36	LEU	17
1	А	80	LEU	15
1	А	7	LYS	15
1	А	33	CYS	15
1	А	10	GLU	14
1	А	58	LYS	14
1	А	16	LYS	13
1	А	56	THR	13
1	А	15	GLN	13



Mol	Chain	Res	Type	Models (Total)
1	А	102	LYS	13
1	А	9	VAL	13
1	А	27	LYS	13
1	А	26	GLU	13
1	А	104	LYS	12
1	А	40	LYS	12
1	А	61	GLU	12
1	А	75	LYS	11
1	А	85	LYS	11
1	А	96	ASP	11
1	А	19	MET	10
1	А	45	LYS	10
1	А	29	GLU	8
1	А	38	ASP	8
1	А	55	LEU	8
1	А	59	LYS	7
1	А	12	LYS	7
1	А	62	LYS	7
1	А	73	GLU	5
1	A	41	GLU	5
1	A	84	SER	4
1	A	49	SER	4
1	A	103	SER	3
1	А	42	SER	3
1	A	76	HIS	1
1	А	48	SER	1

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6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates (i)

There are no carbohydrates in this entry.



6.6 Ligand geometry (i)

4 ligands are modelled in this entry.

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.

Mal	Tuno	Chain	Dog	Link		Bond leng	gths
MOI	туре	Unam	nes		Counts	RMSZ	$\#Z{>}2$
2	HEC	А	233	1	26,50,50	$1.64{\pm}0.01$	2 ± 0 (7±0%)
2	HEC	А	282	1	26,50,50	$1.64{\pm}0.02$	2 ± 0 (7±0%)
2	HEC	А	251	1	26,50,50	$1.66 {\pm} 0.03$	2 ± 0 (7±0%)
2	HEC	А	305	1	26,50,50	$1.67 {\pm} 0.01$	2 ± 0 (7±0%)

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.

Mal	Turne	Chain	Dec	Tink		Bond ang	les
	туре	Cham	nes		Counts	RMSZ	#Z>2
2	HEC	А	233	1	18,82,82	$1.35 {\pm} 0.00$	0±0 (0±0%)
2	HEC	А	282	1	18,82,82	$1.35 {\pm} 0.00$	0±0 (0±0%)
2	HEC	А	251	1	18,82,82	$1.35 {\pm} 0.00$	0±0 (0±0%)
2	HEC	А	305	1	18,82,82	$1.35 {\pm} 0.00$	0±0 (0±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
2	HEC	А	251	1	-	$0\pm0,\!6,\!54,\!54$	-
2	HEC	А	305	1	-	$0\pm0,\!6,\!54,\!54$	-
2	HEC	А	282	1	-	$0\pm0,\!6,\!54,\!54$	-
2	HEC	А	233	1	-	$0\pm0,\!6,\!54,\!54$	-



Mol	Chain	Res	Type	Atoms	Z	${ m Observed}({ m \AA})$	$\operatorname{Ideal}(\operatorname{\AA})$	Models	
								Worst	Total
2	А	282	HEC	C3C-C2C	5.20	1.35	1.40	3	20
2	А	305	HEC	C3C-C2C	5.19	1.35	1.40	9	20
2	А	305	HEC	C3B-C2B	5.19	1.35	1.40	12	20
2	А	282	HEC	C3B-C2B	5.18	1.35	1.40	2	20
2	А	251	HEC	C3B-C2B	5.18	1.35	1.40	9	20
2	А	251	HEC	C3C-C2C	5.17	1.35	1.40	11	20
2	А	233	HEC	C3B-C2B	5.16	1.35	1.40	12	20
2	А	233	HEC	C3C-C2C	5.15	1.35	1.40	9	20

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

There are no bond-angle outliers.

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 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.

















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 (i)

No chemical shift data were provided

