



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2018 – 11:21 AM EST

PDB ID : 1CF9
Title : Structure of the mutant VAL169CYS of catalase HP11 from Escherichia coli
Authors : Mate, M.J.; Loewen, P.C.; Fita, I.
Deposited on : 1999-03-24
Resolution : 1.80 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030736
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030736

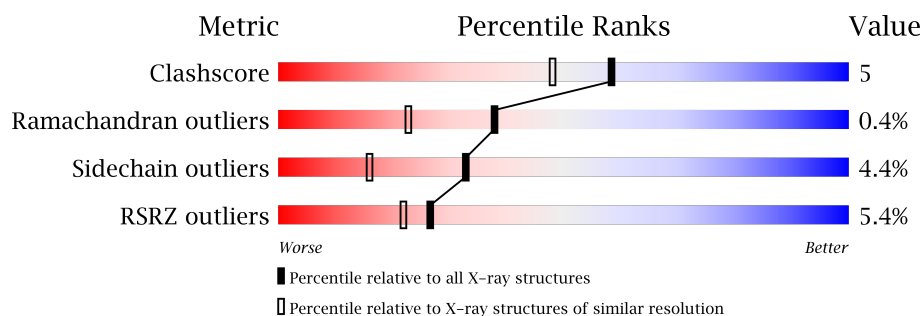
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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))
Clashscore	112137	5742 (1.80-1.80)
Ramachandran outliers	110173	5676 (1.80-1.80)
Sidechain outliers	110143	5675 (1.80-1.80)
RSRZ outliers	101464	4906 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	753	<div> <div>4%</div> <div>79%</div> <div>13%</div> <div>...</div> </div>
1	B	753	<div> <div>7%</div> <div>77%</div> <div>17%</div> <div>..</div> </div>
1	C	753	<div> <div>5%</div> <div>77%</div> <div>16%</div> <div>...</div> </div>
1	D	753	<div> <div>4%</div> <div>77%</div> <div>18%</div> <div>..</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 25850 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 PROTEIN (CATALASE HP11).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	727	Total	C	N	O	S	0	1	0
			5748	3649	1005	1081	13			
1	B	727	Total	C	N	O	S	0	1	0
			5748	3649	1005	1081	13			
1	C	727	Total	C	N	O	S	0	1	0
			5748	3649	1005	1081	13			
1	D	727	Total	C	N	O	S	0	1	0
			5748	3649	1005	1081	13			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	169	CYS	VAL	ENGINEERED MUTATION	UNP P21179
B	169	CYS	VAL	ENGINEERED MUTATION	UNP P21179
C	169	CYS	VAL	ENGINEERED MUTATION	UNP P21179
D	169	CYS	VAL	ENGINEERED MUTATION	UNP P21179

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	727	Total	O	0	0
			727	727		
3	B	616	Total	O	0	0
			616	616		
3	C	638	Total	O	0	0
			638	638		
3	D	705	Total	O	0	0
			705	705		

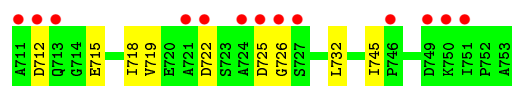
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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 ($\text{RSRZ} > 2$). 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.

Chain A:

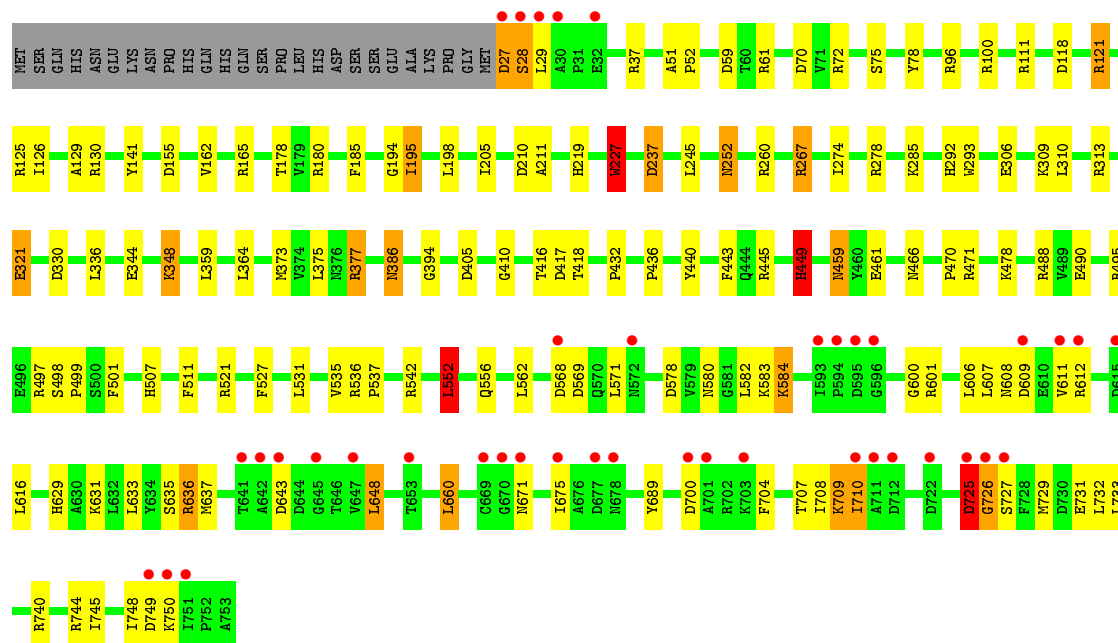
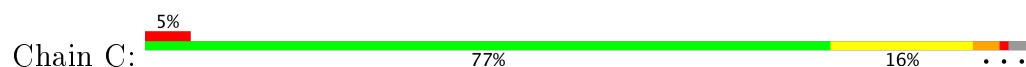
Chain B:

7% 17%

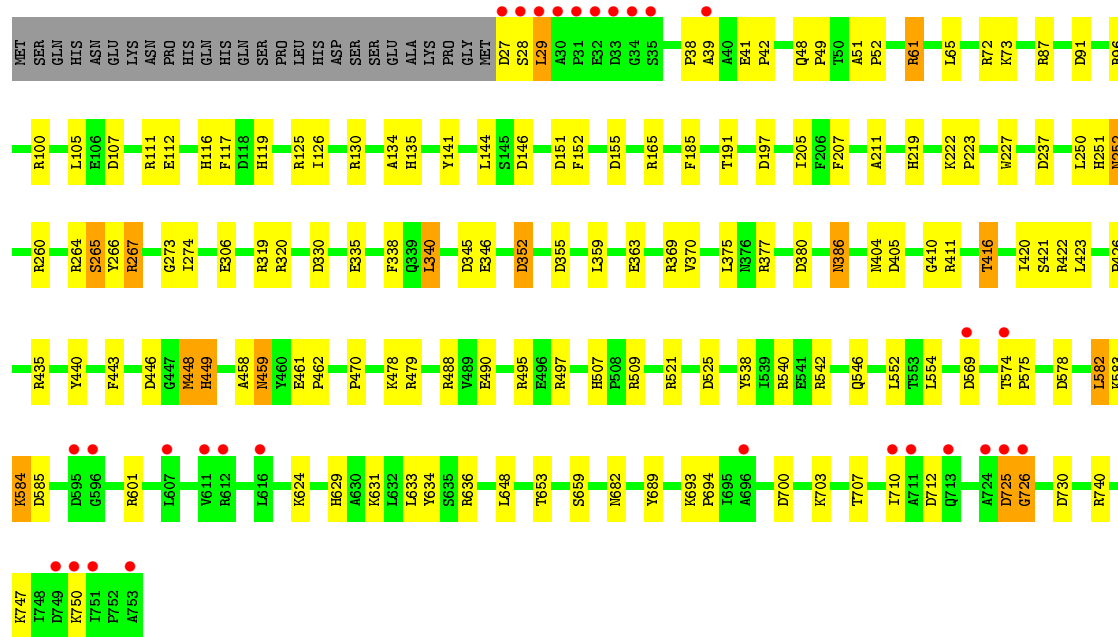
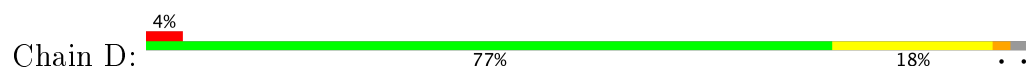
S613	F443	Q444	R290	D118	MET
A614	Q445	R291	D119	H118	SER
D615	R292	H293	D120	E120	GLN
L616	H448	H449	R121	R121	HIS
A618	M459	Q308	H126	V127	ASN
L619	P470	K309	A129	H128	PRO
K624	K478	L310	R130	R130	HIS
H629	E487	D830	H135	H135	GLN
L633	M492	E335	K142	K142	PRO
Y634	V494	D352	D146	D146	LEU
M637	R495	D355	D155	D155	HIS
V640	F501	L359	K158	K158	ASP
T641	H507	L364	R165	R165	SER
A642	P508	R369	C169	C169	SER
D643	E519	L375	R180	R180	GLU
D644	Q520	R376	F185	F185	ALA
G645	R521	R377	D197	D197	LYS
T646	V535	N386	I205	I205	PRO
V647	R536	H392	F206	F206	GLY
L648	P537	H395	F207	F207	MET
P649	R540	D568	H219	H219	D27
L650	L582	D569	W227	W227	S28
T653	O570	L571	D237	D237	L29
L660	L572	M580	T238	T238	A30
A664	K583	K584	Y242	Y242	P31
C669	D595	G596	P247	P247	E32
G670	R601	V602	H251	H251	D33
N671	V603	D418	N252	N252	G34
L672	M608	L411	Q419	Q419	S35
L673	D609	F413	I420	I420	H36
D674	E610	T416	R260	R260	R37
A676	P612	D417	S265	S265	P38
D677	T700	T418	T266	T266	A39
N682	F704	Q438	I274	I274	A40
A696	T707	Y440	R378	R378	Q48
D700	L719				P49
A701					T50
R702					D59
K703					T60
F704					A61
T707					L65
L719					R72



• Molecule 1: PROTEIN (CATALASE HP1I)



• Molecule 1: PROTEIN (CATALASE HP1I)



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	93.47Å 133.04Å 122.22Å 90.00° 109.64° 90.00°	Depositor
Resolution (Å)	20.00 – 1.80 19.76 – 1.77	Depositor EDS
% Data completeness (in resolution range)	88.3 (20.00-1.80) 83.6 (19.76-1.77)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	9.00	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.60 (at 1.77Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.181 , 0.237 0.179 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	15.2	Xtriage
Anisotropy	0.416	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 64.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.028 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	25850	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 4.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.75	1/5908 (0.0%)	1.69	91/8033 (1.1%)
1	B	0.72	0/5908	1.49	61/8033 (0.8%)
1	C	0.74	0/5908	1.51	68/8033 (0.8%)
1	D	0.71	0/5908	1.50	74/8033 (0.9%)
All	All	0.73	1/23632 (0.0%)	1.55	294/32132 (0.9%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	2	4
1	C	1	2
1	D	0	2
All	All	3	8

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	28	SER	N-CA	-5.46	1.35	1.46

All (294) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	479	ARG	NE-CZ-NH2	-50.60	95.00	120.30
1	A	479	ARG	NE-CZ-NH1	35.58	138.09	120.30
1	B	377	ARG	CD-NE-CZ	22.63	155.28	123.60
1	A	61	ARG	NE-CZ-NH1	-19.53	110.53	120.30
1	C	180	ARG	NE-CZ-NH1	16.75	128.67	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	377	ARG	NE-CZ-NH2	-16.30	112.15	120.30
1	C	725	ASP	N-CA-CB	15.90	139.23	110.60
1	C	445	ARG	NE-CZ-NH1	15.59	128.10	120.30
1	B	61	ARG	CD-NE-CZ	15.26	144.97	123.60
1	A	27	ASP	O-C-N	-15.16	98.44	122.70
1	B	495	ARG	NE-CZ-NH1	14.13	127.37	120.30
1	D	61	ARG	CD-NE-CZ	13.80	142.92	123.60
1	D	495	ARG	NE-CZ-NH1	13.64	127.12	120.30
1	D	497	ARG	NE-CZ-NH1	13.62	127.11	120.30
1	D	725	ASP	CA-CB-CG	13.60	143.32	113.40
1	D	740	ARG	NE-CZ-NH1	13.45	127.03	120.30
1	A	710	ILE	CB-CA-C	13.40	138.40	111.60
1	C	72	ARG	NE-CZ-NH2	-13.19	113.70	120.30
1	D	260	ARG	NE-CZ-NH2	-13.17	113.72	120.30
1	B	61	ARG	NE-CZ-NH1	12.97	126.78	120.30
1	C	636	ARG	NE-CZ-NH2	-12.50	114.05	120.30
1	B	61	ARG	NE-CZ-NH2	-12.09	114.26	120.30
1	D	740	ARG	NE-CZ-NH2	-11.84	114.38	120.30
1	B	445	ARG	NE-CZ-NH1	11.80	126.20	120.30
1	D	112	GLU	OE1-CD-OE2	11.40	136.98	123.30
1	A	740	ARG	NE-CZ-NH2	-11.37	114.62	120.30
1	D	636	ARG	NE-CZ-NH1	10.94	125.77	120.30
1	C	521	ARG	NE-CZ-NH2	-10.90	114.85	120.30
1	D	100	ARG	NE-CZ-NH1	10.86	125.73	120.30
1	B	290	ARG	NE-CZ-NH2	-10.48	115.06	120.30
1	A	27	ASP	CA-C-N	10.31	139.89	117.20
1	D	497	ARG	NE-CZ-NH2	-10.22	115.19	120.30
1	D	320	ARG	NE-CZ-NH2	-10.20	115.20	120.30
1	C	536	ARG	NE-CZ-NH2	-9.88	115.36	120.30
1	B	435	ARG	NE-CZ-NH1	9.85	125.22	120.30
1	C	471	ARG	NE-CZ-NH2	9.79	125.20	120.30
1	C	96	ARG	NE-CZ-NH2	-9.79	115.40	120.30
1	C	377	ARG	NE-CZ-NH1	-9.78	115.41	120.30
1	A	319	ARG	NE-CZ-NH2	-9.70	115.45	120.30
1	C	636	ARG	CD-NE-CZ	9.68	137.15	123.60
1	D	96	ARG	NE-CZ-NH1	9.55	125.07	120.30
1	A	27	ASP	CA-CB-CG	9.43	134.14	113.40
1	A	344	GLU	CA-CB-CG	9.42	134.12	113.40
1	D	107	ASP	CB-CG-OD2	9.39	126.75	118.30
1	B	72	ARG	NE-CZ-NH2	-9.37	115.62	120.30
1	A	130	ARG	NE-CZ-NH2	-9.18	115.71	120.30
1	B	417	ASP	CB-CG-OD2	-9.07	110.14	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	185	PHE	CB-CG-CD2	-9.00	114.50	120.80
1	B	411	ARG	NE-CZ-NH2	8.97	124.78	120.30
1	D	377	ARG	NH1-CZ-NH2	8.97	129.27	119.40
1	A	712	ASP	CB-CA-C	8.94	128.28	110.40
1	C	180	ARG	NE-CZ-NH2	-8.83	115.89	120.30
1	C	141	TYR	CB-CG-CD2	-8.77	115.74	121.00
1	C	130	ARG	NE-CZ-NH1	8.66	124.63	120.30
1	A	495	ARG	NE-CZ-NH2	-8.56	116.02	120.30
1	D	320	ARG	NE-CZ-NH1	8.56	124.58	120.30
1	B	536	ARG	NE-CZ-NH2	-8.50	116.05	120.30
1	A	740	ARG	NE-CZ-NH1	8.45	124.53	120.30
1	C	278	ARG	NE-CZ-NH2	-8.44	116.08	120.30
1	A	28	SER	C-N-CA	-8.39	100.71	121.70
1	A	350	ASP	CB-CG-OD1	-8.39	110.75	118.30
1	A	61	ARG	CD-NE-CZ	-8.38	111.87	123.60
1	A	29	LEU	N-CA-C	8.36	133.58	111.00
1	D	146	ASP	CB-CG-OD1	8.30	125.77	118.30
1	D	155	ASP	CB-CG-OD1	8.28	125.75	118.30
1	C	490	GLU	OE1-CD-OE2	-8.25	113.39	123.30
1	D	542	ARG	NE-CZ-NH2	-8.18	116.21	120.30
1	A	435	ARG	NE-CZ-NH1	-8.09	116.25	120.30
1	A	609	ASP	CB-CG-OD2	-8.07	111.03	118.30
1	A	411	ARG	NE-CZ-NH2	8.05	124.32	120.30
1	D	601	ARG	NE-CZ-NH1	8.01	124.30	120.30
1	C	471	ARG	NE-CZ-NH1	-7.94	116.33	120.30
1	A	265	SER	N-CA-CB	-7.92	98.62	110.50
1	C	636	ARG	NE-CZ-NH1	7.91	124.25	120.30
1	C	100	ARG	NE-CZ-NH1	7.90	124.25	120.30
1	A	712	ASP	N-CA-CB	-7.85	96.47	110.60
1	A	744	ARG	NE-CZ-NH1	-7.85	116.38	120.30
1	A	260	ARG	NE-CZ-NH2	-7.83	116.38	120.30
1	C	700	ASP	CB-CG-OD1	7.75	125.27	118.30
1	A	601	ARG	NE-CZ-NH1	7.74	124.17	120.30
1	C	740	ARG	NE-CZ-NH1	7.69	124.15	120.30
1	C	449	HIS	CA-CB-CG	-7.64	100.61	113.60
1	A	267	ARG	CD-NE-CZ	7.62	134.27	123.60
1	C	278	ARG	NE-CZ-NH1	7.61	124.11	120.30
1	A	417	ASP	CB-CG-OD2	-7.60	111.46	118.30
1	D	411	ARG	NE-CZ-NH1	7.59	124.09	120.30
1	C	121	ARG	CD-NE-CZ	7.55	134.17	123.60
1	B	521	ARG	NE-CZ-NH1	-7.54	116.53	120.30
1	C	405	ASP	CB-CG-OD2	7.53	125.08	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	278	ARG	NE-CZ-NH2	-7.48	116.56	120.30
1	B	180	ARG	NE-CZ-NH2	-7.47	116.56	120.30
1	A	369	ARG	CD-NE-CZ	7.47	134.05	123.60
1	A	112	GLU	OE1-CD-OE2	7.30	132.06	123.30
1	A	445	ARG	NE-CZ-NH1	7.29	123.94	120.30
1	D	265	SER	N-CA-CB	-7.28	99.58	110.50
1	A	290	ARG	NE-CZ-NH2	-7.28	116.66	120.30
1	D	319	ARG	NE-CZ-NH1	7.25	123.92	120.30
1	A	185	PHE	CB-CG-CD1	7.22	125.86	120.80
1	B	37	ARG	CD-NE-CZ	7.20	133.68	123.60
1	A	445	ARG	NE-CZ-NH2	-7.14	116.73	120.30
1	B	118	ASP	CB-CG-OD1	7.14	124.72	118.30
1	B	242	TYR	CB-CG-CD2	-7.10	116.74	121.00
1	B	377	ARG	NE-CZ-NH2	-7.08	116.76	120.30
1	A	350	ASP	CB-CA-C	7.06	124.52	110.40
1	D	497	ARG	CD-NE-CZ	7.05	133.48	123.60
1	C	155	ASP	CB-CG-OD1	7.03	124.63	118.30
1	A	725	ASP	CB-CG-OD1	6.95	124.55	118.30
1	B	501	PHE	CB-CG-CD2	-6.93	115.95	120.80
1	C	601	ARG	NE-CZ-NH2	-6.92	116.84	120.30
1	A	643	ASP	CB-CG-OD1	6.90	124.51	118.30
1	A	121	ARG	NE-CZ-NH2	-6.88	116.86	120.30
1	C	542	ARG	NE-CZ-NH1	6.87	123.73	120.30
1	C	495	ARG	NE-CZ-NH1	6.86	123.73	120.30
1	D	449	HIS	CA-CB-CG	6.86	125.25	113.60
1	D	130	ARG	NE-CZ-NH2	-6.85	116.88	120.30
1	A	96	ARG	NE-CZ-NH2	-6.81	116.90	120.30
1	B	96	ARG	NE-CZ-NH2	-6.80	116.90	120.30
1	A	479	ARG	NH1-CZ-NH2	6.78	126.86	119.40
1	A	61	ARG	NH1-CZ-NH2	6.78	126.86	119.40
1	C	725	ASP	CA-C-O	-6.78	105.87	120.10
1	D	585	ASP	CB-CG-OD2	6.78	124.40	118.30
1	A	488	ARG	NE-CZ-NH2	-6.76	116.92	120.30
1	B	445	ARG	NH1-CZ-NH2	-6.76	111.97	119.40
1	A	183	ARG	NE-CZ-NH2	6.68	123.64	120.30
1	D	72	ARG	NE-CZ-NH1	-6.67	116.97	120.30
1	A	344	GLU	OE1-CD-OE2	-6.67	115.30	123.30
1	C	377	ARG	NH1-CZ-NH2	6.62	126.69	119.40
1	A	259	ASP	CB-CG-OD1	6.62	124.26	118.30
1	B	352	ASP	CB-CG-OD1	6.62	124.26	118.30
1	C	744	ARG	NE-CZ-NH1	-6.60	117.00	120.30
1	C	141	TYR	CB-CG-CD1	6.59	124.96	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	488	ARG	NE-CZ-NH2	-6.56	117.02	120.30
1	D	152	PHE	CB-CG-CD2	-6.54	116.22	120.80
1	B	130	ARG	NE-CZ-NH2	-6.51	117.04	120.30
1	D	540	ARG	NE-CZ-NH1	6.51	123.56	120.30
1	D	306	GLU	OE1-CD-OE2	-6.50	115.50	123.30
1	A	488	ARG	NE-CZ-NH1	6.47	123.54	120.30
1	C	306	GLU	CA-CB-CG	6.46	127.62	113.40
1	A	713	GLN	N-CA-CB	-6.44	99.00	110.60
1	D	352	ASP	CB-CG-OD1	6.41	124.07	118.30
1	D	264	ARG	NE-CZ-NH1	6.39	123.50	120.30
1	A	709	LYS	C-N-CA	-6.38	105.75	121.70
1	A	377	ARG	NE-CZ-NH2	-6.36	117.12	120.30
1	B	612	ARG	CB-CA-C	6.35	123.10	110.40
1	C	609	ASP	CB-CG-OD1	6.33	124.00	118.30
1	A	69	GLU	OE1-CD-OE2	-6.33	115.71	123.30
1	D	509	ARG	NE-CZ-NH1	6.31	123.45	120.30
1	C	72	ARG	NE-CZ-NH1	6.28	123.44	120.30
1	D	207	PHE	CB-CG-CD2	-6.28	116.40	120.80
1	B	72	ARG	NE-CZ-NH1	6.26	123.43	120.30
1	A	369	ARG	NE-CZ-NH1	6.26	123.43	120.30
1	A	578	ASP	CB-CG-OD1	6.25	123.92	118.30
1	B	405	ASP	CB-CG-OD2	6.25	123.92	118.30
1	D	197	ASP	CB-CG-OD1	6.25	123.92	118.30
1	A	259	ASP	CB-CG-OD2	-6.24	112.68	118.30
1	A	644	ASP	CB-CG-OD1	6.23	123.91	118.30
1	B	501	PHE	CB-CG-CD1	6.23	125.16	120.80
1	D	435	ARG	NE-CZ-NH1	6.16	123.38	120.30
1	D	448	MET	CG-SD-CE	6.16	110.05	100.20
1	D	96	ARG	NE-CZ-NH2	-6.15	117.23	120.30
1	D	446	ASP	CB-CG-OD2	6.14	123.83	118.30
1	A	182	ILE	CA-CB-CG1	-6.14	99.34	111.00
1	B	59	ASP	CB-CA-C	-6.13	98.14	110.40
1	B	146	ASP	CB-CG-OD1	6.12	123.81	118.30
1	B	121	ARG	NE-CZ-NH2	-6.12	117.24	120.30
1	B	291	PHE	CB-CG-CD2	6.10	125.07	120.80
1	B	369	ARG	NE-CZ-NH1	-6.10	117.25	120.30
1	D	458	ALA	CB-CA-C	-6.10	100.95	110.10
1	D	380	ASP	CB-CG-OD2	-6.08	112.83	118.30
1	D	320	ARG	CD-NE-CZ	6.06	132.09	123.60
1	A	612	ARG	NE-CZ-NH2	-6.04	117.28	120.30
1	D	61	ARG	CB-CG-CD	6.00	127.21	111.60
1	A	637	MET	CG-SD-CE	5.99	109.79	100.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	479	ARG	CB-CA-C	-5.96	98.49	110.40
1	A	107	ASP	CB-CG-OD2	-5.92	112.97	118.30
1	A	611	VAL	CB-CA-C	-5.92	100.16	111.40
1	C	260	ARG	NE-CZ-NH1	-5.90	117.35	120.30
1	D	525	ASP	CB-CG-OD1	5.90	123.61	118.30
1	C	130	ARG	NE-CZ-NH2	-5.90	117.35	120.30
1	C	521	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	B	59	ASP	N-CA-CB	5.86	121.16	110.60
1	C	267	ARG	NE-CZ-NH2	5.84	123.22	120.30
1	D	416	THR	CA-CB-CG2	5.84	120.58	112.40
1	A	320	ARG	NE-CZ-NH2	-5.82	117.39	120.30
1	D	538	TYR	CB-CG-CD1	-5.81	117.51	121.00
1	C	497	ARG	NE-CZ-NH1	-5.80	117.40	120.30
1	B	100	ARG	NE-CZ-NH2	-5.78	117.41	120.30
1	C	100	ARG	NE-CZ-NH2	-5.75	117.42	120.30
1	B	355	ASP	CB-CG-OD1	5.75	123.47	118.30
1	D	29	LEU	CB-CA-C	5.73	121.09	110.20
1	D	631	LYS	CA-CB-CG	5.70	125.94	113.40
1	A	509	ARG	NE-CZ-NH1	5.69	123.14	120.30
1	C	631	LYS	N-CA-CB	5.64	120.76	110.60
1	C	37	ARG	NE-CZ-NH2	-5.64	117.48	120.30
1	D	521	ARG	NE-CZ-NH1	-5.64	117.48	120.30
1	B	487	GLU	OE1-CD-OE2	-5.62	116.56	123.30
1	C	70	ASP	CB-CG-OD2	-5.60	113.26	118.30
1	C	178	THR	CA-CB-CG2	-5.60	104.56	112.40
1	C	511	PHE	CB-CG-CD1	-5.59	116.88	120.80
1	B	601	ARG	CA-CB-CG	5.59	125.69	113.40
1	D	111	ARG	NE-CZ-NH1	-5.58	117.51	120.30
1	C	495	ARG	CD-NE-CZ	5.57	131.39	123.60
1	B	602	VAL	CB-CA-C	-5.57	100.82	111.40
1	C	59	ASP	CB-CG-OD1	5.56	123.31	118.30
1	D	479	ARG	CD-NE-CZ	5.55	131.37	123.60
1	A	495	ARG	NE-CZ-NH1	5.54	123.07	120.30
1	D	490	GLU	OE1-CD-OE2	-5.53	116.66	123.30
1	D	134	ALA	CB-CA-C	-5.53	101.80	110.10
1	C	78	TYR	CB-CG-CD1	-5.53	117.68	121.00
1	A	72	ARG	N-CA-CB	5.53	120.55	110.60
1	C	260	ARG	NE-CZ-NH2	5.51	123.05	120.30
1	B	725	ASP	N-CA-CB	-5.50	100.69	110.60
1	B	725	ASP	CB-CA-C	-5.50	99.40	110.40
1	A	540	ARG	NE-CZ-NH2	-5.49	117.56	120.30
1	A	155	ASP	CB-CG-OD2	-5.49	113.36	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	482	PHE	CB-CG-CD1	5.49	124.64	120.80
1	C	501	PHE	CB-CG-CD2	-5.49	116.96	120.80
1	D	141	TYR	CB-CG-CD2	-5.49	117.71	121.00
1	A	28	SER	CA-C-N	-5.48	105.14	117.20
1	C	648	LEU	CA-CB-CG	5.47	127.89	115.30
1	D	100	ARG	NH1-CZ-NH2	-5.47	113.38	119.40
1	C	194	GLY	CA-C-O	5.47	130.44	120.60
1	A	377	ARG	CA-CB-CG	-5.46	101.40	113.40
1	A	48	GLN	CA-CB-CG	5.45	125.39	113.40
1	B	72	ARG	CD-NE-CZ	5.45	131.23	123.60
1	D	125	ARG	NE-CZ-NH2	-5.44	117.58	120.30
1	C	210	ASP	CB-CG-OD2	5.43	123.19	118.30
1	A	126[A]	ILE	CB-CA-C	5.42	122.45	111.60
1	A	126[B]	ILE	CB-CA-C	5.42	122.45	111.60
1	C	542	ARG	NH1-CZ-NH2	-5.40	113.46	119.40
1	D	91	ASP	CB-CG-OD2	5.40	123.16	118.30
1	B	260	ARG	NE-CZ-NH1	-5.38	117.61	120.30
1	C	59	ASP	CB-CG-OD2	-5.38	113.46	118.30
1	D	422	ARG	NE-CZ-NH1	-5.37	117.62	120.30
1	C	111	ARG	CD-NE-CZ	5.37	131.11	123.60
1	A	414	SER	N-CA-CB	-5.37	102.45	110.50
1	B	207	PHE	O-C-N	-5.37	114.12	122.70
1	C	643	ASP	CB-CG-OD1	5.36	123.13	118.30
1	D	355	ASP	CB-CG-OD1	5.34	123.11	118.30
1	D	100	ARG	CD-NE-CZ	5.33	131.06	123.60
1	B	519	GLU	OE1-CD-OE2	-5.32	116.92	123.30
1	C	710	ILE	CB-CA-C	-5.31	100.98	111.60
1	D	346	GLU	OE1-CD-OE2	-5.29	116.95	123.30
1	A	542	ARG	NE-CZ-NH1	5.29	122.94	120.30
1	B	130	ARG	NE-CZ-NH1	5.29	122.94	120.30
1	A	479	ARG	CG-CD-NE	-5.28	100.72	111.80
1	A	61	ARG	CB-CG-CD	-5.26	97.91	111.60
1	D	151	ASP	CB-CG-OD2	5.26	123.04	118.30
1	A	644	ASP	OD1-CG-OD2	-5.26	113.31	123.30
1	A	536	ARG	NE-CZ-NH2	5.24	122.92	120.30
1	C	552	LEU	CA-CB-CG	5.23	127.33	115.30
1	A	121	ARG	CD-NE-CZ	5.23	130.92	123.60
1	B	640	VAL	N-CA-CB	5.23	123.00	111.50
1	D	345	ASP	CB-CG-OD2	-5.22	113.60	118.30
1	C	237	ASP	CB-CG-OD1	-5.22	113.61	118.30
1	B	290	ARG	NH1-CZ-NH2	5.21	125.13	119.40
1	C	501	PHE	CB-CG-CD1	5.21	124.45	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	659	SER	N-CA-CB	5.21	118.31	110.50
1	B	259	ASP	CB-CG-OD1	5.20	122.98	118.30
1	D	435	ARG	NE-CZ-NH2	-5.19	117.70	120.30
1	B	707	THR	N-CA-CB	5.19	120.16	110.30
1	A	41	GLU	CA-CB-CG	5.19	124.81	113.40
1	D	266	TYR	CB-CG-CD2	-5.17	117.89	121.00
1	D	421	SER	N-CA-CB	5.17	118.25	110.50
1	B	704	PHE	CB-CG-CD2	-5.16	117.19	120.80
1	A	125	ARG	NE-CZ-NH2	-5.16	117.72	120.30
1	D	411	ARG	NE-CZ-NH2	-5.16	117.72	120.30
1	B	402	PHE	CB-CG-CD1	-5.15	117.19	120.80
1	D	725	ASP	CB-CG-OD1	5.15	122.94	118.30
1	A	479	ARG	CA-CB-CG	5.14	124.70	113.40
1	B	494	VAL	CB-CA-C	-5.12	101.68	111.40
1	A	646	THR	N-CA-CB	5.12	120.02	110.30
1	B	27	ASP	CA-C-N	-5.11	105.96	117.20
1	C	601	ARG	NE-CZ-NH1	5.11	122.85	120.30
1	D	87	ARG	NE-CZ-NH2	5.11	122.85	120.30
1	A	488	ARG	CD-NE-CZ	-5.10	116.45	123.60
1	A	595	ASP	CB-CG-OD1	5.10	122.89	118.30
1	D	207	PHE	O-C-N	-5.09	114.55	122.70
1	B	126[A]	ILE	CB-CA-C	5.08	121.77	111.60
1	B	126[B]	ILE	CB-CA-C	5.08	121.77	111.60
1	A	91	ASP	CB-CG-OD1	-5.08	113.72	118.30
1	B	242	TYR	CD1-CE1-CZ	-5.08	115.23	119.80
1	B	495	ARG	NH1-CZ-NH2	-5.08	113.81	119.40
1	C	292	HIS	CB-CA-C	-5.08	100.24	110.40
1	C	445	ARG	NH1-CZ-NH2	-5.08	113.81	119.40
1	A	711	ALA	CA-C-O	5.08	130.76	120.10
1	A	28	SER	N-CA-CB	5.07	118.11	110.50
1	B	601	ARG	NE-CZ-NH2	5.07	122.83	120.30
1	C	227	TRP	CA-CB-CG	5.06	123.32	113.70
1	D	267	ARG	NE-CZ-NH1	-5.05	117.78	120.30
1	A	242	TYR	CB-CG-CD1	-5.03	117.98	121.00
1	B	100	ARG	NE-CZ-NH1	5.03	122.81	120.30
1	A	334	TYR	CG-CD2-CE2	-5.02	117.28	121.30
1	B	540	ARG	NE-CZ-NH1	-5.00	117.80	120.30

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	28	SER	CA

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Mol	Chain	Res	Type	Atom
1	A	29	LEU	CA
1	C	725	ASP	CA

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	27	ASP	Mainchain,Peptide
1	A	394	GLY	Mainchain
1	A	710	ILE	Mainchain
1	C	394	GLY	Mainchain
1	C	725	ASP	Mainchain
1	D	273	GLY	Mainchain
1	D	423	LEU	Mainchain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5748	0	5580	62	5
1	B	5748	0	5580	92	1
1	C	5748	0	5580	65	0
1	D	5748	0	5580	65	0
2	A	43	0	30	3	0
2	B	43	0	30	4	0
2	C	43	0	30	2	0
2	D	43	0	30	3	0
3	A	727	0	0	10	0
3	B	616	0	0	17	5
3	C	638	0	0	6	1
3	D	705	0	0	9	0
All	All	25850	0	22440	250	6

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 5.

All (250) 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:B:126[B]:ILE:HD12	2:B:754:HEM:HMD1	1.43	0.99
1:C:126[B]:ILE:HD12	2:C:754:HEM:HMD1	1.48	0.96
1:D:39:ALA:H	1:D:48:GLN:HE21	1.16	0.93
1:B:710:ILE:HD13	1:B:718:ILE:HG13	1.59	0.84
1:A:28:SER:O	1:A:29:LEU:HG	1.77	0.84
1:D:39:ALA:H	1:D:48:GLN:NE2	1.77	0.81
1:B:583:LYS:HE2	1:B:583:LYS:H	1.45	0.81
1:C:27:ASP:O	1:C:28:SER:HB2	1.80	0.81
1:D:267:ARG:HG3	3:D:1243:HOH:O	1.83	0.79
1:B:309:LYS:HG3	3:B:1353:HOH:O	1.83	0.78
1:C:310:LEU:HD13	1:C:660:LEU:HB3	1.65	0.77
1:A:126[A]:ILE:HD12	1:D:117:PHE:CZ	2.20	0.76
1:B:126[A]:ILE:HD13	1:C:121:ARG:NH2	2.00	0.75
1:C:267:ARG:HH12	1:C:600:GLY:HA3	1.51	0.75
1:C:527:PHE:O	1:C:531:LEU:HD13	1.87	0.74
1:B:267:ARG:HG3	3:B:1361:HOH:O	1.87	0.74
1:B:310:LEU:HD13	1:B:660:LEU:HB3	1.70	0.74
1:B:603:VAL:HG22	1:B:664:ALA:HB3	1.69	0.74
1:A:479:ARG:NH1	1:A:479:ARG:HG2	2.05	0.71
1:A:488:ARG:HH11	1:B:492:ASN:ND2	1.88	0.71
1:A:29:LEU:HD23	1:A:30:ALA:O	1.91	0.71
1:A:51:ALA:HB1	1:A:52:PRO:HD2	1.71	0.70
1:C:267:ARG:HD2	3:C:998:HOH:O	1.89	0.70
1:A:611:VAL:HG23	3:A:1053:HOH:O	1.92	0.69
1:D:386:ASN:C	1:D:386:ASN:HD22	1.95	0.69
1:D:725:ASP:O	3:D:1208:HOH:O	2.11	0.69
1:A:726:GLY:HA3	3:A:1399:HOH:O	1.94	0.68
1:C:708:ILE:HG13	1:C:710:ILE:HG12	1.76	0.68
1:B:386:ASN:C	1:B:386:ASN:HD22	1.98	0.67
1:B:449:HIS:ND1	3:B:1357:HOH:O	2.26	0.67
1:B:309:LYS:HG2	1:B:660:LEU:HD11	1.76	0.66
1:C:309:LYS:HE2	3:C:1387:HOH:O	1.97	0.65
1:A:245:LEU:HD22	1:D:29:LEU:HD13	1.79	0.65
1:D:448:MET:HG2	3:D:1457:HOH:O	1.97	0.65
1:B:37:ARG:HD2	3:B:1367:HOH:O	1.99	0.63
1:C:552:LEU:HD22	1:C:556:GLN:HG3	1.80	0.63
1:D:126[A]:ILE:HG22	2:D:754:HEM:HMD1	1.81	0.62
1:C:607:LEU:HD22	1:C:611:VAL:HG21	1.82	0.62
1:A:488:ARG:HH11	1:B:492:ASN:HD21	1.46	0.62
1:B:583:LYS:CE	1:B:583:LYS:H	2.13	0.62
1:B:710:ILE:HG23	1:B:715:GLU:HG2	1.82	0.61
1:C:386:ASN:HD22	1:C:386:ASN:C	2.04	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:449:HIS:NE2	3:B:1356:HOH:O	2.31	0.61
1:D:126[A]:ILE:CG2	2:D:754:HEM:HMD1	2.31	0.61
1:D:375:LEU:N	1:D:375:LEU:HD12	2.15	0.60
1:B:29:LEU:HD13	1:C:245:LEU:HD22	1.82	0.60
1:A:126[B]:ILE:HD11	3:D:1453:HOH:O	2.01	0.60
1:B:448:MET:HE3	3:B:1358:HOH:O	2.02	0.60
1:C:704:PHE:O	1:C:707:THR:HG22	2.02	0.60
1:B:126[B]:ILE:CD1	2:B:754:HEM:HMD1	2.26	0.59
1:C:578:ASP:HB2	1:C:582:LEU:O	2.01	0.59
1:B:583:LYS:O	1:B:584:LYS:HB3	2.02	0.59
1:A:317:PHE:O	1:A:321:GLU:HB2	2.04	0.57
1:A:121:ARG:HG2	1:D:126[B]:ILE:HD13	1.87	0.57
1:A:488:ARG:NH1	1:B:492:ASN:ND2	2.53	0.57
1:B:75:SER:HA	3:B:1368:HOH:O	2.04	0.56
1:B:344:GLU:H	1:B:344:GLU:CD	2.08	0.56
1:A:488:ARG:NH1	1:B:492:ASN:HD21	2.04	0.56
1:D:726:GLY:O	1:D:730:ASP:OD1	2.24	0.56
1:A:182:ILE:HD12	1:A:207:PHE:CE2	2.40	0.56
1:A:28:SER:CB	3:A:1359:HOH:O	2.54	0.56
1:A:27:ASP:HB3	1:A:28:SER:OG	2.07	0.55
1:A:73:LYS:HE2	3:C:951:HOH:O	2.05	0.55
1:A:386:ASN:C	1:A:386:ASN:HD22	2.09	0.55
1:B:126[B]:ILE:CD1	1:C:118:ASP:HA	2.37	0.55
1:D:420:ILE:HD12	1:D:426:PRO:HA	1.89	0.54
1:B:126[B]:ILE:HD11	1:B:418:THR:OG1	2.08	0.54
1:A:461:GLU:HA	1:A:462:PRO:C	2.28	0.54
1:B:330:ASP:OD2	1:B:629:HIS:HE1	1.91	0.54
1:D:39:ALA:N	1:D:48:GLN:HE21	1.96	0.54
1:B:449:HIS:CE1	3:B:1356:HOH:O	2.61	0.53
1:C:359:LEU:H	1:C:507:HIS:HD2	1.56	0.53
3:A:1474:HOH:O	1:D:126[B]:ILE:HD11	2.08	0.53
1:B:443:PHE:CZ	1:B:470:PRO:HD2	2.44	0.53
1:B:646:THR:HA	3:B:1145:HOH:O	2.08	0.53
1:D:443:PHE:CZ	1:D:470:PRO:HD2	2.44	0.53
1:A:278:ARG:HH22	1:A:487:GLU:CD	2.12	0.52
1:A:552:LEU:HD21	1:A:571:LEU:O	2.10	0.52
1:A:583:LYS:O	1:A:584:LYS:HB3	2.08	0.52
1:C:165:ARG:HE	1:C:386:ASN:HD21	1.57	0.52
1:D:578:ASP:HB3	1:D:582:LEU:O	2.09	0.52
1:A:443:PHE:CZ	1:A:470:PRO:HD2	2.44	0.52
1:D:416:THR:HG23	3:D:1355:HOH:O	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:583:LYS:O	1:C:584:LYS:HB3	2.09	0.52
1:B:165:ARG:HE	1:B:386:ASN:HD21	1.57	0.52
1:A:459:ASN:ND2	1:B:219:HIS:HB3	2.25	0.52
1:A:707:THR:HG23	3:A:1402:HOH:O	2.09	0.52
1:B:155:ASP:HB3	1:B:158:LYS:HG3	1.92	0.52
1:B:38:PRO:HA	1:B:48:GLN:OE1	2.10	0.52
1:B:562:LEU:HA	1:C:637:MET:HB2	1.91	0.52
1:B:624:LYS:HB2	3:B:1060:HOH:O	2.09	0.52
1:B:126[B]:ILE:HD13	1:C:118:ASP:HA	1.90	0.52
1:B:126[B]:ILE:HD12	2:B:754:HEM:CMD	2.30	0.51
1:D:144:LEU:HD11	1:D:370:VAL:HG13	1.93	0.51
1:B:438:CYS:HB2	1:B:439:PRO:HD2	1.92	0.51
1:A:28:SER:HB2	3:A:1359:HOH:O	2.08	0.51
1:D:700:ASP:O	1:D:703:LYS:HG3	2.10	0.51
1:D:359:LEU:H	1:D:507:HIS:HD2	1.58	0.51
1:A:682:ASN:HB3	1:A:707:THR:HG21	1.91	0.51
1:C:416:THR:HA	3:C:1381:HOH:O	2.11	0.51
3:B:1357:HOH:O	1:D:449:HIS:CE1	2.63	0.51
1:D:634:TYR:O	1:D:653:THR:HA	2.11	0.51
1:D:689:TYR:CE1	1:D:710:ILE:HD11	2.46	0.51
1:A:165:ARG:HE	1:A:386:ASN:HD21	1.58	0.51
1:B:637:MET:HB2	1:C:562:LEU:HA	1.93	0.51
1:C:126[B]:ILE:HD11	1:C:418:THR:OG1	2.11	0.51
1:B:118:ASP:HA	1:C:126[B]:ILE:CD1	2.42	0.50
1:A:70:ASP:OD2	3:A:1479:HOH:O	2.19	0.50
1:B:682:ASN:OD1	1:B:707:THR:HG21	2.12	0.50
1:C:725:ASP:O	1:C:726:GLY:C	2.49	0.50
1:D:165:ARG:HE	1:D:386:ASN:HD21	1.59	0.49
1:B:274:ILE:HD12	2:B:754:HEM:HMB1	1.94	0.49
1:A:120:GLU:HB2	1:D:126[A]:ILE:CD1	2.41	0.49
1:D:363:GLU:HB2	1:D:582:LEU:HD21	1.94	0.49
1:B:521:ARG:HE	1:B:745:ILE:HG21	1.78	0.49
3:B:924:HOH:O	1:D:52:PRO:HG3	2.11	0.49
1:A:28:SER:O	1:A:29:LEU:CG	2.55	0.49
1:A:36:HIS:CD2	1:A:36:HIS:H	2.31	0.49
1:B:413:PHE:HB2	1:D:105:LEU:HD11	1.94	0.48
1:D:750:LYS:HG3	1:D:750:LYS:O	2.14	0.48
1:A:745:ILE:O	1:A:748:ILE:HG12	2.14	0.48
1:A:411:ARG:HG2	2:A:754:HEM:C2C	2.49	0.48
1:B:416:THR:HA	3:B:1370:HOH:O	2.13	0.48
1:B:308:GLN:OE1	1:C:313:ARG:NH1	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:267:ARG:HD2	3:B:976:HOH:O	2.13	0.48
1:B:583:LYS:CD	1:B:583:LYS:H	2.26	0.48
1:C:729:MET:O	1:C:733:LEU:HD13	2.14	0.48
1:A:479:ARG:HH11	1:A:479:ARG:HG2	1.79	0.47
1:B:27:ASP:O	1:B:28:SER:HB2	2.14	0.47
1:D:330:ASP:OD2	1:D:629:HIS:HE1	1.97	0.47
1:B:710:ILE:CD1	1:B:718:ILE:HG13	2.36	0.47
1:B:126[A]:ILE:HD13	1:C:121:ARG:CZ	2.44	0.47
1:B:29:LEU:HD13	1:C:245:LEU:HD13	1.96	0.47
1:B:634:TYR:O	1:B:653:THR:HA	2.15	0.47
1:B:293:TRP:CZ3	1:B:336:LEU:HB2	2.50	0.47
1:C:211:ALA:CB	1:C:410:GLY:HA3	2.45	0.47
1:C:745:ILE:O	1:C:748:ILE:HG12	2.15	0.47
1:B:364:LEU:HD11	1:B:580:ASN:HB2	1.97	0.46
1:B:50:THR:HG21	1:C:227:TRP:CZ3	2.50	0.46
1:B:395:HIS:HE1	3:D:1445:HOH:O	1.97	0.46
1:C:219:HIS:HB3	1:D:459:ASN:ND2	2.30	0.46
1:A:51:ALA:HB1	1:A:52:PRO:CD	2.44	0.46
1:C:330:ASP:OD2	1:C:629:HIS:HE1	1.99	0.46
1:C:364:LEU:HD11	1:C:580:ASN:HB2	1.97	0.46
1:C:727:SER:O	1:C:731:GLU:HG3	2.15	0.46
1:D:251:HIS:CE1	1:D:507:HIS:HB3	2.51	0.46
1:B:535:VAL:O	1:B:537:PRO:HD3	2.15	0.46
1:B:36:HIS:CD2	1:B:37:ARG:HE	2.34	0.46
1:B:359:LEU:H	1:B:507:HIS:HD2	1.63	0.46
1:D:725:ASP:O	1:D:726:GLY:C	2.54	0.46
1:A:126[A]:ILE:HG22	2:A:754:HEM:HMD1	1.97	0.45
1:D:629:HIS:HD2	3:D:1068:HOH:O	1.99	0.45
1:A:335:GLU:OE1	1:A:369:ARG:HG3	2.17	0.45
1:B:165:ARG:HE	1:B:386:ASN:ND2	2.14	0.45
1:B:420:ILE:HG21	1:D:119:HIS:CE1	2.51	0.45
1:D:338:PHE:HB3	1:D:340:LEU:HD13	1.98	0.45
1:B:448:MET:HG2	3:B:1358:HOH:O	2.17	0.45
1:B:521:ARG:NE	1:B:745:ILE:HG21	2.32	0.45
1:C:732:LEU:C	1:C:732:LEU:HD13	2.37	0.45
1:C:321:GLU:HG2	3:C:1201:HOH:O	2.17	0.45
1:D:747:LYS:NZ	3:D:1349:HOH:O	2.47	0.45
1:B:197:ASP:OD2	1:B:395:HIS:HD2	2.00	0.44
1:B:252:ASN:HA	1:B:252:ASN:HD22	1.61	0.44
1:A:477:PRO:HB2	1:A:478:LYS:HD2	1.99	0.44
1:D:583:LYS:O	1:D:584:LYS:HB3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:703:LYS:HD2	3:D:1409:HOH:O	2.17	0.44
1:B:118:ASP:HA	1:C:126[B]:ILE:HD13	1.99	0.44
1:D:274:ILE:HD12	2:D:754:HEM:HMB1	1.99	0.44
1:B:369:ARG:HG2	3:B:1110:HOH:O	2.18	0.44
1:C:459:ASN:ND2	1:D:219:HIS:HB3	2.33	0.44
1:A:634:TYR:HB3	1:A:650:ILE:HD13	2.00	0.44
1:A:120:GLU:HB2	1:D:126[A]:ILE:HD11	2.00	0.43
1:C:274:ILE:HD12	2:C:754:HEM:HMB1	2.00	0.43
1:B:426:PRO:HB2	1:D:116:HIS:CD2	2.53	0.43
1:A:341:ILE:HD12	1:A:353:LEU:HD21	2.00	0.43
1:B:615:ASP:O	1:B:619:ILE:HG13	2.17	0.43
1:C:359:LEU:C	1:C:359:LEU:HD12	2.39	0.43
1:C:443:PHE:CZ	1:C:470:PRO:HD2	2.54	0.43
1:D:252:ASN:HD22	1:D:252:ASN:HA	1.63	0.43
1:D:41:GLU:CD	1:D:42:PRO:HD2	2.38	0.43
1:C:165:ARG:HE	1:C:386:ASN:ND2	2.16	0.43
1:D:38:PRO:HB3	1:D:49:PRO:HD2	2.00	0.43
1:D:682:ASN:HB3	1:D:707:THR:HG21	2.00	0.43
1:D:404:ASN:O	1:D:405:ASP:C	2.56	0.43
1:A:260:ARG:HD3	1:A:590:LEU:HD21	2.01	0.43
1:C:162:VAL:HG21	1:C:373:MET:SD	2.59	0.43
1:D:222:LYS:HB3	1:D:223:PRO:HD2	2.00	0.43
1:D:461:GLU:HA	1:D:462:PRO:C	2.38	0.43
1:B:36:HIS:HD1	1:B:36:HIS:H	1.66	0.43
1:A:37:ARG:NH2	1:C:466:ASN:HA	2.34	0.43
1:A:76:GLU:O	1:A:77:ASN:HB2	2.19	0.42
1:B:119:HIS:CE1	1:D:420:ILE:HG21	2.54	0.42
1:A:91:ASP:OD2	1:C:461:GLU:OE2	2.36	0.42
1:C:535:VAL:O	1:C:537:PRO:HD3	2.19	0.42
1:B:251:HIS:HA	1:B:508:PRO:HG3	2.02	0.42
1:C:749:ASP:HB3	1:C:750:LYS:NZ	2.34	0.42
1:A:165:ARG:HE	1:A:386:ASN:ND2	2.17	0.42
1:A:37:ARG:HH21	1:C:466:ASN:HA	1.84	0.42
1:B:696:ALA:CB	1:B:719:VAL:HB	2.49	0.42
1:C:293:TRP:CZ3	1:C:336:LEU:HB2	2.54	0.42
1:B:65:LEU:HD21	1:B:135:HIS:CG	2.55	0.42
1:D:583:LYS:HB2	1:D:583:LYS:NZ	2.35	0.42
1:A:207:PHE:O	1:A:249:THR:HA	2.19	0.42
1:D:335:GLU:OE1	1:D:369:ARG:HG2	2.20	0.42
1:B:507:HIS:N	1:B:508:PRO:CD	2.82	0.42
1:C:125:ARG:HB2	1:C:129:ALA:HA	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:51:ALA:HB1	1:C:52:PRO:HD2	2.02	0.42
1:A:511:PHE:O	1:A:515:GLN:HG2	2.19	0.42
1:D:51:ALA:HB1	1:D:52:PRO:HD2	2.02	0.42
1:D:250:LEU:HD11	1:D:546:GLN:HE21	1.85	0.42
1:D:375:LEU:N	1:D:375:LEU:CD1	2.82	0.41
1:B:128:HIS:ND1	1:B:169:CYS:HA	2.34	0.41
1:C:689:TYR:CE1	1:C:710:ILE:HD11	2.55	0.41
1:A:610:GLU:OE2	1:A:643:ASP:HA	2.19	0.41
1:C:195:ILE:HD11	1:C:436:PRO:HA	2.02	0.41
1:B:91:ASP:OD2	1:D:461:GLU:OE2	2.38	0.41
1:A:478:LYS:HE2	1:A:478:LYS:HB3	1.79	0.41
1:C:449:HIS:CE1	3:C:1369:HOH:O	2.74	0.41
1:A:104:LEU:HB3	3:A:901:HOH:O	2.20	0.41
1:A:578:ASP:HB3	1:A:582:LEU:O	2.20	0.41
1:B:118:ASP:OD2	1:C:417:ASP:OD2	2.38	0.41
1:B:294:LYS:HG3	3:B:1286:HOH:O	2.20	0.41
1:A:158:LYS:HB3	3:A:1097:HOH:O	2.19	0.41
1:A:631:LYS:HD3	3:A:1188:HOH:O	2.20	0.41
1:A:155:ASP:OD1	1:A:156:PRO:HD2	2.21	0.41
1:B:459:ASN:H	1:B:459:ASN:HD22	1.68	0.41
1:D:386:ASN:C	1:D:386:ASN:ND2	2.68	0.41
1:B:682:ASN:CG	1:B:707:THR:HG21	2.41	0.41
1:C:709:LYS:HD2	1:C:709:LYS:N	2.36	0.41
1:D:222:LYS:HB3	1:D:223:PRO:CD	2.51	0.41
1:B:608:ASN:O	1:B:611:VAL:HG23	2.21	0.41
1:C:252:ASN:HD22	1:C:252:ASN:HA	1.66	0.41
1:C:344:GLU:O	1:C:348:LYS:NZ	2.50	0.41
1:D:65:LEU:HD21	1:D:135:HIS:CG	2.56	0.41
1:B:616:LEU:HA	1:B:616:LEU:HD23	1.93	0.41
1:C:583:LYS:O	1:C:584:LYS:CB	2.68	0.41
1:B:732:LEU:HD13	1:B:732:LEU:C	2.40	0.41
1:C:608:ASN:OD1	1:C:671:ASN:N	2.54	0.41
1:A:460:TYR:CE1	1:B:238:THR:HB	2.56	0.40
1:B:392:HIS:HB3	1:B:395:HIS:CD2	2.56	0.40
1:B:335:GLU:OE1	1:B:369:ARG:HD2	2.21	0.40
1:B:251:HIS:CE1	1:B:507:HIS:HB3	2.56	0.40
1:C:675:ILE:HG13	1:C:704:PHE:HZ	1.86	0.40
1:D:211:ALA:CB	1:D:410:GLY:HA3	2.51	0.40
1:D:574:THR:OG1	1:D:575:PRO:HD2	2.21	0.40
1:D:693:LYS:HA	1:D:694:PRO:HD3	1.97	0.40
1:B:648:LEU:HA	1:B:649:PRO:HD3	1.91	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:498:SER:HA	1:C:499:PRO:HD3	1.98	0.40
1:A:229:ILE:HA	1:A:230:PRO:HA	1.88	0.40
1:A:126[A]:ILE:CG2	2:A:754:HEM:HMD1	2.51	0.40

All (6) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:479:ARG:NH2	3:B:1105:HOH:O[2_545]	1.88	0.32
1:A:479:ARG:NH2	3:B:1315:HOH:O[2_545]	1.91	0.29
1:A:61:ARG:NH1	3:B:881:HOH:O[2_545]	2.03	0.17
1:A:479:ARG:NH1	3:B:1315:HOH:O[2_545]	2.16	0.04
1:B:146:ASP:OD1	3:C:1114:HOH:O[2_555]	2.17	0.03
1:A:479:ARG:CZ	3:B:1315:HOH:O[2_545]	2.19	0.01

5.3 Torsion angles

5.3.1 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 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	726/753 (96%)	706 (97%)	17 (2%)	3 (0%)	38	23
1	B	726/753 (96%)	707 (97%)	16 (2%)	3 (0%)	38	23
1	C	726/753 (96%)	707 (97%)	16 (2%)	3 (0%)	38	23
1	D	726/753 (96%)	707 (97%)	16 (2%)	3 (0%)	38	23
All	All	2904/3012 (96%)	2827 (97%)	65 (2%)	12 (0%)	38	23

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	711	ALA
1	B	28	SER

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Mol	Chain	Res	Type
1	C	28	SER
1	D	28	SER
1	A	726	GLY
1	B	726	GLY
1	C	726	GLY
1	D	726	GLY
1	B	584	LYS
1	A	75	SER
1	C	75	SER
1	D	584	LYS

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	613/636 (96%)	590 (96%)	23 (4%)	38	21
1	B	613/636 (96%)	587 (96%)	26 (4%)	34	17
1	C	613/636 (96%)	577 (94%)	36 (6%)	23	8
1	D	613/636 (96%)	588 (96%)	25 (4%)	35	18
All	All	2452/2544 (96%)	2342 (96%)	110 (4%)	33	15

All (110) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	73	LYS
1	A	126[A]	ILE
1	A	126[B]	ILE
1	A	185	PHE
1	A	191	THR
1	A	205	ILE
1	A	227	TRP
1	A	237	ASP
1	A	252	ASN
1	A	375	LEU
1	A	386	ASN

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Mol	Chain	Res	Type
1	A	392	HIS
1	A	440	TYR
1	A	459	ASN
1	A	478	LYS
1	A	479	ARG
1	A	552	LEU
1	A	565	GLU
1	A	616	LEU
1	A	631	LYS
1	A	710	ILE
1	A	713	GLN
1	A	750	LYS
1	B	37	ARG
1	B	126[A]	ILE
1	B	126[B]	ILE
1	B	142	LYS
1	B	185	PHE
1	B	205	ILE
1	B	227	TRP
1	B	237	ASP
1	B	247	PRO
1	B	252	ASN
1	B	265	SER
1	B	375	LEU
1	B	386	ASN
1	B	440	TYR
1	B	459	ASN
1	B	478	LYS
1	B	562	LEU
1	B	571	LEU
1	B	583	LYS
1	B	601	ARG
1	B	613	SER
1	B	633	LEU
1	B	647	VAL
1	B	703	LYS
1	B	712	ASP
1	B	722	ASP
1	C	27	ASP
1	C	29	LEU
1	C	61	ARG
1	C	185	PHE

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Mol	Chain	Res	Type
1	C	195	ILE
1	C	198	LEU
1	C	205	ILE
1	C	227	TRP
1	C	237	ASP
1	C	252	ASN
1	C	285	LYS
1	C	321	GLU
1	C	348	LYS
1	C	375	LEU
1	C	377	ARG
1	C	386	ASN
1	C	432	PRO
1	C	440	TYR
1	C	449	HIS
1	C	459	ASN
1	C	478	LYS
1	C	552	LEU
1	C	568	ASP
1	C	569	ASP
1	C	571	LEU
1	C	584	LYS
1	C	606	LEU
1	C	612	ARG
1	C	616	LEU
1	C	633	LEU
1	C	635	SER
1	C	636	ARG
1	C	648	LEU
1	C	660	LEU
1	C	709	LYS
1	C	725	ASP
1	D	27	ASP
1	D	61	ARG
1	D	73	LYS
1	D	185	PHE
1	D	191	THR
1	D	205	ILE
1	D	227	TRP
1	D	237	ASP
1	D	252	ASN
1	D	265	SER

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Mol	Chain	Res	Type
1	D	340	LEU
1	D	352	ASP
1	D	386	ASN
1	D	440	TYR
1	D	459	ASN
1	D	478	LYS
1	D	488	ARG
1	D	552	LEU
1	D	554	LEU
1	D	569	ASP
1	D	582	LEU
1	D	624	LYS
1	D	633	LEU
1	D	648	LEU
1	D	712	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	HIS
1	A	128	HIS
1	A	368	GLN
1	A	386	ASN
1	A	449	HIS
1	A	459	ASN
1	A	515	GLN
1	A	713	GLN
1	B	128	HIS
1	B	157	ASN
1	B	252	ASN
1	B	386	ASN
1	B	395	HIS
1	B	459	ASN
1	B	492	ASN
1	B	507	HIS
1	B	629	HIS
1	C	128	HIS
1	C	252	ASN
1	C	368	GLN
1	C	386	ASN
1	C	459	ASN
1	C	507	HIS

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Mol	Chain	Res	Type
1	C	629	HIS
1	C	671	ASN
1	D	48	GLN
1	D	128	HIS
1	D	252	ASN
1	D	386	ASN
1	D	449	HIS
1	D	459	ASN
1	D	507	HIS
1	D	546	GLN
1	D	556	GLN
1	D	629	HIS
1	D	671	ASN
1	D	713	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

4 ligands 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	HEM	A	754	1	28,50,50	2.21	11 (39%)	17,82,82	2.00	5 (29%)
2	HEM	B	754	1	28,50,50	2.05	7 (25%)	17,82,82	2.06	6 (35%)
2	HEM	C	754	1	28,50,50	1.96	9 (32%)	17,82,82	1.79	5 (29%)
2	HEM	D	754	1	28,50,50	2.12	11 (39%)	17,82,82	1.66	5 (29%)

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	HEM	A	754	1	-	0/6/54/54	0/0/8/8
2	HEM	B	754	1	-	0/6/54/54	0/0/8/8
2	HEM	C	754	1	-	0/6/54/54	0/0/8/8
2	HEM	D	754	1	-	0/6/54/54	0/0/8/8

All (38) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	754	HEM	C3C-C2C	-6.04	1.32	1.40
2	B	754	HEM	C3B-C2B	-5.45	1.33	1.40
2	D	754	HEM	C3C-C2C	-4.83	1.34	1.40
2	B	754	HEM	C3C-C2C	-4.57	1.34	1.40
2	C	754	HEM	C3B-C2B	-4.47	1.34	1.40
2	D	754	HEM	C3B-C2B	-4.31	1.34	1.40
2	A	754	HEM	C3B-C2B	-3.82	1.35	1.40
2	C	754	HEM	C3C-C2C	-3.80	1.35	1.40
2	D	754	HEM	C4B-NB	2.01	1.40	1.36
2	C	754	HEM	C1D-ND	2.01	1.40	1.36
2	D	754	HEM	CAA-C2A	2.02	1.55	1.52
2	D	754	HEM	CMC-C2C	2.08	1.56	1.51
2	B	754	HEM	CMA-C3A	2.12	1.55	1.51
2	B	754	HEM	CAD-C3D	2.13	1.56	1.52
2	D	754	HEM	CMD-C2D	2.14	1.56	1.51
2	A	754	HEM	C4B-NB	2.23	1.40	1.36
2	A	754	HEM	CMC-C2C	2.25	1.56	1.51
2	A	754	HEM	C1D-ND	2.29	1.41	1.36
2	D	754	HEM	CMA-C3A	2.30	1.56	1.51
2	C	754	HEM	C4C-NC	2.35	1.39	1.36
2	C	754	HEM	CAA-C2A	2.42	1.56	1.52
2	A	754	HEM	C3B-CAB	2.45	1.52	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	754	HEM	CAD-C3D	2.46	1.57	1.52
2	C	754	HEM	CMA-C3A	2.50	1.56	1.51
2	A	754	HEM	CAD-C3D	2.61	1.57	1.52
2	B	754	HEM	CAA-C2A	2.66	1.56	1.52
2	C	754	HEM	C3C-CAC	2.66	1.53	1.47
2	A	754	HEM	CAA-C2A	2.72	1.56	1.52
2	C	754	HEM	C1B-NB	2.77	1.40	1.36
2	A	754	HEM	C1C-NC	3.04	1.40	1.36
2	B	754	HEM	C3C-CAC	3.07	1.53	1.47
2	D	754	HEM	C1C-NC	3.19	1.40	1.36
2	A	754	HEM	C4D-ND	3.38	1.40	1.36
2	B	754	HEM	C3B-CAB	3.38	1.54	1.47
2	D	754	HEM	C3C-CAC	3.48	1.54	1.47
2	A	754	HEM	C3C-CAC	3.48	1.54	1.47
2	C	754	HEM	C3B-CAB	3.56	1.54	1.47
2	D	754	HEM	C3B-CAB	3.73	1.55	1.47

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	754	HEM	CMD-C2D-C1D	-4.19	122.02	128.46
2	A	754	HEM	CBD-CAD-C3D	-4.14	104.58	112.47
2	A	754	HEM	CAA-CBA-CGA	-4.03	105.77	112.66
2	C	754	HEM	CMD-C2D-C1D	-4.03	122.28	128.46
2	B	754	HEM	CAA-CBA-CGA	-3.70	106.34	112.66
2	D	754	HEM	CBD-CAD-C3D	-3.56	105.67	112.47
2	B	754	HEM	CMA-C3A-C4A	-3.44	123.18	128.46
2	A	754	HEM	CMD-C2D-C1D	-3.32	123.36	128.46
2	C	754	HEM	CAA-CBA-CGA	-2.84	107.81	112.66
2	D	754	HEM	CMA-C3A-C4A	-2.76	124.22	128.46
2	A	754	HEM	CMA-C3A-C4A	-2.51	124.61	128.46
2	D	754	HEM	CAA-CBA-CGA	-2.43	108.50	112.66
2	C	754	HEM	CBD-CAD-C3D	-2.15	108.37	112.47
2	D	754	HEM	CMD-C2D-C1D	-2.01	125.38	128.46
2	B	754	HEM	CMC-C2C-C3C	2.08	128.75	124.89
2	D	754	HEM	CMB-C2B-C3B	2.31	129.18	124.89
2	C	754	HEM	CMB-C2B-C3B	2.41	129.36	124.89
2	B	754	HEM	CAD-CBD-CGD	2.49	116.92	112.66
2	A	754	HEM	CMD-C2D-C3D	2.67	129.97	124.94
2	C	754	HEM	CMD-C2D-C3D	2.74	130.11	124.94
2	B	754	HEM	CMD-C2D-C3D	2.81	130.24	124.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	754	HEM	3	0
2	B	754	HEM	4	0
2	C	754	HEM	2	0
2	D	754	HEM	3	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	727/753 (96%)	-0.36	33 (4%) 34 29	8, 16, 52, 85	0
1	B	727/753 (96%)	-0.23	56 (7%) 14 11	9, 17, 52, 85	0
1	C	727/753 (96%)	-0.35	40 (5%) 26 21	9, 17, 52, 85	0
1	D	727/753 (96%)	-0.38	29 (3%) 39 33	8, 16, 51, 85	0
All	All	2908/3012 (96%)	-0.33	158 (5%) 26 22	8, 17, 52, 85	0

All (158) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	27	ASP	10.9
1	B	27	ASP	7.9
1	A	29	LEU	7.7
1	A	28	SER	7.0
1	A	27	ASP	6.8
1	B	726	GLY	6.1
1	B	614	ALA	6.1
1	C	725	ASP	5.9
1	A	32	GLU	5.8
1	B	29	LEU	5.8
1	B	641	THR	5.8
1	C	28	SER	5.3
1	C	726	GLY	5.3
1	A	35	SER	5.3
1	C	750	LYS	5.3
1	C	642	ALA	5.2
1	C	27	ASP	5.2
1	C	751	ILE	5.1
1	B	645	GLY	5.1
1	C	677	ASP	5.0
1	A	712	ASP	5.0

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Mol	Chain	Res	Type	RSRZ
1	D	750	LYS	4.9
1	A	711	ALA	4.9
1	B	34	GLY	4.9
1	B	750	LYS	4.8
1	A	34	GLY	4.7
1	B	642	ALA	4.6
1	D	32	GLU	4.6
1	B	647	VAL	4.6
1	C	645	GLY	4.5
1	D	29	LEU	4.5
1	D	726	GLY	4.3
1	C	612	ARG	4.2
1	A	710	ILE	4.2
1	B	673	ALA	4.2
1	B	677	ASP	4.1
1	D	33	ASP	4.1
1	D	711	ALA	4.0
1	B	721	ALA	4.0
1	C	595	ASP	3.9
1	C	675	ILE	3.9
1	A	750	LYS	3.8
1	D	35	SER	3.8
1	B	676	ALA	3.8
1	D	34	GLY	3.8
1	C	594	PRO	3.7
1	A	642	ALA	3.7
1	D	28	SER	3.7
1	B	568	ASP	3.7
1	A	612	ARG	3.6
1	A	611	VAL	3.6
1	B	611	VAL	3.5
1	B	712	ASP	3.5
1	B	610	GLU	3.4
1	B	711	ALA	3.4
1	D	595	ASP	3.4
1	B	612	ARG	3.4
1	B	32	GLU	3.4
1	D	39	ALA	3.3
1	B	701	ALA	3.3
1	B	644	ASP	3.3
1	B	33	ASP	3.3
1	C	711	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
1	C	647	VAL	3.2
1	D	710	ILE	3.2
1	B	596	GLY	3.2
1	B	39	ALA	3.2
1	C	701	ALA	3.2
1	C	643	ASP	3.2
1	B	670	GLY	3.2
1	D	612	ARG	3.1
1	C	641	THR	3.1
1	B	595	ASP	3.1
1	C	596	GLY	3.1
1	A	33	ASP	3.1
1	C	29	LEU	3.1
1	A	753	ALA	3.1
1	B	28	SER	3.0
1	A	713	GLN	3.0
1	B	646	THR	3.0
1	C	700	ASP	3.0
1	A	751	ILE	3.0
1	A	39	ALA	3.0
1	C	611	VAL	3.0
1	C	653	THR	2.9
1	B	713	GLN	2.9
1	B	609	ASP	2.9
1	B	749	ASP	2.9
1	D	30	ALA	2.8
1	B	727	SER	2.8
1	A	709	LYS	2.8
1	B	617	LEU	2.8
1	B	608	ASN	2.8
1	A	596	GLY	2.8
1	B	722	ASP	2.8
1	C	678	ASN	2.8
1	D	725	ASP	2.8
1	C	722	ASP	2.7
1	A	726	GLY	2.7
1	B	710	ILE	2.7
1	A	607	LEU	2.6
1	B	672	ILE	2.6
1	B	634	TYR	2.6
1	D	596	GLY	2.6
1	B	643	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	703	LYS	2.6
1	A	675	ILE	2.6
1	C	712	ASP	2.5
1	B	725	ASP	2.5
1	C	671	ASN	2.5
1	D	696	ALA	2.5
1	A	645	GLY	2.5
1	C	727	SER	2.5
1	D	753	ALA	2.4
1	C	593	ILE	2.4
1	A	669	CYS	2.4
1	B	569	ASP	2.4
1	B	700	ASP	2.4
1	B	669	CYS	2.4
1	C	669	CYS	2.4
1	B	37	ARG	2.4
1	C	572	ASN	2.4
1	C	30	ALA	2.4
1	D	749	ASP	2.4
1	B	650	ILE	2.4
1	B	724	ALA	2.3
1	A	646	THR	2.3
1	B	621	LYS	2.3
1	D	31	PRO	2.3
1	B	746	PRO	2.3
1	D	569	ASP	2.3
1	A	613	SER	2.3
1	D	713	GLN	2.3
1	B	59	ASP	2.3
1	A	31	PRO	2.3
1	D	724	ALA	2.3
1	C	32	GLU	2.2
1	B	572	ASN	2.2
1	D	751	ILE	2.2
1	D	616	LEU	2.2
1	B	31	PRO	2.2
1	A	640	VAL	2.2
1	C	670	GLY	2.2
1	A	38	PRO	2.1
1	C	568	ASP	2.1
1	D	607	LEU	2.1
1	A	673	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	611	VAL	2.1
1	B	751	ILE	2.1
1	C	710	ILE	2.1
1	C	615	ASP	2.1
1	A	41	GLU	2.1
1	C	749	ASP	2.0
1	C	609	ASP	2.0
1	A	30	ALA	2.0
1	B	40	ALA	2.0
1	B	675	ILE	2.0
1	D	574	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	HEM	A	754	43/43	0.98	0.07	0.29	7,12,16,22	0
2	HEM	C	754	43/43	0.98	0.07	0.26	8,12,16,22	0
2	HEM	D	754	43/43	0.98	0.06	-0.16	7,12,16,22	0
2	HEM	B	754	43/43	0.98	0.06	-0.37	8,12,16,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.