



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 04:42 am GMT

PDB ID : 3TTU
Title : Structure of F413Y/H128N double variant of E. coli KatE
Authors : Loewen, P.C.; Jha, V.
Deposited on : 2011-09-15
Resolution : 1.89 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 : trunk28620
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) : recalc28949

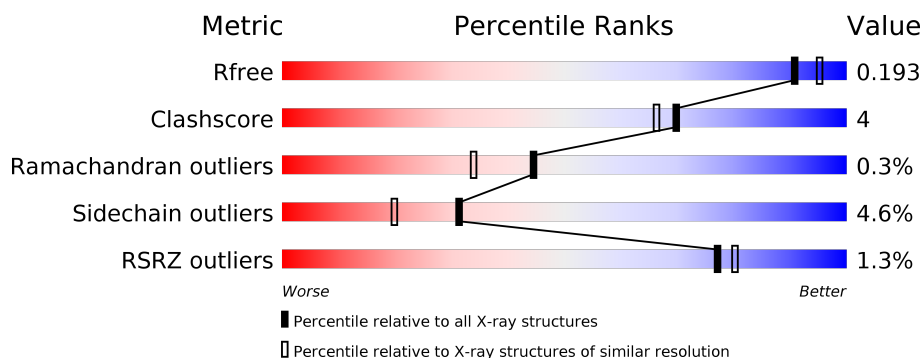
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.89 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	5047 (1.90-1.90)
Clashscore	112137	5731 (1.90-1.90)
Ramachandran outliers	110173	5669 (1.90-1.90)
Sidechain outliers	110143	5670 (1.90-1.90)
RSRZ outliers	101464	5100 (1.90-1.90)

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 style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> % 86% 10% ... </div> </div>
1	B	753	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 2% 85% 9% ... </div> </div>
1	C	753	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> % 83% 11% ... </div> </div>
1	D	753	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> % 86% 8% ... </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 25986 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 Catalase HP11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	726	Total	C	N	O	S	0	1	0
			5743	3645	1005	1081	12			
1	B	726	Total	C	N	O	S	0	1	0
			5744	3646	1005	1081	12			
1	C	726	Total	C	N	O	S	0	1	0
			5743	3645	1005	1081	12			
1	D	726	Total	C	N	O	S	0	1	0
			5744	3646	1005	1081	12			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	128	ASN	HIS	ENGINEERED MUTATION	UNP P21179
A	413	TYR	PHE	ENGINEERED MUTATION	UNP P21179
B	128	ASN	HIS	ENGINEERED MUTATION	UNP P21179
B	413	TYR	PHE	ENGINEERED MUTATION	UNP P21179
C	128	ASN	HIS	ENGINEERED MUTATION	UNP P21179
C	413	TYR	PHE	ENGINEERED MUTATION	UNP P21179
D	128	ASN	HIS	ENGINEERED MUTATION	UNP P21179
D	413	TYR	PHE	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

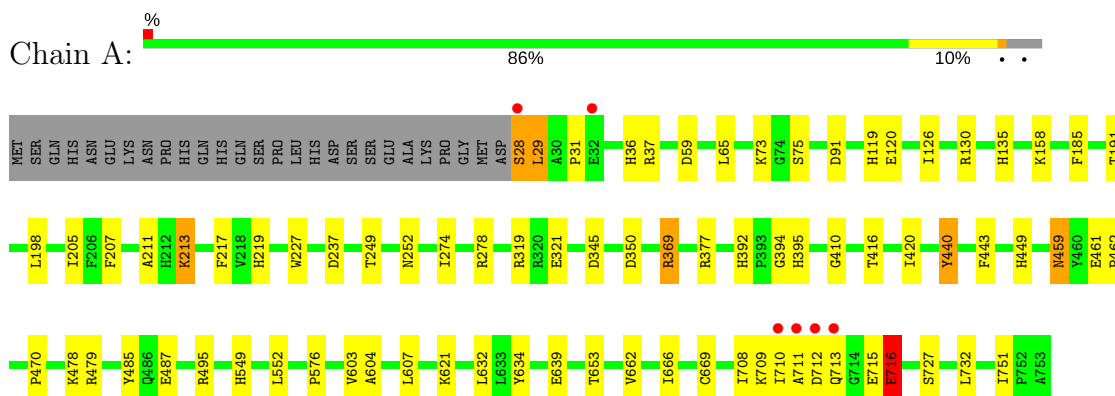
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	772	Total	O	0	0
			772	772		
3	B	639	Total	O	0	0
			639	639		
3	C	680	Total	O	0	0
			680	680		
3	D	749	Total	O	0	0
			749	749		

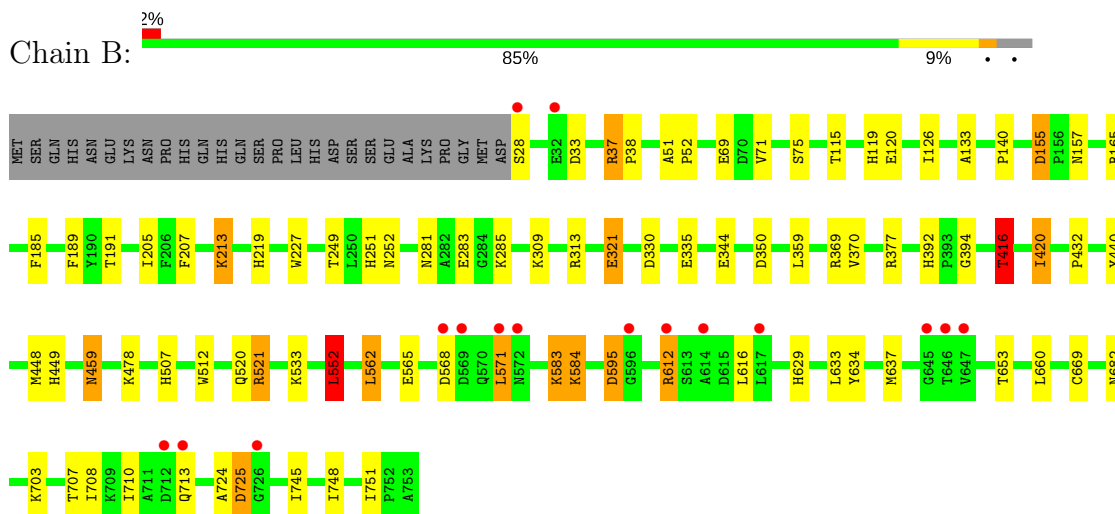
3 Residue-property plots [i](#)

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 ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

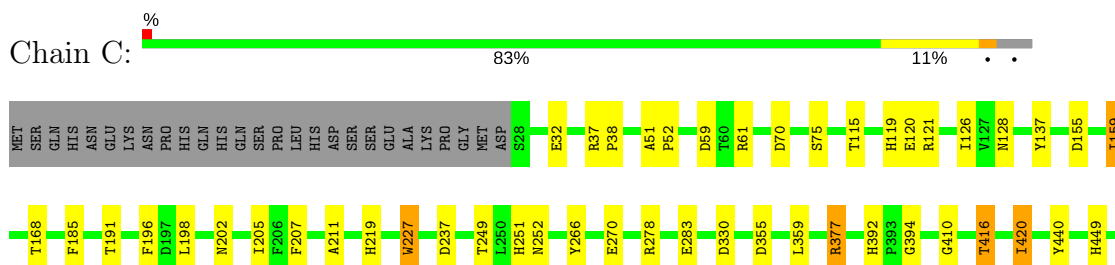
• Molecule 1: Catalase HPII

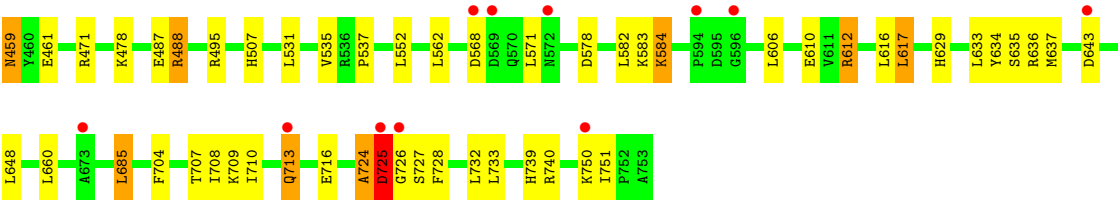


• Molecule 1: Catalase HPII

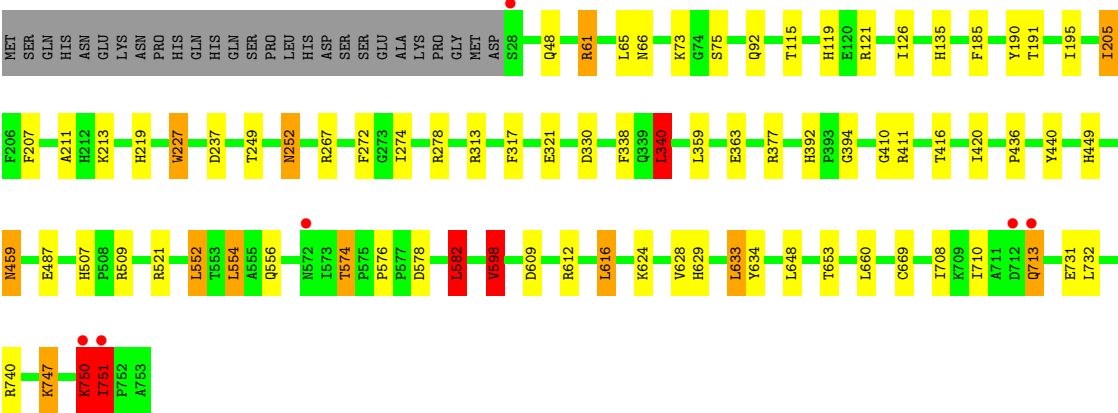
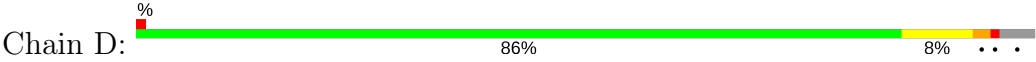


• Molecule 1: Catalase HPII





● Molecule 1: Catalase HP11



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	93.62Å 132.96Å 122.67Å 90.00° 109.39° 90.00°	Depositor
Resolution (Å)	35.46 – 1.89 35.46 – 1.89	Depositor EDS
% Data completeness (in resolution range)	84.3 (35.46-1.89) 84.3 (35.46-1.89)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.17 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.144 , 0.193 0.144 , 0.193	Depositor DCC
R_{free} test set	9439 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	15.3	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 42.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	25986	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% 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	1.10	5/5903 (0.1%)	0.93	9/8026 (0.1%)
1	B	1.06	8/5903 (0.1%)	0.92	9/8026 (0.1%)
1	C	1.05	3/5903 (0.1%)	0.93	14/8026 (0.2%)
1	D	1.08	5/5903 (0.1%)	0.96	15/8026 (0.2%)
All	All	1.07	21/23612 (0.1%)	0.93	47/32104 (0.1%)

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	0	1
1	C	0	2
All	All	0	3

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	669	CYS	CB-SG	7.50	1.95	1.82
1	B	321	GLU	CB-CG	7.35	1.66	1.52
1	B	321	GLU	CG-CD	-6.36	1.42	1.51
1	B	71	VAL	CB-CG1	6.08	1.65	1.52
1	D	317	PHE	CE2-CZ	6.03	1.48	1.37
1	B	344	GLU	CB-CG	-6.00	1.40	1.52
1	A	321	GLU	CD-OE1	5.99	1.32	1.25
1	A	440	TYR	CE1-CZ	5.79	1.46	1.38
1	B	157	ASN	CB-CG	5.65	1.64	1.51
1	B	189	PHE	CE1-CZ	5.61	1.48	1.37
1	B	69	GLU	CB-CG	5.57	1.62	1.52
1	D	190	TYR	CD1-CE1	5.52	1.47	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	669	CYS	CB-SG	5.50	1.91	1.82
1	C	196	PHE	CE1-CZ	5.39	1.47	1.37
1	A	485	TYR	CD2-CE2	5.31	1.47	1.39
1	D	272	PHE	CE2-CZ	5.28	1.47	1.37
1	C	227	TRP	CB-CG	5.22	1.59	1.50
1	D	321	GLU	CD-OE1	5.13	1.31	1.25
1	B	133	ALA	CA-CB	5.08	1.63	1.52
1	A	716	GLU	CB-CG	5.07	1.61	1.52
1	C	266	TYR	CD2-CE2	5.02	1.46	1.39

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	61	ARG	NE-CZ-NH2	13.20	126.90	120.30
1	D	61	ARG	NE-CZ-NH1	-9.79	115.41	120.30
1	C	37	ARG	NE-CZ-NH2	-8.90	115.85	120.30
1	A	350	ASP	CB-CG-OD1	-8.38	110.76	118.30
1	C	377	ARG	NE-CZ-NH1	-6.98	116.81	120.30
1	D	521	ARG	NE-CZ-NH2	-6.68	116.96	120.30
1	B	595	ASP	CB-CG-OD2	-6.52	112.44	118.30
1	B	350	ASP	CB-CG-OD1	-6.51	112.44	118.30
1	C	59	ASP	CB-CG-OD2	-6.48	112.47	118.30
1	D	582	LEU	CB-CG-CD1	6.40	121.88	111.00
1	D	616	LEU	CB-CG-CD2	6.38	121.85	111.00
1	B	33	ASP	CB-CG-OD1	6.32	123.99	118.30
1	B	416	THR	CA-CB-CG2	-6.26	103.63	112.40
1	D	554	LEU	CB-CG-CD2	6.26	121.64	111.00
1	C	355	ASP	CB-CG-OD2	6.22	123.89	118.30
1	A	377	ARG	NE-CZ-NH2	-6.16	117.22	120.30
1	D	121	ARG	NE-CZ-NH1	6.15	123.38	120.30
1	C	59	ASP	CB-CG-OD1	6.12	123.81	118.30
1	B	37	ARG	NE-CZ-NH1	-6.06	117.27	120.30
1	A	345	ASP	CB-CG-OD1	5.93	123.64	118.30
1	B	165	ARG	NE-CZ-NH1	-5.89	117.36	120.30
1	D	213	LYS	CD-CE-NZ	-5.85	98.25	111.70
1	C	420	ILE	CG1-CB-CG2	-5.79	98.66	111.40
1	B	552	LEU	CA-CB-CG	5.75	128.53	115.30
1	C	416	THR	CA-CB-CG2	-5.69	104.44	112.40
1	A	130	ARG	NE-CZ-NH1	5.65	123.12	120.30
1	D	554	LEU	CA-CB-CG	5.62	128.23	115.30
1	A	213	LYS	CD-CE-NZ	-5.62	98.77	111.70
1	C	471	ARG	NE-CZ-NH2	-5.61	117.49	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	70	ASP	CB-CG-OD1	-5.58	113.28	118.30
1	D	598	VAL	CG1-CB-CG2	5.58	119.83	110.90
1	C	685	LEU	CB-CG-CD1	5.56	120.45	111.00
1	A	130	ARG	NE-CZ-NH2	-5.55	117.52	120.30
1	C	471	ARG	NE-CZ-NH1	5.45	123.03	120.30
1	D	740	ARG	NE-CZ-NH1	5.44	123.02	120.30
1	B	521	ARG	NE-CZ-NH2	5.41	123.00	120.30
1	C	495	ARG	NE-CZ-NH1	-5.32	117.64	120.30
1	A	495	ARG	NE-CZ-NH2	-5.25	117.68	120.30
1	A	621	LYS	CD-CE-NZ	-5.25	99.63	111.70
1	D	633	LEU	CB-CG-CD1	5.21	119.86	111.00
1	D	340	LEU	CB-CG-CD1	5.21	119.85	111.00
1	D	609	ASP	CB-CG-OD2	5.11	122.90	118.30
1	C	617	LEU	CA-CB-CG	5.10	127.03	115.30
1	C	155	ASP	CB-CG-OD2	5.09	122.88	118.30
1	A	59	ASP	CB-CG-OD2	-5.05	113.76	118.30
1	B	313	ARG	NE-CZ-NH2	-5.02	117.79	120.30
1	D	377	ARG	NE-CZ-NH2	-5.01	117.80	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	708	ILE	Peptide
1	C	724	ALA	Peptide
1	C	725	ASP	Peptide

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	5743	0	5576	51	0
1	B	5744	0	5580	54	0
1	C	5743	0	5576	57	0
1	D	5744	0	5580	52	0
2	A	43	0	30	1	0
2	B	43	0	30	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	43	0	30	0	0
2	D	43	0	30	2	0
3	A	772	0	0	11	0
3	B	639	0	0	11	0
3	C	680	0	0	14	0
3	D	749	0	0	10	1
All	All	25986	0	22432	190	1

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 4.

All (190) 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:D:449[B]:HIS:CE1	3:D:3274:HOH:O	1.68	1.28
1:C:449[A]:HIS:CE1	3:C:3277:HOH:O	1.86	1.23
1:B:449[B]:HIS:CE1	3:B:3275:HOH:O	1.90	1.22
1:C:449[A]:HIS:NE2	3:C:3277:HOH:O	1.69	1.20
1:A:449[A]:HIS:CE1	3:A:3276:HOH:O	1.96	1.16
1:B:449[B]:HIS:NE2	3:B:3275:HOH:O	1.77	1.14
3:B:2705:HOH:O	1:D:73:LYS:HD3	1.47	1.13
1:B:416:THR:HG21	3:B:3233:HOH:O	1.47	1.12
1:A:449[A]:HIS:CD2	1:C:449[A]:HIS:CD2	2.40	1.08
1:B:521:ARG:HD3	3:B:3047:HOH:O	1.53	1.08
1:D:449[B]:HIS:NE2	3:D:3274:HOH:O	1.71	1.01
1:B:612:ARG:HH11	1:B:612:ARG:HB2	1.27	0.95
1:A:639:GLU:HG3	3:A:2414:HOH:O	1.75	0.85
3:B:2705:HOH:O	1:D:73:LYS:CD	2.13	0.84
1:B:583:LYS:NZ	1:B:583:LYS:H	1.76	0.84
1:B:449[B]:HIS:CD2	1:D:449[B]:HIS:CD2	2.67	0.83
1:A:449[A]:HIS:NE2	3:A:3276:HOH:O	2.04	0.83
1:A:449[A]:HIS:CD2	1:C:449[A]:HIS:HD2	1.94	0.81
1:B:392:HIS:CD2	1:B:394:GLY:H	1.99	0.81
1:D:267:ARG:HG3	3:D:1920:HOH:O	1.82	0.78
1:A:479:ARG:NH2	3:A:2607:HOH:O	2.16	0.76
1:D:750:LYS:HD2	1:D:751:ILE:H	1.51	0.74
1:B:708:ILE:HG13	1:B:710:ILE:HG12	1.68	0.74
1:C:392:HIS:CD2	1:C:394:GLY:H	2.06	0.74
1:A:392:HIS:CD2	1:A:394:GLY:H	2.06	0.72
1:B:533:LYS:HE3	3:C:2623:HOH:O	1.89	0.71
1:C:612:ARG:HG3	1:C:612:ARG:HH11	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:SER:OG	1:A:28:SER:O	2.10	0.70
1:B:119:HIS:CE1	1:D:420:ILE:HG21	2.28	0.69
1:D:750:LYS:HD2	1:D:751:ILE:N	2.07	0.69
1:A:392:HIS:HD2	1:A:394:GLY:H	1.42	0.67
1:B:629:HIS:HD2	3:B:1046:HOH:O	1.77	0.67
1:C:283:GLU:OE1	3:C:2292:HOH:O	2.13	0.67
1:B:392:HIS:HD2	1:B:394:GLY:H	1.43	0.66
1:D:731:GLU:OE2	3:D:3028:HOH:O	2.14	0.65
1:C:629:HIS:HD2	3:C:1129:HOH:O	1.80	0.65
1:B:583:LYS:O	1:B:584:LYS:HB3	1.96	0.65
1:A:449[B]:HIS:CG	1:C:449[B]:HIS:CG	2.67	0.65
1:A:751:ILE:O	1:A:751:ILE:HD12	1.97	0.64
1:B:583:LYS:HZ3	1:B:583:LYS:H	1.45	0.64
1:C:137:TYR:HB2	1:C:159:ILE:CD1	2.28	0.64
1:C:727:SER:HA	3:C:2714:HOH:O	1.97	0.64
1:B:448:MET:HG3	1:B:449[A]:HIS:CD2	2.32	0.64
1:B:552:LEU:HD21	1:B:571:LEU:HD12	1.80	0.64
1:B:583:LYS:HZ2	1:B:583:LYS:H	1.45	0.64
3:B:2705:HOH:O	1:D:73:LYS:CE	2.44	0.63
1:A:29:LEU:CB	3:C:2405:HOH:O	2.46	0.63
1:C:392:HIS:HD2	1:C:394:GLY:H	1.44	0.63
1:C:583:LYS:O	1:C:584:LYS:HB3	1.98	0.63
1:D:392:HIS:CD2	1:D:394:GLY:H	2.17	0.62
1:D:629:HIS:HD2	3:D:1554:HOH:O	1.82	0.62
1:B:281:ASN:OD1	1:B:283:GLU:HG3	2.00	0.62
1:C:330:ASP:OD1	1:C:629:HIS:HE1	1.83	0.62
1:B:682:ASN:HB3	1:B:707:THR:HG21	1.82	0.61
1:C:704:PHE:O	1:C:707:THR:HG22	1.99	0.61
1:A:29:LEU:HB2	3:C:2405:HOH:O	2.01	0.61
1:C:612:ARG:HH11	1:C:612:ARG:CG	2.14	0.60
1:C:708:ILE:HG13	1:C:710:ILE:HG12	1.82	0.60
1:B:449[A]:HIS:CG	1:D:449[A]:HIS:CG	2.55	0.60
1:D:330:ASP:OD1	1:D:629:HIS:HE1	1.85	0.59
1:D:747:LYS:O	1:D:750:LYS:HE2	2.03	0.58
1:D:392:HIS:HE1	1:D:416:THR:OG1	1.86	0.58
1:A:449[A]:HIS:HD2	1:C:449[A]:HIS:CD2	2.18	0.58
1:A:36:HIS:CD2	1:A:36:HIS:H	2.22	0.58
1:B:724:ALA:O	1:B:725:ASP:O	2.21	0.57
1:D:750:LYS:O	1:D:751:ILE:O	2.23	0.56
1:A:36:HIS:HE1	3:A:1872:HOH:O	1.89	0.56
1:A:392:HIS:HE1	1:A:416:THR:OG1	1.90	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:612:ARG:NH1	1:B:612:ARG:HB2	2.10	0.55
1:B:330:ASP:OD1	1:B:629:HIS:HE1	1.90	0.55
1:D:61:ARG:HH11	1:D:66:ASN:HA	1.73	0.54
1:A:29:LEU:HD22	3:C:2405:HOH:O	2.08	0.54
1:D:359:LEU:H	1:D:507:HIS:HD2	1.54	0.54
1:B:38:PRO:HG2	1:B:51:ALA:HB2	1.89	0.53
1:C:612:ARG:HG3	1:C:612:ARG:NH1	2.21	0.53
1:C:578:ASP:HB2	1:C:582:LEU:O	2.08	0.53
1:A:710:ILE:HG12	1:A:715:GLU:OE1	2.08	0.53
1:D:392:HIS:HD2	1:D:394:GLY:H	1.55	0.53
1:A:603:VAL:HG11	1:A:666:ILE:HD12	1.91	0.53
1:A:120:GLU:HB2	1:D:126:ILE:CD1	2.39	0.53
1:A:478:LYS:HG2	3:A:1955:HOH:O	2.08	0.53
1:A:278:ARG:HH12	1:A:487:GLU:CD	2.13	0.52
1:A:119:HIS:CE1	1:C:420:ILE:HG21	2.45	0.52
1:C:359:LEU:H	1:C:507:HIS:HD2	1.57	0.52
1:C:416:THR:CG2	3:C:3238:HOH:O	2.58	0.52
1:C:392:HIS:HE1	1:C:416:THR:OG1	1.92	0.52
1:C:724:ALA:O	1:C:725:ASP:HB2	2.10	0.52
1:B:533:LYS:CE	3:C:2623:HOH:O	2.53	0.51
1:B:120:GLU:HB2	1:C:126:ILE:HD11	1.93	0.51
1:C:535:VAL:O	1:C:537:PRO:HD3	2.10	0.51
1:A:607:LEU:HD11	1:A:632:LEU:HB3	1.92	0.51
1:A:710:ILE:CG1	1:A:715:GLU:OE1	2.59	0.51
1:D:509:ARG:HD2	1:D:576:PRO:HD2	1.92	0.51
1:C:38:PRO:HG2	1:C:51:ALA:HB2	1.92	0.51
1:D:708:ILE:HG13	1:D:710:ILE:HG12	1.92	0.50
1:B:359:LEU:H	1:B:507:HIS:HD2	1.58	0.50
1:A:274:ILE:HD12	2:A:760:HEM:HMB1	1.92	0.50
1:A:219:HIS:HB3	1:B:459:ASN:ND2	2.27	0.50
1:C:610:GLU:O	1:C:610:GLU:HG3	2.12	0.50
1:D:115:THR:O	1:D:119:HIS:HD2	1.94	0.50
1:B:612:ARG:NH1	1:B:669:CYS:SG	2.85	0.49
1:A:459:ASN:ND2	1:B:219:HIS:HB3	2.27	0.49
1:D:205:ILE:HD13	1:D:205:ILE:H	1.77	0.49
1:C:219:HIS:HB3	1:D:459:ASN:ND2	2.27	0.49
1:A:449[B]:HIS:CD2	3:A:1077:HOH:O	2.65	0.49
1:D:598:VAL:HG13	1:D:628:VAL:CG2	2.42	0.49
1:B:420:ILE:HG21	1:D:119:HIS:CE1	2.48	0.49
1:B:533:LYS:HE2	3:B:3100:HOH:O	2.11	0.48
1:D:363:GLU:HB2	1:D:582:LEU:HD21	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:392:HIS:HE1	1:B:416:THR:OG1	1.96	0.48
1:C:115:THR:O	1:C:119:HIS:HD2	1.97	0.48
1:A:634:TYR:O	1:A:653:THR:HA	2.13	0.48
1:A:91:ASP:OD1	1:C:461:GLU:OE1	2.32	0.48
1:A:207:PHE:CD1	1:A:217:PHE:CZ	3.02	0.48
1:C:137:TYR:HB2	1:C:159:ILE:HD11	1.97	0.47
1:B:126:ILE:CD1	1:C:120:GLU:HB2	2.45	0.47
1:D:65:LEU:HD21	1:D:135:HIS:CG	2.50	0.47
1:B:28:SER:HB2	3:D:2425:HOH:O	2.15	0.47
1:B:309:LYS:HD2	1:B:660:LEU:HD11	1.97	0.47
1:C:610:GLU:OE1	1:C:643:ASP:HA	2.15	0.47
1:D:211:ALA:CB	1:D:410:GLY:HA3	2.45	0.46
1:A:603:VAL:HG11	1:A:666:ILE:CD1	2.46	0.46
1:A:716:GLU:HG2	3:A:1656:HOH:O	2.15	0.46
1:C:207:PHE:O	1:C:249:THR:HA	2.15	0.46
1:A:65:LEU:HD21	1:A:135:HIS:CG	2.50	0.46
1:B:637:MET:HB2	1:C:562:LEU:HA	1.98	0.46
1:D:713:GLN:O	1:D:713:GLN:HG2	2.15	0.46
1:A:449[B]:HIS:CD2	1:C:449[B]:HIS:CG	3.01	0.46
1:C:459:ASN:ND2	1:D:219:HIS:HB3	2.31	0.46
1:D:556:GLN:NE2	3:D:2773:HOH:O	2.48	0.45
1:A:158:LYS:HD3	3:A:2278:HOH:O	2.16	0.45
1:A:395:HIS:HE1	3:A:3270:HOH:O	1.99	0.45
1:A:213:LYS:HD3	1:D:92:GLN:HA	1.99	0.45
1:B:478:LYS:HD2	3:B:2857:HOH:O	2.17	0.45
1:D:274:ILE:HD12	2:D:760:HEM:HMB1	1.99	0.45
1:C:51:ALA:HB1	1:C:52:PRO:HD2	1.98	0.45
1:B:335:GLU:OE1	1:B:369:ARG:HD2	2.17	0.44
1:C:488:ARG:HD3	3:C:2379:HOH:O	2.16	0.44
1:C:739:HIS:CD2	1:C:740:ARG:HG2	2.52	0.44
1:B:37:ARG:HD3	3:B:2886:HOH:O	2.17	0.44
1:D:207:PHE:O	1:D:249:THR:HA	2.16	0.44
1:A:207:PHE:O	1:A:249:THR:HA	2.18	0.44
1:A:211:ALA:CB	1:A:410:GLY:HA3	2.48	0.44
1:A:459:ASN:C	1:A:459:ASN:HD22	2.20	0.44
1:D:338:PHE:HB3	1:D:340:LEU:HD13	2.00	0.44
1:C:202:ASN:HA	1:C:270:GLU:O	2.18	0.43
1:D:750:LYS:O	1:D:751:ILE:C	2.57	0.43
1:A:31:PRO:HD2	1:A:36:HIS:HB3	1.99	0.43
1:C:416:THR:HG21	3:C:3238:HOH:O	2.18	0.43
1:D:552:LEU:HA	1:D:552:LEU:HD22	1.85	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:725:ASP:HB3	1:C:726:GLY:H	1.50	0.43
1:D:634:TYR:O	1:D:653:THR:HA	2.18	0.43
1:C:128:ASN:HA	1:C:168:THR:O	2.18	0.43
1:B:562:LEU:HA	1:C:637:MET:HB2	1.99	0.43
1:D:411:ARG:HG2	2:D:760:HEM:C2C	2.54	0.43
1:B:634:TYR:O	1:B:653:THR:HA	2.19	0.43
1:B:251:HIS:CE1	1:B:507:HIS:HB3	2.54	0.43
1:C:713:GLN:HG3	1:C:713:GLN:H	1.31	0.43
1:C:716:GLU:OE2	1:C:716:GLU:HA	2.18	0.42
1:D:359:LEU:H	1:D:507:HIS:CD2	2.35	0.42
1:D:578:ASP:HB2	3:D:2129:HOH:O	2.18	0.42
1:C:725:ASP:HA	1:C:728:PHE:HB3	2.00	0.42
1:B:359:LEU:H	1:B:507:HIS:CD2	2.35	0.42
1:D:195:ILE:HD11	1:D:436:PRO:HA	2.02	0.42
1:B:52:PRO:HG3	3:D:1451:HOH:O	2.19	0.42
1:A:449[A]:HIS:CG	1:C:449[A]:HIS:CD2	3.03	0.42
1:A:443:PHE:CZ	1:A:470:PRO:HD2	2.55	0.42
1:A:549:HIS:O	1:A:576:PRO:HD3	2.20	0.42
1:B:512:TRP:CH2	1:B:520:GLN:HB3	2.54	0.41
1:B:745:ILE:O	1:B:748:ILE:HG12	2.20	0.41
1:C:278:ARG:HH12	1:C:487:GLU:CD	2.22	0.41
1:C:211:ALA:CB	1:C:410:GLY:HA3	2.50	0.41
1:B:213:LYS:HE3	1:B:213:LYS:HB3	1.78	0.41
1:A:369:ARG:HG2	3:A:1078:HOH:O	2.19	0.41
1:B:115:THR:O	1:B:119:HIS:HD2	2.03	0.41
1:B:207:PHE:O	1:B:249:THR:HA	2.20	0.41
1:C:507:HIS:HE1	3:C:926:HOH:O	2.03	0.41
1:B:725:ASP:OD2	1:B:725:ASP:C	2.58	0.41
1:D:574:THR:HG22	3:D:1614:HOH:O	2.21	0.41
1:D:278:ARG:HH12	1:D:487:GLU:CD	2.24	0.41
1:C:634:TYR:CG	1:C:635:SER:N	2.89	0.41
1:A:319:ARG:HD3	1:D:227:TRP:O	2.19	0.41
1:A:604:ALA:HB2	1:A:662:VAL:HG11	2.02	0.41
1:A:461:GLU:HA	1:A:462:PRO:C	2.41	0.41
1:B:126:ILE:HD12	1:C:121:ARG:CZ	2.51	0.41
1:B:140:PRO:HG2	1:B:155:ASP:O	2.21	0.41
1:D:313:ARG:HG3	1:D:660:LEU:HD12	2.02	0.41
1:D:578:ASP:HB3	1:D:582:LEU:O	2.20	0.40
1:C:251:HIS:CE1	1:C:507:HIS:HB3	2.56	0.40
1:D:207:PHE:CD2	1:D:252:ASN:HB3	2.56	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:2178:HOH:O	3:D:2976:HOH:O[1_655]	2.09	0.11

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	725/753 (96%)	706 (97%)	17 (2%)	2 (0%)	44	34
1	B	725/753 (96%)	703 (97%)	19 (3%)	3 (0%)	38	26
1	C	725/753 (96%)	704 (97%)	19 (3%)	2 (0%)	44	34
1	D	725/753 (96%)	703 (97%)	19 (3%)	3 (0%)	38	26
All	All	2900/3012 (96%)	2816 (97%)	74 (3%)	10 (0%)	44	34

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	711	ALA
1	B	725	ASP
1	C	725	ASP
1	D	750	LYS
1	D	751	ILE
1	B	75	SER
1	C	75	SER
1	D	75	SER
1	A	75	SER
1	B	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	612/636 (96%)	589 (96%)	23 (4%)	38	27
1	B	612/636 (96%)	583 (95%)	29 (5%)	30	19
1	C	612/636 (96%)	576 (94%)	36 (6%)	23	12
1	D	612/636 (96%)	587 (96%)	25 (4%)	35	24
All	All	2448/2544 (96%)	2335 (95%)	113 (5%)	31	20

All (113) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	SER
1	A	29	LEU
1	A	37	ARG
1	A	73	LYS
1	A	126	ILE
1	A	185	PHE
1	A	191	THR
1	A	198	LEU
1	A	205	ILE
1	A	227	TRP
1	A	237	ASP
1	A	252	ASN
1	A	369	ARG
1	A	420	ILE
1	A	440	TYR
1	A	459	ASN
1	A	552	LEU
1	A	709	LYS
1	A	712	ASP
1	A	713	GLN
1	A	716	GLU
1	A	727	SER
1	A	732	LEU
1	B	155	ASP
1	B	185	PHE
1	B	191	THR
1	B	205	ILE
1	B	213	LYS

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Mol	Chain	Res	Type
1	B	227	TRP
1	B	252	ASN
1	B	285	LYS
1	B	321	GLU
1	B	370	VAL
1	B	377	ARG
1	B	416	THR
1	B	420	ILE
1	B	432	PRO
1	B	440	TYR
1	B	459	ASN
1	B	552	LEU
1	B	562	LEU
1	B	565	GLU
1	B	568	ASP
1	B	571	LEU
1	B	583	LYS
1	B	595	ASP
1	B	612	ARG
1	B	616	LEU
1	B	633	LEU
1	B	703	LYS
1	B	713	GLN
1	B	751	ILE
1	C	32	GLU
1	C	61	ARG
1	C	159	ILE
1	C	185	PHE
1	C	191	THR
1	C	198	LEU
1	C	205	ILE
1	C	227	TRP
1	C	237	ASP
1	C	252	ASN
1	C	377	ARG
1	C	440	TYR
1	C	459	ASN
1	C	478	LYS
1	C	488	ARG
1	C	531	LEU
1	C	552	LEU
1	C	568	ASP

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Mol	Chain	Res	Type
1	C	571	LEU
1	C	584	LYS
1	C	606	LEU
1	C	612	ARG
1	C	616	LEU
1	C	617	LEU
1	C	633	LEU
1	C	636	ARG
1	C	648	LEU
1	C	660	LEU
1	C	685	LEU
1	C	709	LYS
1	C	713	GLN
1	C	725	ASP
1	C	732	LEU
1	C	733	LEU
1	C	750	LYS
1	C	751	ILE
1	D	48	GLN
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	340	LEU
1	D	440	TYR
1	D	459	ASN
1	D	552	LEU
1	D	554	LEU
1	D	574	THR
1	D	582	LEU
1	D	598	VAL
1	D	612	ARG
1	D	616	LEU
1	D	624	LYS
1	D	633	LEU
1	D	648	LEU
1	D	713	GLN
1	D	732	LEU
1	D	747	LYS
1	D	750	LYS

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Mol	Chain	Res	Type
1	D	751	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	HIS
1	A	252	ASN
1	A	368	GLN
1	A	392	HIS
1	A	459	ASN
1	A	515	GLN
1	B	252	ASN
1	B	392	HIS
1	B	459	ASN
1	B	507	HIS
1	B	629	HIS
1	C	252	ASN
1	C	392	HIS
1	C	459	ASN
1	C	507	HIS
1	C	556	GLN
1	C	629	HIS
1	C	671	ASN
1	D	48	GLN
1	D	128	ASN
1	D	252	ASN
1	D	392	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

5.3.3 RNA ⓘ

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	760	1	28,50,50	1.95	8 (28%)	17,82,82	2.45	8 (47%)
2	HEM	B	760	1	28,50,50	2.11	9 (32%)	17,82,82	1.83	5 (29%)
2	HEM	C	760	1	28,50,50	2.09	9 (32%)	17,82,82	2.60	7 (41%)
2	HEM	D	760	1	28,50,50	2.09	9 (32%)	17,82,82	2.20	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	760	1	-	0/6/54/54	0/0/8/8
2	HEM	B	760	1	-	0/6/54/54	0/0/8/8
2	HEM	C	760	1	-	0/6/54/54	0/0/8/8
2	HEM	D	760	1	-	0/6/54/54	0/0/8/8

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	760	HEM	C3B-C2B	-5.38	1.33	1.40
2	B	760	HEM	C3B-C2B	-4.78	1.34	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	760	HEM	C3C-C2C	-4.06	1.35	1.40
2	B	760	HEM	C3C-C2C	-3.88	1.35	1.40
2	A	760	HEM	C3C-C2C	-3.85	1.35	1.40
2	A	760	HEM	C3B-C2B	-2.69	1.36	1.40
2	C	760	HEM	C3C-C2C	-2.58	1.36	1.40
2	D	760	HEM	C3B-C2B	-2.50	1.37	1.40
2	B	760	HEM	C4A-NA	2.08	1.40	1.36
2	C	760	HEM	C1A-NA	2.09	1.40	1.36
2	B	760	HEM	C4D-ND	2.17	1.39	1.36
2	D	760	HEM	CMC-C2C	2.26	1.56	1.51
2	C	760	HEM	C4D-ND	2.32	1.39	1.36
2	A	760	HEM	C3B-CAB	2.55	1.52	1.47
2	D	760	HEM	CMB-C2B	2.56	1.57	1.51
2	C	760	HEM	CMA-C3A	2.56	1.56	1.51
2	A	760	HEM	C4A-NA	2.58	1.41	1.36
2	C	760	HEM	C4C-NC	2.64	1.39	1.36
2	D	760	HEM	C1C-NC	2.70	1.40	1.36
2	B	760	HEM	CMA-C3A	2.75	1.57	1.51
2	B	760	HEM	CMC-C2C	2.81	1.57	1.51
2	D	760	HEM	CMD-C2D	2.84	1.57	1.51
2	A	760	HEM	C3C-CAC	3.00	1.53	1.47
2	B	760	HEM	C3B-CAB	3.01	1.53	1.47
2	A	760	HEM	CAA-C2A	3.11	1.57	1.52
2	C	760	HEM	C3C-CAC	3.20	1.54	1.47
2	A	760	HEM	CMC-C2C	3.24	1.58	1.51
2	D	760	HEM	C3B-CAB	3.36	1.54	1.47
2	A	760	HEM	C3D-C2D	3.63	1.48	1.37
2	B	760	HEM	C3D-C2D	3.74	1.48	1.37
2	C	760	HEM	C3B-CAB	3.79	1.55	1.47
2	C	760	HEM	C3D-C2D	3.82	1.49	1.37
2	B	760	HEM	C3C-CAC	3.86	1.55	1.47
2	D	760	HEM	C3D-C2D	4.21	1.50	1.37
2	D	760	HEM	C3C-CAC	4.45	1.56	1.47

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	760	HEM	CBD-CAD-C3D	-5.91	101.20	112.47
2	C	760	HEM	CAA-CBA-CGA	-5.64	103.02	112.66
2	D	760	HEM	CBD-CAD-C3D	-5.27	102.42	112.47
2	A	760	HEM	CAA-CBA-CGA	-4.55	104.89	112.66
2	C	760	HEM	CBD-CAD-C3D	-4.26	104.34	112.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	760	HEM	CMA-C3A-C4A	-3.90	122.47	128.46
2	B	760	HEM	CAA-CBA-CGA	-3.57	106.56	112.66
2	D	760	HEM	CAA-CBA-CGA	-3.49	106.70	112.66
2	B	760	HEM	CBD-CAD-C3D	-3.29	106.19	112.47
2	C	760	HEM	C1D-C2D-C3D	-3.20	104.77	107.00
2	D	760	HEM	CMA-C3A-C4A	-2.89	124.03	128.46
2	C	760	HEM	CBA-CAA-C2A	-2.87	107.00	112.48
2	A	760	HEM	C3C-C4C-NC	-2.53	106.16	110.94
2	D	760	HEM	C1D-C2D-C3D	-2.51	105.25	107.00
2	C	760	HEM	C3B-C4B-NB	-2.44	106.05	109.21
2	B	760	HEM	C3C-C4C-NC	-2.36	106.50	110.94
2	B	760	HEM	C1D-C2D-C3D	-2.29	105.40	107.00
2	A	760	HEM	CMD-C2D-C1D	-2.09	125.25	128.46
2	A	760	HEM	C3B-C4B-NB	-2.08	106.52	109.21
2	B	760	HEM	C4C-C3C-C2C	2.12	108.38	106.90
2	A	760	HEM	CMB-C2B-C3B	2.18	128.94	124.89
2	A	760	HEM	C4A-C3A-C2A	2.27	108.58	107.00
2	C	760	HEM	C4A-C3A-C2A	2.55	108.77	107.00
2	A	760	HEM	C4C-C3C-C2C	2.81	108.86	106.90
2	D	760	HEM	CMB-C2B-C3B	2.83	130.15	124.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	760	HEM	1	0
2	D	760	HEM	2	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	726/753 (96%)	-0.55	6 (0%) 86 87	6, 12, 27, 42	1 (0%)
1	B	726/753 (96%)	-0.44	16 (2%) 62 66	7, 14, 34, 47	1 (0%)
1	C	726/753 (96%)	-0.48	11 (1%) 74 77	7, 14, 34, 46	1 (0%)
1	D	726/753 (96%)	-0.55	6 (0%) 86 87	6, 12, 28, 42	1 (0%)
All	All	2904/3012 (96%)	-0.50	39 (1%) 77 80	6, 13, 31, 47	4 (0%)

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	32	GLU	3.9
1	C	726	GLY	3.8
1	A	710	ILE	3.6
1	B	28	SER	3.4
1	B	713	GLN	3.3
1	D	28	SER	3.1
1	D	750	LYS	3.1
1	A	28	SER	3.0
1	A	32	GLU	2.9
1	A	711	ALA	2.9
1	D	713	GLN	2.9
1	B	647	VAL	2.9
1	B	568	ASP	2.8
1	D	712	ASP	2.8
1	B	646	THR	2.7
1	B	617	LEU	2.7
1	B	712	ASP	2.6
1	B	596	GLY	2.5
1	C	596	GLY	2.5
1	D	751	ILE	2.5
1	B	572	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	614	ALA	2.4
1	B	571	LEU	2.4
1	C	750	LYS	2.4
1	B	645	GLY	2.3
1	C	568	ASP	2.3
1	A	712	ASP	2.3
1	C	643	ASP	2.2
1	B	726	GLY	2.2
1	C	673	ALA	2.2
1	C	594	PRO	2.2
1	B	612	ARG	2.1
1	C	572	ASN	2.1
1	B	569	ASP	2.1
1	C	725	ASP	2.1
1	C	713	GLN	2.1
1	D	572	ASN	2.1
1	A	713	GLN	2.0
1	C	569	ASP	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	760	43/43	0.98	0.10	-0.01	3,7,10,13	0
2	HEM	B	760	43/43	0.98	0.07	-0.18	6,8,11,12	0
2	HEM	C	760	43/43	0.98	0.08	-0.25	5,9,11,12	0
2	HEM	D	760	43/43	0.98	0.07	-0.64	5,7,9,10	0

6.5 Other polymers [i](#)

There are no such residues in this entry.