



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 07:44 am GMT

PDB ID : 1F5O
Title : 2.9 ANGSTROM CRYSTAL STRUCTURE OF DEOXYGENATED LAM-
PREY HEMOGLOBIN V IN THE SPACE GROUP P2(1)2(1)2(1)
Authors : Heaslet, H.A.; Royer Jr., W.E.
Deposited on : 2000-06-15
Resolution : 2.90 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

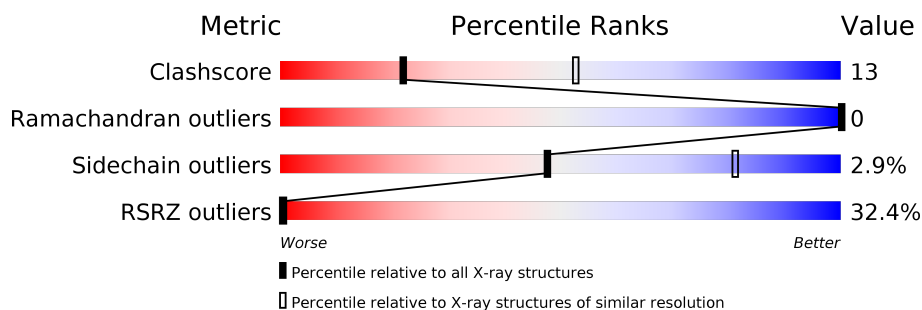
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	1807 (2.90-2.90)
Ramachandran outliers	110173	1768 (2.90-2.90)
Sidechain outliers	110143	1770 (2.90-2.90)
RSRZ outliers	101464	1596 (2.90-2.90)

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	149	<div> <div>36%</div> <div>77%</div> <div>22%</div> <div>.</div> </div>
1	B	149	<div> <div>52%</div> <div>75%</div> <div>23%</div> <div>.</div> </div>
1	C	149	<div> <div>38%</div> <div>73%</div> <div>26%</div> <div>.</div> </div>
1	D	149	<div> <div>28%</div> <div>75%</div> <div>23%</div> <div>.</div> </div>
1	E	149	<div> <div>17%</div> <div>76%</div> <div>23%</div> <div>.</div> </div>
1	F	149	<div> <div>25%</div> <div>74%</div> <div>25%</div> <div>.</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7134 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 HEMOGLOBIN V.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	149	Total	C	N	O	S	0	0	0
			1144	732	189	217	6			
1	B	149	Total	C	N	O	S	0	0	0
			1144	732	189	217	6			
1	C	149	Total	C	N	O	S	0	0	0
			1144	732	189	217	6			
1	D	149	Total	C	N	O	S	0	0	0
			1144	732	189	217	6			
1	E	149	Total	C	N	O	S	0	0	0
			1144	732	189	217	6			
1	F	149	Total	C	N	O	S	0	0	0
			1144	732	189	217	6			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	29	THR	ASN	SEE REMARK 999	UNP P02208
A	86	ALA	VAL	SEE REMARK 999	UNP P02208
B	29	THR	ASN	SEE REMARK 999	UNP P02208
B	86	ALA	VAL	SEE REMARK 999	UNP P02208
C	29	THR	ASN	SEE REMARK 999	UNP P02208
C	86	ALA	VAL	SEE REMARK 999	UNP P02208
D	29	THR	ASN	SEE REMARK 999	UNP P02208
D	86	ALA	VAL	SEE REMARK 999	UNP P02208
E	29	THR	ASN	SEE REMARK 999	UNP P02208
E	86	ALA	VAL	SEE REMARK 999	UNP P02208
F	29	THR	ASN	SEE REMARK 999	UNP P02208
F	86	ALA	VAL	SEE REMARK 999	UNP P02208

- 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
2	E	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	F	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

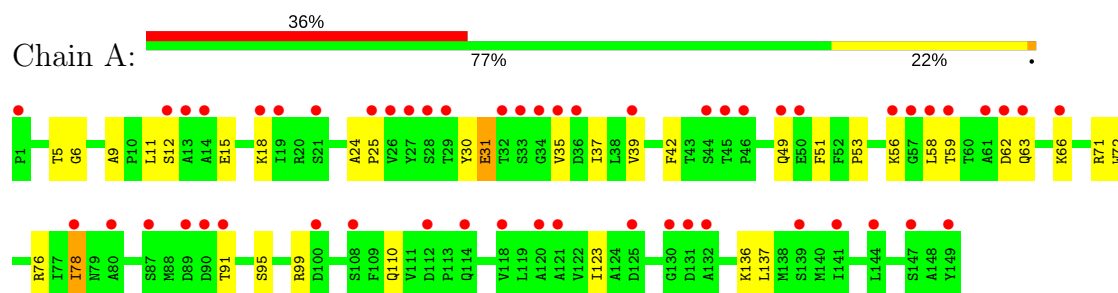
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total O 2 2	0	0
3	B	2	Total O 2 2	0	0
3	C	2	Total O 2 2	0	0
3	D	2	Total O 2 2	0	0
3	E	2	Total O 2 2	0	0
3	F	2	Total O 2 2	0	0

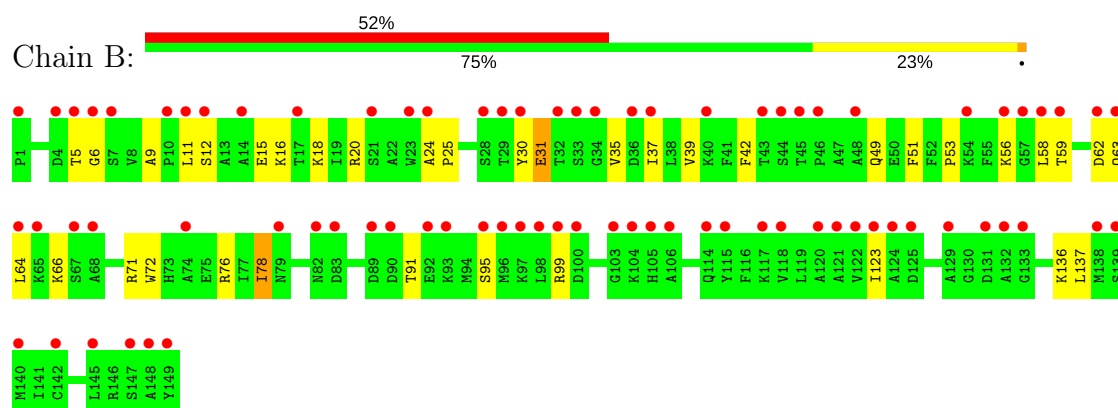
3 Residue-property plots [i](#)

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.

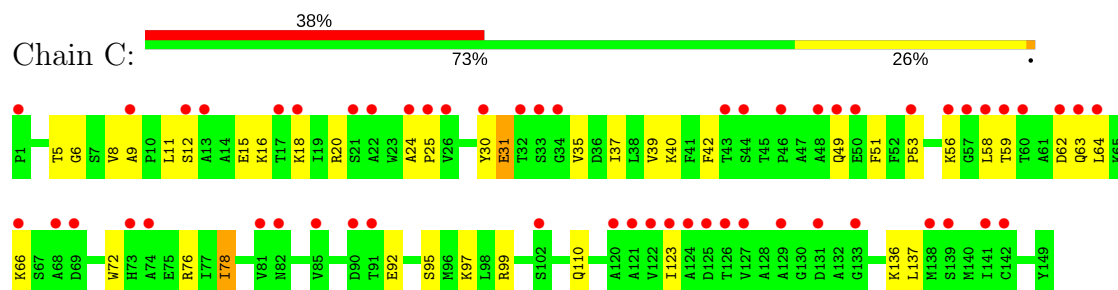
• Molecule 1: HEMOGLOBIN V



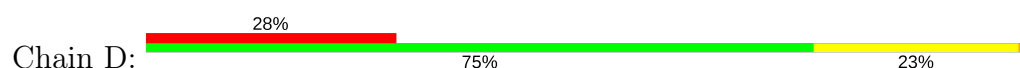
• Molecule 1: HEMOGLOBIN V

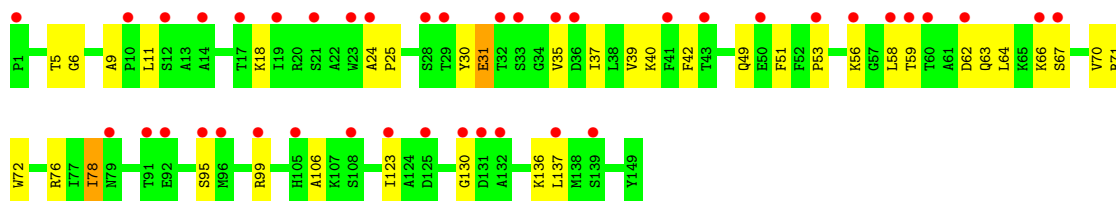


• Molecule 1: HEMOGLOBIN V

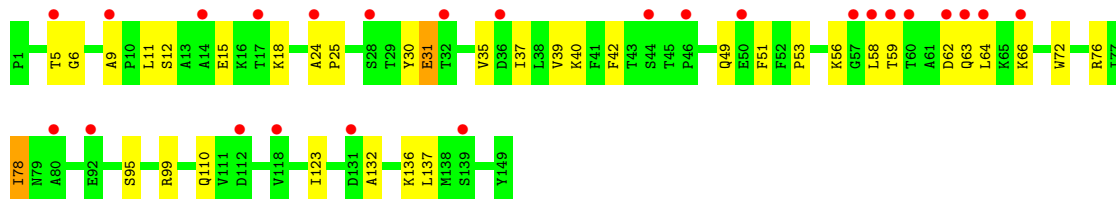
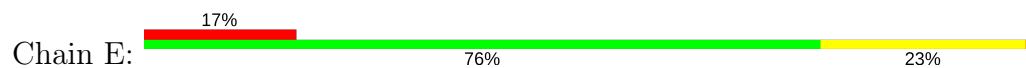


• Molecule 1: HEMOGLOBIN V

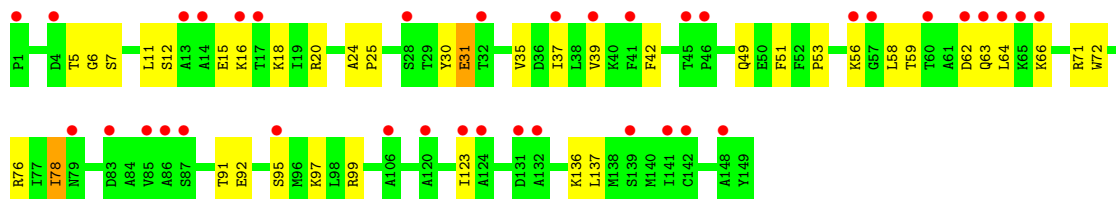
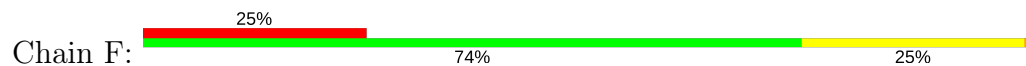




• Molecule 1: HEMOGLOBIN V



• Molecule 1: HEMOGLOBIN V



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	82.50Å 96.20Å 146.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.90 9.99 – 2.90	Depositor EDS
% Data completeness (in resolution range)	95.5 (8.00-2.90) 95.1 (9.99-2.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.44 (at 2.89Å)	Xtriage
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.192 , 0.234 0.337 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	52.3	Xtriage
Anisotropy	0.846	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 71.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.76	EDS
Total number of atoms	7134	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.89% 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	0.43	0/1167	0.56	0/1577
1	B	0.40	0/1167	0.55	0/1577
1	C	0.45	0/1167	0.56	0/1577
1	D	0.42	0/1167	0.56	0/1577
1	E	0.44	0/1167	0.55	0/1577
1	F	0.41	0/1167	0.55	0/1577
All	All	0.42	0/7002	0.55	0/9462

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1144	0	1158	33	1
1	B	1144	0	1158	31	0
1	C	1144	0	1158	31	4
1	D	1144	0	1158	30	2
1	E	1144	0	1158	28	2
1	F	1144	0	1158	27	3
2	A	43	0	30	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	43	0	30	3	0
2	C	43	0	30	3	0
2	D	43	0	30	3	0
2	E	43	0	30	3	0
2	F	43	0	30	3	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
3	E	2	0	0	0	0
3	F	2	0	0	0	0
All	All	7134	0	7128	189	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 13.

All (189) 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:E:24:ALA:HB3	1:E:25:PRO:HD3	1.58	0.85
1:A:31:GLU:OE1	1:B:71:ARG:HD2	1.78	0.82
1:F:24:ALA:HB3	1:F:25:PRO:HD3	1.62	0.80
1:B:72:TRP:CE2	1:B:76:ARG:HD2	2.16	0.80
1:C:24:ALA:HB3	1:C:25:PRO:HD3	1.62	0.80
1:D:24:ALA:HB3	1:D:25:PRO:HD3	1.62	0.80
1:A:24:ALA:HB3	1:A:25:PRO:HD3	1.62	0.80
1:A:72:TRP:CE2	1:A:76:ARG:HD2	2.17	0.79
1:D:18:LYS:HB3	1:D:18:LYS:NZ	1.97	0.79
1:E:18:LYS:NZ	1:E:18:LYS:HB3	1.99	0.78
1:A:31:GLU:OE1	1:B:71:ARG:NH1	2.17	0.77
1:F:18:LYS:NZ	1:F:18:LYS:HB3	1.99	0.77
1:C:18:LYS:NZ	1:C:18:LYS:HB3	2.01	0.76
1:A:18:LYS:HB3	1:A:18:LYS:NZ	2.01	0.75
1:C:11:LEU:HD23	1:C:136:LYS:HD2	1.69	0.75
1:E:72:TRP:CE2	1:E:76:ARG:HD2	2.21	0.75
1:F:72:TRP:CE2	1:F:76:ARG:HD2	2.20	0.75
1:D:72:TRP:CE2	1:D:76:ARG:HD2	2.22	0.75
1:F:11:LEU:HD23	1:F:136:LYS:HD2	1.68	0.75
1:C:72:TRP:CE2	1:C:76:ARG:HD2	2.22	0.74
1:B:24:ALA:HB3	1:B:25:PRO:HD3	1.67	0.74
1:B:11:LEU:HD23	1:B:136:LYS:HD2	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:18:LYS:NZ	1:B:18:LYS:HB3	2.03	0.73
1:E:11:LEU:HD23	1:E:136:LYS:HD2	1.71	0.73
1:D:11:LEU:HD23	1:D:136:LYS:HD2	1.72	0.72
1:A:11:LEU:HD23	1:A:136:LYS:HD2	1.71	0.72
2:D:150:HEM:HMB1	2:D:150:HEM:HBB2	1.73	0.70
1:C:31:GLU:OE1	1:D:71:ARG:HD2	1.93	0.69
2:F:150:HEM:HBB2	2:F:150:HEM:HMB1	1.75	0.68
2:C:150:HEM:HMB1	2:C:150:HEM:HBB2	1.75	0.67
1:E:59:THR:H	1:E:63:GLN:NE2	1.92	0.67
1:C:59:THR:H	1:C:63:GLN:NE2	1.93	0.67
2:A:150:HEM:HMB1	2:A:150:HEM:HBB2	1.77	0.67
1:E:53:PRO:O	1:E:56:LYS:HG3	1.93	0.67
1:C:53:PRO:O	1:C:56:LYS:HG3	1.95	0.66
1:D:59:THR:H	1:D:63:GLN:NE2	1.91	0.66
1:B:59:THR:H	1:B:63:GLN:NE2	1.92	0.66
1:B:53:PRO:O	1:B:56:LYS:HG3	1.96	0.66
1:A:53:PRO:O	1:A:56:LYS:HG3	1.95	0.66
1:A:59:THR:H	1:A:63:GLN:NE2	1.93	0.65
2:B:150:HEM:HMB1	2:B:150:HEM:HBB2	1.78	0.65
1:F:53:PRO:O	1:F:56:LYS:HG3	1.98	0.64
1:F:59:THR:H	1:F:63:GLN:NE2	1.96	0.64
1:A:71:ARG:HD2	1:B:31:GLU:OE1	1.98	0.64
1:D:35:VAL:O	1:D:39:VAL:HG23	1.97	0.63
1:D:53:PRO:O	1:D:56:LYS:HG3	1.97	0.63
1:A:95:SER:O	1:A:99:ARG:HG3	1.98	0.63
1:F:18:LYS:HB3	1:F:18:LYS:HZ3	1.63	0.62
2:E:150:HEM:HMB1	2:E:150:HEM:HBB2	1.81	0.62
1:E:35:VAL:O	1:E:39:VAL:HG23	2.00	0.62
1:F:95:SER:O	1:F:99:ARG:HG3	1.99	0.62
1:F:35:VAL:O	1:F:39:VAL:HG23	2.00	0.62
1:C:95:SER:O	1:C:99:ARG:HG3	2.00	0.61
1:B:35:VAL:O	1:B:39:VAL:HG23	2.00	0.60
1:B:95:SER:O	1:B:99:ARG:HG3	2.00	0.60
1:C:35:VAL:O	1:C:39:VAL:HG23	2.01	0.60
1:E:18:LYS:HZ2	1:E:18:LYS:HB3	1.65	0.60
1:E:95:SER:O	1:E:99:ARG:HG3	2.01	0.60
1:C:18:LYS:HB3	1:C:18:LYS:HZ3	1.68	0.57
1:B:5:THR:HG22	1:B:6:GLY:N	2.19	0.57
1:D:18:LYS:HB3	1:D:18:LYS:HZ2	1.68	0.57
1:C:5:THR:HG22	1:C:6:GLY:N	2.20	0.57
1:A:35:VAL:O	1:A:39:VAL:HG23	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:5:THR:HG22	1:A:6:GLY:N	2.20	0.56
1:D:95:SER:O	1:D:99:ARG:HG3	2.06	0.55
1:D:18:LYS:HB3	1:D:18:LYS:HZ3	1.69	0.55
1:D:5:THR:HG22	1:D:6:GLY:N	2.21	0.55
1:F:5:THR:HG22	1:F:6:GLY:N	2.22	0.55
1:A:18:LYS:HB3	1:A:18:LYS:HZ2	1.71	0.55
1:C:31:GLU:OE1	1:D:71:ARG:NH1	2.33	0.53
1:E:5:THR:HG22	1:E:6:GLY:N	2.23	0.53
1:B:18:LYS:HB3	1:B:18:LYS:HZ2	1.74	0.53
1:E:51:PHE:C	1:E:53:PRO:HD3	2.30	0.52
1:A:72:TRP:HA	1:B:30:TYR:OH	2.10	0.52
1:B:59:THR:H	1:B:63:GLN:HE21	1.57	0.52
1:B:51:PHE:C	1:B:53:PRO:HD3	2.31	0.51
1:C:51:PHE:C	1:C:53:PRO:HD3	2.30	0.51
1:D:30:TYR:HB2	1:D:78:ILE:HG21	1.92	0.51
1:F:51:PHE:C	1:F:53:PRO:HD3	2.31	0.51
1:A:71:ARG:NH1	1:B:31:GLU:OE1	2.43	0.51
1:E:18:LYS:HB3	1:E:18:LYS:HZ3	1.76	0.51
1:F:30:TYR:HB2	1:F:78:ILE:HG21	1.93	0.50
1:D:51:PHE:C	1:D:53:PRO:HD3	2.31	0.50
1:A:30:TYR:HB2	1:A:78:ILE:HG21	1.93	0.50
1:D:62:ASP:OD2	1:D:66:LYS:HE3	2.11	0.50
1:E:30:TYR:HB2	1:E:78:ILE:HG21	1.93	0.50
1:A:51:PHE:C	1:A:53:PRO:HD3	2.32	0.50
1:B:37:ILE:HG21	1:B:123:ILE:HG12	1.93	0.49
1:C:30:TYR:HB2	1:C:78:ILE:HG21	1.94	0.49
1:B:30:TYR:HB2	1:B:78:ILE:HG21	1.94	0.49
2:D:150:HEM:CMB	2:D:150:HEM:HBB2	2.42	0.49
1:B:18:LYS:HZ3	1:B:18:LYS:HB3	1.76	0.48
1:C:59:THR:H	1:C:63:GLN:HE21	1.60	0.48
1:E:37:ILE:HG21	1:E:123:ILE:HG12	1.94	0.48
1:D:42:PHE:CE2	1:D:49:GLN:HG2	2.48	0.48
1:D:58:LEU:N	1:D:58:LEU:HD22	2.28	0.48
1:F:62:ASP:OD2	1:F:66:LYS:HE3	2.13	0.48
1:F:42:PHE:CE2	1:F:49:GLN:HG2	2.48	0.48
2:D:150:HEM:HMC2	2:D:150:HEM:HBC2	1.95	0.48
1:C:42:PHE:CE2	1:C:49:GLN:HG2	2.48	0.48
1:A:72:TRP:CA	1:B:30:TYR:OH	2.61	0.48
1:A:18:LYS:HB3	1:A:18:LYS:HZ3	1.74	0.48
1:E:62:ASP:OD2	1:E:66:LYS:HE3	2.14	0.47
1:E:42:PHE:CE2	1:E:49:GLN:HG2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:42:PHE:CE2	1:B:49:GLN:HG2	2.49	0.47
2:F:150:HEM:HMC2	2:F:150:HEM:HBC2	1.96	0.47
1:F:37:ILE:HG21	1:F:123:ILE:HG12	1.95	0.47
2:C:150:HEM:HBB2	2:C:150:HEM:CMB	2.44	0.47
1:B:5:THR:HG22	1:B:6:GLY:H	1.80	0.47
1:E:59:THR:H	1:E:63:GLN:HE21	1.59	0.47
1:A:42:PHE:CE2	1:A:49:GLN:HG2	2.50	0.47
2:B:150:HEM:CMB	2:B:150:HEM:HBB2	2.45	0.47
1:B:58:LEU:N	1:B:58:LEU:HD22	2.30	0.47
1:C:62:ASP:OD2	1:C:66:LYS:HE3	2.15	0.46
1:B:62:ASP:OD2	1:B:66:LYS:HE3	2.14	0.46
1:C:37:ILE:HG21	1:C:123:ILE:HG12	1.96	0.46
1:C:53:PRO:HB3	1:C:56:LYS:HZ1	1.80	0.46
1:D:59:THR:H	1:D:63:GLN:HE21	1.60	0.46
1:F:59:THR:H	1:F:63:GLN:HE21	1.63	0.46
1:A:5:THR:HG22	1:A:6:GLY:H	1.80	0.46
1:A:59:THR:H	1:A:63:GLN:HE21	1.60	0.46
1:A:37:ILE:HG21	1:A:123:ILE:HG12	1.98	0.46
1:A:58:LEU:HD22	1:A:58:LEU:N	2.31	0.46
1:D:37:ILE:HG21	1:D:123:ILE:HG12	1.98	0.46
1:E:58:LEU:N	1:E:58:LEU:HD22	2.31	0.46
1:B:9:ALA:O	1:B:136:LYS:HD3	2.16	0.46
1:C:58:LEU:HD22	1:C:58:LEU:N	2.31	0.46
1:A:53:PRO:HB3	1:A:56:LYS:HZ1	1.80	0.45
1:C:5:THR:HG22	1:C:6:GLY:H	1.80	0.45
2:A:150:HEM:CMB	2:A:150:HEM:HBB2	2.45	0.45
1:F:18:LYS:HZ2	1:F:18:LYS:HB3	1.79	0.45
1:F:5:THR:HG22	1:F:6:GLY:H	1.82	0.45
1:E:5:THR:HG22	1:E:6:GLY:H	1.82	0.45
1:F:72:TRP:O	1:F:76:ARG:HD3	2.16	0.45
1:D:5:THR:HG22	1:D:6:GLY:H	1.81	0.45
1:A:9:ALA:O	1:A:136:LYS:HD3	2.18	0.44
1:E:31:GLU:HG2	1:E:31:GLU:H	1.26	0.44
1:C:18:LYS:HZ2	1:C:18:LYS:HB3	1.76	0.44
1:A:31:GLU:O	1:A:35:VAL:HG23	2.16	0.44
1:D:40:LYS:HE3	1:D:40:LYS:HB2	1.84	0.44
1:B:72:TRP:O	1:B:76:ARG:HD3	2.17	0.44
1:C:24:ALA:CB	1:C:25:PRO:HD3	2.43	0.44
1:D:9:ALA:O	1:D:136:LYS:HD3	2.18	0.43
1:A:72:TRP:O	1:A:76:ARG:HD3	2.17	0.43
1:A:62:ASP:OD2	1:A:66:LYS:HE3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:51:PHE:O	1:F:53:PRO:HD3	2.18	0.43
2:A:150:HEM:HBC2	2:A:150:HEM:HMC2	2.00	0.43
1:B:12:SER:OG	1:B:15:GLU:HG3	2.19	0.43
1:E:40:LYS:HE3	1:E:40:LYS:HB2	1.83	0.43
1:E:51:PHE:O	1:E:53:PRO:HD3	2.18	0.43
2:F:150:HEM:HBB2	2:F:150:HEM:CMB	2.44	0.43
1:F:12:SER:OG	1:F:15:GLU:HG3	2.19	0.43
1:F:16:LYS:O	1:F:20:ARG:HG3	2.19	0.43
1:D:58:LEU:HB3	1:D:64:LEU:HD23	2.00	0.42
1:A:31:GLU:H	1:A:31:GLU:HG2	1.28	0.42
1:C:40:LYS:HE3	1:C:40:LYS:HB2	1.84	0.42
1:C:58:LEU:HB3	1:C:64:LEU:CD2	2.49	0.42
1:C:58:LEU:HB3	1:C:64:LEU:HD23	2.00	0.42
1:B:16:LYS:O	1:B:20:ARG:HG3	2.19	0.42
1:C:51:PHE:O	1:C:53:PRO:HD3	2.20	0.42
1:A:12:SER:OG	1:A:15:GLU:HG3	2.18	0.42
1:D:53:PRO:HB3	1:D:56:LYS:HZ1	1.83	0.42
1:A:72:TRP:CZ2	1:A:76:ARG:HD2	2.55	0.41
2:C:150:HEM:HBC2	2:C:150:HEM:HMC2	2.02	0.41
1:C:12:SER:OG	1:C:15:GLU:HG3	2.20	0.41
1:F:31:GLU:H	1:F:31:GLU:HG2	1.27	0.41
1:B:51:PHE:O	1:B:53:PRO:HD3	2.20	0.41
1:D:67:SER:HB3	1:D:70:VAL:HG23	2.02	0.41
1:E:12:SER:OG	1:E:15:GLU:HG3	2.20	0.41
1:F:58:LEU:HB3	1:F:64:LEU:HD23	2.02	0.41
1:C:9:ALA:O	1:C:136:LYS:HD3	2.21	0.41
2:E:150:HEM:HBB2	2:E:150:HEM:CMB	2.48	0.41
1:C:72:TRP:O	1:C:76:ARG:HD3	2.20	0.41
1:D:58:LEU:N	1:D:58:LEU:CD2	2.83	0.41
1:E:58:LEU:HB3	1:E:64:LEU:HD23	2.03	0.41
1:E:31:GLU:OE1	1:F:71:ARG:HD2	2.21	0.41
1:E:72:TRP:O	1:E:76:ARG:HD3	2.20	0.41
1:F:53:PRO:HB3	1:F:56:LYS:HZ1	1.85	0.41
1:A:51:PHE:O	1:A:53:PRO:HD3	2.20	0.41
2:B:150:HEM:HBC2	2:B:150:HEM:HMC2	2.02	0.41
1:E:9:ALA:O	1:E:136:LYS:HD3	2.21	0.41
1:F:58:LEU:HD22	1:F:58:LEU:N	2.36	0.41
1:D:31:GLU:H	1:D:31:GLU:HG2	1.28	0.40
1:D:58:LEU:HB3	1:D:64:LEU:CD2	2.51	0.40
2:E:150:HEM:HBC2	2:E:150:HEM:HMC2	2.03	0.40
1:B:58:LEU:HB3	1:B:64:LEU:HD23	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:24:ALA:HB3	1:E:25:PRO:CD	2.42	0.40
1:C:16:LYS:O	1:C:20:ARG:HG3	2.22	0.40
1:D:72:TRP:O	1:D:76:ARG:HD3	2.21	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:C:92:GLU:OE1	1:F:97:LYS:CE[4_556]	1.98	0.22
1:D:130:GLY:O	1:E:132:ALA:N[3_655]	2.00	0.20
1:C:8:VAL:O	1:E:110:GLN:NE2[4_556]	2.03	0.17
1:C:97:LYS:CE	1:F:92:GLU:OE1[4_556]	2.04	0.16
1:A:110:GLN:NE2	1:C:110:GLN:NE2[1_455]	2.18	0.02
1:D:106:ALA:O	1:F:7:SER:OG[4_556]	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	147/149 (99%)	142 (97%)	5 (3%)	0	100	100
1	B	147/149 (99%)	141 (96%)	6 (4%)	0	100	100
1	C	147/149 (99%)	142 (97%)	5 (3%)	0	100	100
1	D	147/149 (99%)	142 (97%)	5 (3%)	0	100	100
1	E	147/149 (99%)	142 (97%)	5 (3%)	0	100	100
1	F	147/149 (99%)	143 (97%)	4 (3%)	0	100	100
All	All	882/894 (99%)	852 (97%)	30 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	122/122 (100%)	118 (97%)	4 (3%)	43	77
1	B	122/122 (100%)	118 (97%)	4 (3%)	43	77
1	C	122/122 (100%)	119 (98%)	3 (2%)	53	83
1	D	122/122 (100%)	119 (98%)	3 (2%)	53	83
1	E	122/122 (100%)	119 (98%)	3 (2%)	53	83
1	F	122/122 (100%)	118 (97%)	4 (3%)	43	77
All	All	732/732 (100%)	711 (97%)	21 (3%)	48	81

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	GLU
1	A	78	ILE
1	A	91	THR
1	A	137	LEU
1	B	31	GLU
1	B	78	ILE
1	B	91	THR
1	B	137	LEU
1	C	31	GLU
1	C	78	ILE
1	C	137	LEU
1	D	31	GLU
1	D	78	ILE
1	D	137	LEU
1	E	31	GLU
1	E	78	ILE
1	E	137	LEU
1	F	31	GLU
1	F	78	ILE
1	F	91	THR
1	F	137	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	GLN
1	A	63	GLN
1	B	49	GLN
1	B	63	GLN
1	C	49	GLN
1	C	63	GLN
1	D	49	GLN
1	D	63	GLN
1	E	49	GLN
1	E	63	GLN
1	F	49	GLN
1	F	63	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](#)

6 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	150	1	28,50,50	1.81	9 (32%)	17,82,82	1.61	3 (17%)
2	HEM	B	150	1	28,50,50	1.92	8 (28%)	17,82,82	1.77	4 (23%)
2	HEM	C	150	1	28,50,50	1.69	7 (25%)	17,82,82	1.65	5 (29%)
2	HEM	D	150	1	28,50,50	1.88	10 (35%)	17,82,82	1.45	2 (11%)
2	HEM	E	150	1	28,50,50	1.96	9 (32%)	17,82,82	1.45	3 (17%)
2	HEM	F	150	1	28,50,50	1.88	10 (35%)	17,82,82	1.61	4 (23%)

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	150	1	-	0/6/54/54	0/0/8/8
2	HEM	B	150	1	-	0/6/54/54	0/0/8/8
2	HEM	C	150	1	-	0/6/54/54	0/0/8/8
2	HEM	D	150	1	-	0/6/54/54	0/0/8/8
2	HEM	E	150	1	-	0/6/54/54	0/0/8/8
2	HEM	F	150	1	-	0/6/54/54	0/0/8/8

All (53) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	150	HEM	C3C-C2C	-4.98	1.33	1.40
2	B	150	HEM	C3B-CAB	-4.46	1.39	1.47
2	D	150	HEM	C3C-C2C	-4.11	1.34	1.40
2	A	150	HEM	C3B-CAB	-4.03	1.39	1.47
2	F	150	HEM	C3C-C2C	-4.03	1.35	1.40
2	D	150	HEM	C3B-CAB	-3.94	1.40	1.47
2	C	150	HEM	C3B-CAB	-3.90	1.40	1.47
2	B	150	HEM	C3C-CAC	-3.78	1.40	1.47
2	E	150	HEM	C3B-CAB	-3.66	1.40	1.47
2	A	150	HEM	C3C-CAC	-3.54	1.40	1.47
2	F	150	HEM	C3B-CAB	-3.46	1.41	1.47
2	D	150	HEM	C3C-CAC	-3.44	1.40	1.47
2	E	150	HEM	C3C-CAC	-3.30	1.41	1.47
2	B	150	HEM	C3C-C2C	-3.14	1.36	1.40
2	F	150	HEM	C3C-CAC	-3.12	1.41	1.47
2	C	150	HEM	C3C-C2C	-3.03	1.36	1.40
2	C	150	HEM	C3C-CAC	-3.03	1.41	1.47
2	D	150	HEM	C3B-C2B	-2.77	1.36	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	150	HEM	C3B-C2B	-2.69	1.36	1.40
2	F	150	HEM	C3B-C2B	-2.66	1.36	1.40
2	A	150	HEM	C3C-C2C	-2.47	1.37	1.40
2	B	150	HEM	CBB-CAB	2.00	1.43	1.28
2	E	150	HEM	CBB-CAB	2.01	1.43	1.28
2	F	150	HEM	CBC-CAC	2.09	1.43	1.28
2	D	150	HEM	C4A-NA	2.09	1.40	1.36
2	D	150	HEM	C4C-NC	2.11	1.39	1.36
2	D	150	HEM	CBB-CAB	2.15	1.44	1.28
2	A	150	HEM	CBC-CAC	2.16	1.44	1.28
2	E	150	HEM	C4D-ND	2.18	1.39	1.36
2	F	150	HEM	CBB-CAB	2.20	1.44	1.28
2	A	150	HEM	C4D-ND	2.22	1.39	1.36
2	F	150	HEM	C4A-NA	2.23	1.40	1.36
2	D	150	HEM	CBC-CAC	2.26	1.44	1.28
2	C	150	HEM	CBB-CAB	2.28	1.44	1.28
2	E	150	HEM	CBC-CAC	2.29	1.45	1.28
2	C	150	HEM	CBC-CAC	2.30	1.45	1.28
2	A	150	HEM	C4C-NC	2.31	1.39	1.36
2	B	150	HEM	CBC-CAC	2.32	1.45	1.28
2	F	150	HEM	C1C-NC	2.38	1.39	1.36
2	A	150	HEM	C1C-NC	2.40	1.39	1.36
2	E	150	HEM	C1C-NC	2.56	1.39	1.36
2	C	150	HEM	C4A-NA	2.59	1.41	1.36
2	E	150	HEM	C4A-NA	2.60	1.41	1.36
2	B	150	HEM	C4A-NA	2.67	1.41	1.36
2	B	150	HEM	C4C-NC	2.77	1.40	1.36
2	D	150	HEM	C1B-NB	2.84	1.40	1.36
2	C	150	HEM	C1B-NB	2.91	1.40	1.36
2	D	150	HEM	C1C-NC	2.94	1.40	1.36
2	F	150	HEM	C4C-NC	3.00	1.40	1.36
2	E	150	HEM	C1B-NB	3.35	1.40	1.36
2	F	150	HEM	C1B-NB	3.47	1.40	1.36
2	A	150	HEM	C1B-NB	3.66	1.41	1.36
2	B	150	HEM	C1B-NB	3.95	1.41	1.36

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	150	HEM	C4A-C3A-C2A	-3.68	104.43	107.00
2	B	150	HEM	C4C-C3C-C2C	-3.25	104.63	106.90
2	F	150	HEM	C4A-C3A-C2A	-3.14	104.81	107.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	150	HEM	C4C-C3C-C2C	-3.09	104.74	106.90
2	C	150	HEM	C4C-C3C-C2C	-3.01	104.80	106.90
2	F	150	HEM	CBA-CAA-C2A	-2.96	106.82	112.48
2	C	150	HEM	C4A-C3A-C2A	-2.93	104.96	107.00
2	A	150	HEM	CBA-CAA-C2A	-2.83	107.08	112.48
2	A	150	HEM	C4A-C3A-C2A	-2.82	105.03	107.00
2	A	150	HEM	C4C-C3C-C2C	-2.74	104.98	106.90
2	E	150	HEM	C4A-C3A-C2A	-2.73	105.09	107.00
2	D	150	HEM	CBA-CAA-C2A	-2.55	107.61	112.48
2	C	150	HEM	CBA-CAA-C2A	-2.54	107.62	112.48
2	E	150	HEM	CBA-CAA-C2A	-2.38	107.94	112.48
2	D	150	HEM	C4A-C3A-C2A	-2.24	105.44	107.00
2	C	150	HEM	CAD-C3D-C2D	-2.16	122.83	129.00
2	C	150	HEM	CAA-C2A-C3A	-2.14	122.90	129.00
2	B	150	HEM	CBA-CAA-C2A	-2.06	108.55	112.48
2	F	150	HEM	CAA-C2A-C3A	-2.01	123.26	129.00
2	E	150	HEM	C3B-C4B-NB	2.16	112.00	109.21
2	B	150	HEM	C3B-C4B-NB	2.17	112.01	109.21

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	150	HEM	3	0
2	B	150	HEM	3	0
2	C	150	HEM	3	0
2	D	150	HEM	3	0
2	E	150	HEM	3	0
2	F	150	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	149/149 (100%)	1.80	53 (35%) 0 0	32, 56, 91, 108	0
1	B	149/149 (100%)	2.31	78 (52%) 0 0	32, 57, 91, 103	0
1	C	149/149 (100%)	1.94	56 (37%) 0 0	39, 61, 90, 119	0
1	D	149/149 (100%)	1.53	41 (27%) 1 0	33, 58, 92, 113	0
1	E	149/149 (100%)	1.00	25 (16%) 2 1	24, 47, 84, 116	0
1	F	149/149 (100%)	1.45	37 (24%) 1 0	38, 55, 81, 125	0
All	All	894/894 (100%)	1.67	290 (32%) 0 0	24, 56, 91, 125	0

All (290) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	36	ASP	9.0
1	A	132	ALA	6.6
1	E	60	THR	6.2
1	A	1	PRO	6.1
1	B	62	ASP	6.1
1	C	59	THR	6.1
1	B	6	GLY	6.0
1	D	59	THR	5.9
1	B	7	SER	5.7
1	C	57	GLY	5.6
1	B	63	GLN	5.5
1	F	56	LYS	5.4
1	E	139	SER	5.3
1	D	17	THR	5.3
1	D	91	THR	5.3
1	B	10	PRO	5.1
1	C	142	CYS	5.0
1	C	17	THR	5.0
1	B	68	ALA	4.9

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Mol	Chain	Res	Type	RSRZ
1	C	24	ALA	4.9
1	D	24	ALA	4.9
1	B	12	SER	4.9
1	A	50	GLU	4.8
1	A	36	ASP	4.8
1	A	121	ALA	4.7
1	C	13	ALA	4.6
1	E	57	GLY	4.6
1	A	49	GLN	4.6
1	C	12	SER	4.6
1	B	59	THR	4.5
1	C	43	THR	4.5
1	B	142	CYS	4.5
1	C	125	ASP	4.5
1	F	32	THR	4.4
1	B	92	GLU	4.4
1	A	34	GLY	4.4
1	F	57	GLY	4.4
1	D	67	SER	4.4
1	A	33	SER	4.3
1	B	11	LEU	4.3
1	C	58	LEU	4.3
1	D	125	ASP	4.3
1	A	59	THR	4.1
1	B	17	THR	4.1
1	A	12	SER	4.1
1	B	21	SER	4.1
1	B	120	ALA	4.1
1	F	86	ALA	4.0
1	C	1	PRO	4.0
1	B	131	ASP	4.0
1	C	53	PRO	4.0
1	B	56	LYS	4.0
1	C	60	THR	3.9
1	A	58	LEU	3.9
1	D	108	SER	3.9
1	B	139	SER	3.9
1	B	99	ARG	3.8
1	A	18	LYS	3.8
1	A	32	THR	3.8
1	E	59	THR	3.7
1	B	95	SER	3.7

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Mol	Chain	Res	Type	RSRZ
1	C	69	ASP	3.7
1	B	148	ALA	3.7
1	C	121	ALA	3.7
1	B	32	THR	3.7
1	A	44	SER	3.7
1	C	123	ILE	3.6
1	B	90	ASP	3.6
1	B	122	VAL	3.6
1	B	114	GLN	3.5
1	D	131	ASP	3.5
1	E	36	ASP	3.5
1	A	27	TYR	3.5
1	D	62	ASP	3.5
1	E	44	SER	3.5
1	D	139	SER	3.4
1	F	1	PRO	3.4
1	C	66	LYS	3.4
1	C	124	ALA	3.4
1	B	46	PRO	3.3
1	C	102	SER	3.3
1	C	44	SER	3.3
1	C	32	THR	3.3
1	B	140	MET	3.3
1	C	26	VAL	3.3
1	E	5	THR	3.3
1	D	96	MET	3.3
1	F	66	LYS	3.2
1	C	25	PRO	3.2
1	F	85	VAL	3.2
1	F	60	THR	3.2
1	A	13	ALA	3.2
1	D	79	ASN	3.2
1	D	66	LYS	3.2
1	F	45	THR	3.2
1	E	9	ALA	3.1
1	A	112	ASP	3.1
1	B	147	SER	3.1
1	B	121	ALA	3.1
1	D	35	VAL	3.1
1	B	117	LYS	3.1
1	D	32	THR	3.1
1	F	64	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	96	MET	3.1
1	B	1	PRO	3.1
1	F	142	CYS	3.1
1	B	40	LYS	3.1
1	A	46	PRO	3.1
1	C	56	LYS	3.0
1	E	58	LEU	3.0
1	B	57	GLY	3.0
1	C	63	GLN	3.0
1	A	28	SER	3.0
1	F	139	SER	3.0
1	C	90	ASP	3.0
1	C	82	ASN	3.0
1	A	118	VAL	3.0
1	B	82	ASN	3.0
1	D	60	THR	3.0
1	F	132	ALA	2.9
1	C	126	THR	2.9
1	B	64	LEU	2.9
1	D	50	GLU	2.9
1	B	79	ASN	2.9
1	A	62	ASP	2.9
1	D	130	GLY	2.9
1	F	83	ASP	2.9
1	F	120	ALA	2.9
1	F	123	ILE	2.9
1	A	56	LYS	2.9
1	B	118	VAL	2.9
1	D	123	ILE	2.9
1	B	106	ALA	2.8
1	B	93	LYS	2.8
1	F	17	THR	2.8
1	D	1	PRO	2.8
1	A	29	THR	2.8
1	A	80	ALA	2.8
1	B	124	ALA	2.8
1	B	132	ALA	2.8
1	A	57	GLY	2.8
1	D	36	ASP	2.8
1	A	21	SER	2.8
1	D	10	PRO	2.8
1	F	37	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	105	HIS	2.8
1	E	50	GLU	2.8
1	D	28	SER	2.8
1	B	97	LYS	2.8
1	C	18	LYS	2.8
1	F	65	LYS	2.8
1	A	114	GLN	2.8
1	B	54	LYS	2.7
1	A	87	SER	2.7
1	B	29	THR	2.7
1	B	33	SER	2.7
1	F	106	ALA	2.7
1	F	141	ILE	2.7
1	B	98	LEU	2.7
1	B	104	LYS	2.7
1	F	124	ALA	2.7
1	B	145	LEU	2.7
1	B	44	SER	2.7
1	D	14	ALA	2.7
1	C	30	TYR	2.7
1	A	39	VAL	2.7
1	C	129	ALA	2.7
1	B	133	GLY	2.7
1	D	95	SER	2.6
1	F	63	GLN	2.6
1	B	48	ALA	2.6
1	B	100	ASP	2.6
1	A	63	GLN	2.6
1	F	39	VAL	2.6
1	F	62	ASP	2.6
1	A	78	ILE	2.6
1	C	64	LEU	2.6
1	B	115	TYR	2.6
1	B	123	ILE	2.6
1	C	22	ALA	2.6
1	D	92	GLU	2.5
1	A	66	LYS	2.5
1	C	131	ASP	2.5
1	B	43	THR	2.5
1	C	34	GLY	2.5
1	E	62	ASP	2.5
1	A	125	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	62	ASP	2.5
1	C	81	VAL	2.5
1	A	147	SER	2.5
1	B	37	ILE	2.5
1	A	61	ALA	2.5
1	F	13	ALA	2.5
1	B	30	TYR	2.5
1	C	33	SER	2.5
1	B	5	THR	2.4
1	A	131	ASP	2.4
1	B	45	THR	2.4
1	D	29	THR	2.4
1	D	43	THR	2.4
1	A	26	VAL	2.4
1	F	87	SER	2.4
1	B	23	TRP	2.4
1	A	120	ALA	2.4
1	B	74	ALA	2.4
1	E	64	LEU	2.4
1	C	91	THR	2.4
1	D	23	TRP	2.4
1	F	46	PRO	2.4
1	C	133	GLY	2.4
1	D	99	ARG	2.4
1	B	24	ALA	2.4
1	B	28	SER	2.4
1	C	9	ALA	2.4
1	B	65	LYS	2.4
1	A	91	THR	2.4
1	A	14	ALA	2.4
1	C	74	ALA	2.3
1	D	56	LYS	2.3
1	E	92	GLU	2.3
1	C	122	VAL	2.3
1	A	25	PRO	2.3
1	B	129	ALA	2.3
1	E	66	LYS	2.3
1	C	21	SER	2.3
1	F	16	LYS	2.3
1	E	24	ALA	2.3
1	F	28	SER	2.2
1	D	137	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	4	ASP	2.2
1	A	144	LEU	2.2
1	A	130	GLY	2.2
1	B	125	ASP	2.2
1	C	68	ALA	2.2
1	D	58	LEU	2.2
1	E	14	ALA	2.2
1	A	45	THR	2.2
1	D	105	HIS	2.2
1	C	138	MET	2.2
1	B	83	ASP	2.2
1	F	148	ALA	2.2
1	F	4	ASP	2.2
1	F	131	ASP	2.2
1	A	141	ILE	2.2
1	F	41	PHE	2.2
1	D	12	SER	2.2
1	D	33	SER	2.2
1	E	63	GLN	2.2
1	F	95	SER	2.2
1	C	73	HIS	2.2
1	A	149	TYR	2.2
1	E	118	VAL	2.2
1	F	14	ALA	2.2
1	C	49	GLN	2.2
1	B	103	GLY	2.1
1	A	90	ASP	2.1
1	B	89	ASP	2.1
1	D	132	ALA	2.1
1	B	138	MET	2.1
1	B	14	ALA	2.1
1	C	48	ALA	2.1
1	D	53	PRO	2.1
1	E	112	ASP	2.1
1	C	141	ILE	2.1
1	A	35	VAL	2.1
1	B	34	GLY	2.1
1	E	28	SER	2.1
1	C	50	GLU	2.1
1	E	17	THR	2.1
1	A	100	ASP	2.1
1	F	79	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	139	SER	2.1
1	A	89	ASP	2.1
1	C	127	VAL	2.1
1	D	21	SER	2.1
1	C	46	PRO	2.1
1	E	46	PRO	2.1
1	B	58	LEU	2.0
1	A	139	SER	2.0
1	E	32	THR	2.0
1	A	108	SER	2.0
1	D	19	ILE	2.0
1	B	149	TYR	2.0
1	E	80	ALA	2.0
1	C	85	VAL	2.0
1	B	67	SER	2.0
1	C	120	ALA	2.0
1	D	41	PHE	2.0
1	A	19	ILE	2.0
1	E	131	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	D	150	43/43	0.81	0.27	-0.74	38,38,38,38	0
2	HEM	C	150	43/43	0.83	0.25	-1.00	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	HEM	A	150	43/43	0.85	0.24	-1.03	52,52,52,52	0
2	HEM	E	150	43/43	0.89	0.21	-1.03	40,40,40,40	0
2	HEM	B	150	43/43	0.80	0.27	-1.11	38,38,38,38	0
2	HEM	F	150	43/43	0.88	0.21	-1.33	42,42,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.