



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:53 AM GMT

PDB ID : 2LH6
Title : X-RAY STRUCTURAL INVESTIGATION OF LEGHEMOGLOBIN. VI. STRUCTURE OF ACETATE-FERRILEGHEMOGLOBIN AT A RESOLUTION OF 2.0 ANGSTROMS (RUSSIAN)
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Deposited on : 1982-04-23
Resolution : 2.00 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

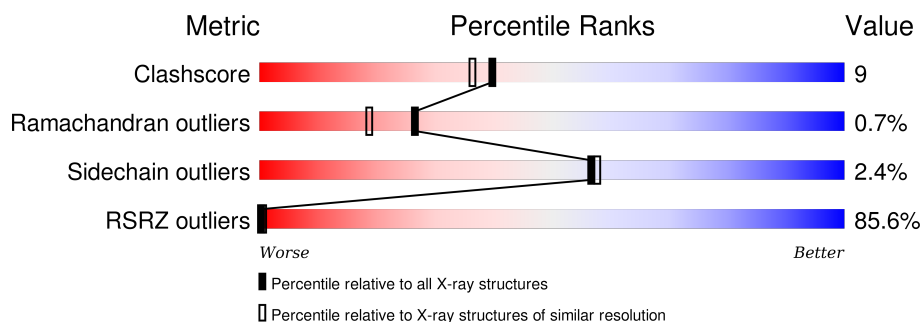
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	153	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 1297 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.

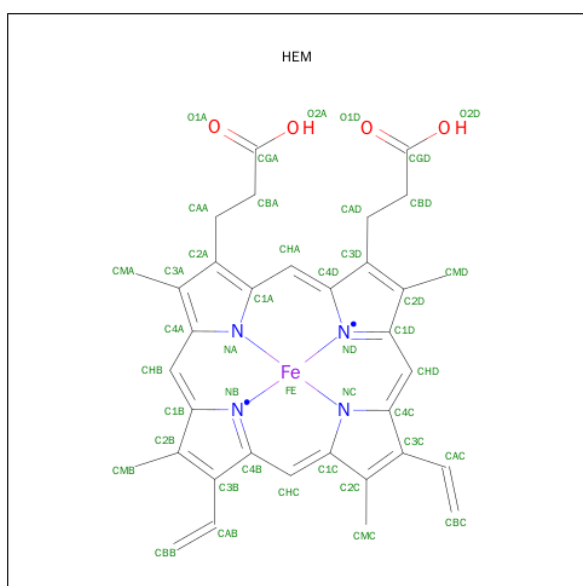
- Molecule 1 is a protein called LEGHEMOGLOBIN A (NICOTINATE MET).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	153	Total	C	N	O	S	35	1	0
			1180	761	193	225	1			

There are 2 discrepancies between the modelled and reference sequences:

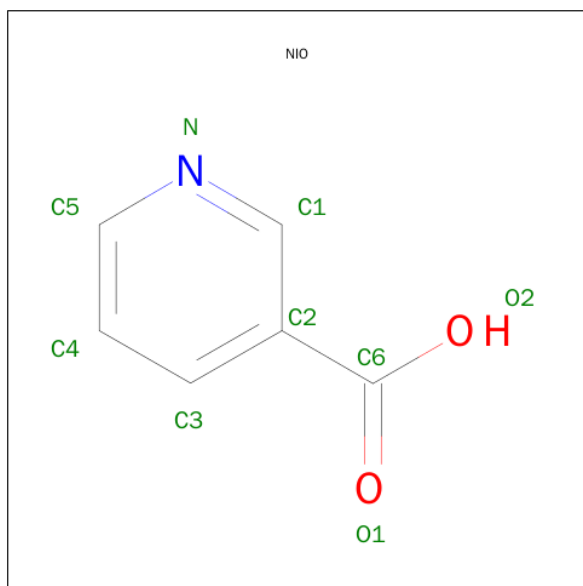
Chain	Residue	Modelled	Actual	Comment	Reference
A	79	GLU	GLN	CONFLICT	UNP P02240
A	150	ASP	ASN	CONFLICT	UNP P02240

- 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	C	Fe	N	O	3	0
			43	34	1	4	4		

- Molecule 3 is NICOTINIC ACID (three-letter code: NIO) (formula: $C_6H_5NO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			9	6	1	2		

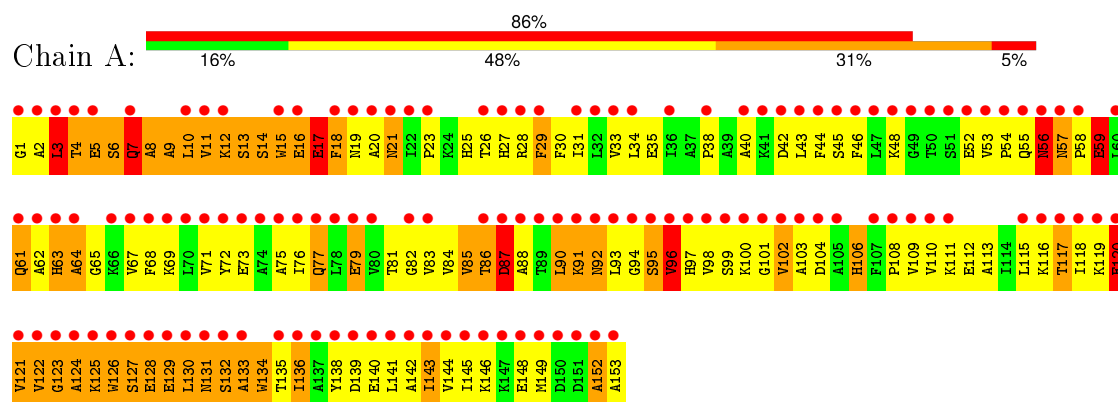
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	65	Total	O	0	0
			65	65		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

- Molecule 1: LEGHEMOGLOBIN A (NICOTINATE MET)



4 Data and refinement statistics

Property	Value	Source
Space group	B 1 1 2	Depositor
Cell constants a, b, c, α , β , γ	92.92Å 38.64Å 52.36Å 90.00° 90.00° 99.60°	Depositor
Resolution (Å)	(Not available) – 2.00 9.99 – 1.99	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-2.00) 91.9 (9.99-1.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	unknown	Depositor
R, R_{free}	(Not available) , (Not available) 0.485 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	20.7	Xtriage
Anisotropy	0.214	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	1.74 , 416.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ¹	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtriage
Outliers	0 of 11555 reflections	Xtriage
F_o, F_c correlation	0.53	EDS
Total number of atoms	1297	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.51% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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, NIO

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	3.44	169/1214 (13.9%)	2.25	49/1648 (3.0%)

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	9

All (169) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	95	SER	CB-OG	11.22	1.56	1.42
1	A	138	TYR	CB-CG	10.76	1.67	1.51
1	A	112	GLU	CG-CD	10.36	1.67	1.51
1	A	138	TYR	CZ-OH	10.25	1.55	1.37
1	A	15	TRP	CD2-CE2	9.74	1.53	1.41
1	A	132[A]	SER	CA-CB	9.72	1.67	1.52
1	A	132[B]	SER	CA-CB	9.72	1.67	1.52
1	A	132[C]	SER	CA-CB	9.72	1.67	1.52
1	A	123	GLY	CA-C	9.12	1.66	1.51
1	A	120	GLU	CG-CD	9.07	1.65	1.51
1	A	106	HIS	CB-CG	8.86	1.66	1.50
1	A	94	GLY	CA-C	8.70	1.65	1.51
1	A	35	GLU	CD-OE2	8.63	1.35	1.25
1	A	15	TRP	CB-CG	8.53	1.65	1.50
1	A	148	GLU	CD-OE2	8.47	1.34	1.25
1	A	72	TYR	CE1-CZ	8.24	1.49	1.38
1	A	65	GLY	C-O	8.23	1.36	1.23
1	A	18	PHE	CB-CG	8.23	1.65	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	129	GLU	CD-OE1	7.96	1.34	1.25
1	A	101	GLY	CA-C	7.85	1.64	1.51
1	A	44	PHE	CB-CG	7.84	1.64	1.51
1	A	13	SER	CA-CB	7.72	1.64	1.52
1	A	138	TYR	CD2-CE2	7.71	1.50	1.39
1	A	144	VAL	CB-CG2	7.64	1.68	1.52
1	A	110	VAL	CB-CG2	7.58	1.68	1.52
1	A	111	LYS	N-CA	7.56	1.61	1.46
1	A	124	ALA	N-CA	7.49	1.61	1.46
1	A	15	TRP	CZ3-CH2	7.43	1.51	1.40
1	A	134	TRP	N-CA	7.41	1.61	1.46
1	A	85	VAL	CB-CG2	7.41	1.68	1.52
1	A	16	GLU	CG-CD	7.39	1.63	1.51
1	A	140	GLU	CB-CG	7.39	1.66	1.52
1	A	59	GLU	CD-OE1	-7.28	1.17	1.25
1	A	72	TYR	CG-CD2	7.27	1.48	1.39
1	A	40	ALA	CA-CB	7.26	1.67	1.52
1	A	46	PHE	CB-CG	7.25	1.63	1.51
1	A	72	TYR	C-O	7.24	1.37	1.23
1	A	113	ALA	CA-CB	7.23	1.67	1.52
1	A	84	VAL	CB-CG1	7.21	1.68	1.52
1	A	138	TYR	CD1-CE1	7.20	1.50	1.39
1	A	104	ASP	N-CA	7.17	1.60	1.46
1	A	88	ALA	N-CA	7.14	1.60	1.46
1	A	11	VAL	CB-CG1	7.14	1.67	1.52
1	A	121	VAL	CB-CG2	7.07	1.67	1.52
1	A	79	GLU	CB-CG	7.07	1.65	1.52
1	A	28	ARG	CZ-NH1	7.02	1.42	1.33
1	A	6	SER	CA-CB	6.98	1.63	1.52
1	A	27	HIS	CE1-NE2	6.97	1.48	1.32
1	A	35	GLU	CD-OE1	-6.94	1.18	1.25
1	A	73	GLU	CG-CD	6.94	1.62	1.51
1	A	124	ALA	C-O	6.90	1.36	1.23
1	A	102	VAL	CB-CG1	6.89	1.67	1.52
1	A	68	PHE	C-O	6.86	1.36	1.23
1	A	61	GLN	C-O	6.84	1.36	1.23
1	A	95	SER	N-CA	6.83	1.60	1.46
1	A	128	GLU	CD-OE2	-6.80	1.18	1.25
1	A	68	PHE	CG-CD2	6.80	1.49	1.38
1	A	109	VAL	CA-CB	6.79	1.69	1.54
1	A	15	TRP	NE1-CE2	-6.78	1.28	1.37
1	A	15	TRP	C-O	6.76	1.36	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	111	LYS	CD-CE	6.76	1.68	1.51
1	A	15	TRP	CD1-NE1	6.75	1.49	1.38
1	A	128	GLU	CG-CD	6.73	1.62	1.51
1	A	145	ILE	N-CA	6.72	1.59	1.46
1	A	45	SER	CB-OG	6.71	1.50	1.42
1	A	86	THR	N-CA	6.70	1.59	1.46
1	A	13	SER	CB-OG	-6.69	1.33	1.42
1	A	148	GLU	CB-CG	6.68	1.64	1.52
1	A	99	SER	N-CA	6.61	1.59	1.46
1	A	5	GLU	CD-OE1	-6.61	1.18	1.25
1	A	11	VAL	N-CA	6.59	1.59	1.46
1	A	27	HIS	CG-ND1	6.58	1.53	1.38
1	A	68	PHE	CE1-CZ	6.56	1.49	1.37
1	A	99	SER	C-O	6.55	1.35	1.23
1	A	14	SER	CB-OG	-6.54	1.33	1.42
1	A	9	ALA	CA-CB	6.50	1.66	1.52
1	A	97	HIS	CA-CB	6.42	1.68	1.53
1	A	122	VAL	N-CA	6.42	1.59	1.46
1	A	90	LEU	CA-CB	6.41	1.68	1.53
1	A	75	ALA	N-CA	6.36	1.59	1.46
1	A	149	MET	C-O	6.31	1.35	1.23
1	A	152	ALA	C-O	6.31	1.35	1.23
1	A	55	GLN	C-O	6.29	1.35	1.23
1	A	102	VAL	N-CA	6.28	1.58	1.46
1	A	75	ALA	C-O	6.28	1.35	1.23
1	A	52	GLU	CG-CD	-6.19	1.42	1.51
1	A	18	PHE	N-CA	6.15	1.58	1.46
1	A	79	GLU	C-O	6.13	1.35	1.23
1	A	97	HIS	CG-CD2	-6.13	1.25	1.35
1	A	106	HIS	ND1-CE1	6.13	1.50	1.34
1	A	140	GLU	CD-OE2	6.10	1.32	1.25
1	A	82	GLY	CA-C	6.09	1.61	1.51
1	A	120	GLU	CA-CB	6.04	1.67	1.53
1	A	96	VAL	CB-CG1	6.03	1.65	1.52
1	A	77	GLN	CG-CD	6.03	1.65	1.51
1	A	67	VAL	CB-CG2	6.01	1.65	1.52
1	A	8	ALA	C-O	6.01	1.34	1.23
1	A	4	THR	C-O	6.00	1.34	1.23
1	A	30	PHE	CG-CD2	-6.00	1.29	1.38
1	A	111	LYS	CB-CG	5.99	1.68	1.52
1	A	45	SER	N-CA	5.92	1.58	1.46
1	A	91	LYS	CD-CE	5.91	1.66	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	141	LEU	N-CA	5.91	1.58	1.46
1	A	53	VAL	CA-CB	5.91	1.67	1.54
1	A	52	GLU	N-CA	5.90	1.58	1.46
1	A	98	VAL	CB-CG2	5.86	1.65	1.52
1	A	76	ILE	C-O	5.85	1.34	1.23
1	A	68	PHE	N-CA	5.83	1.58	1.46
1	A	130	LEU	N-CA	5.77	1.57	1.46
1	A	115	LEU	N-CA	5.75	1.57	1.46
1	A	143	ILE	CA-CB	5.69	1.68	1.54
1	A	127	SER	CA-CB	5.69	1.61	1.52
1	A	3	LEU	CA-CB	5.66	1.66	1.53
1	A	133	ALA	CA-C	5.66	1.67	1.52
1	A	127	SER	C-O	5.63	1.34	1.23
1	A	138	TYR	N-CA	5.59	1.57	1.46
1	A	69	LYS	C-O	5.58	1.33	1.23
1	A	140	GLU	CG-CD	-5.55	1.43	1.51
1	A	43	LEU	CA-CB	5.54	1.66	1.53
1	A	58	PRO	CA-C	-5.54	1.41	1.52
1	A	71	VAL	CB-CG1	5.53	1.64	1.52
1	A	79	GLU	CD-OE2	5.51	1.31	1.25
1	A	92	ASN	C-O	5.50	1.33	1.23
1	A	85	VAL	CA-C	5.50	1.67	1.52
1	A	63	HIS	CB-CG	5.47	1.59	1.50
1	A	64	ALA	N-CA	5.45	1.57	1.46
1	A	38	PRO	N-CA	5.37	1.56	1.47
1	A	61	GLN	N-CA	5.36	1.57	1.46
1	A	63	HIS	ND1-CE1	5.35	1.48	1.34
1	A	100	LYS	C-N	-5.34	1.23	1.33
1	A	125	LYS	CD-CE	5.34	1.64	1.51
1	A	144	VAL	CA-C	5.32	1.66	1.52
1	A	11	VAL	CA-CB	-5.31	1.43	1.54
1	A	7	GLN	N-CA	5.28	1.56	1.46
1	A	87	ASP	CA-C	5.25	1.66	1.52
1	A	84	VAL	N-CA	5.25	1.56	1.46
1	A	13	SER	N-CA	-5.25	1.35	1.46
1	A	136	ILE	CA-CB	5.25	1.67	1.54
1	A	5	GLU	CG-CD	5.23	1.59	1.51
1	A	148	GLU	CG-CD	-5.22	1.44	1.51
1	A	134	TRP	CD2-CE2	-5.21	1.35	1.41
1	A	110	VAL	CA-C	5.19	1.66	1.52
1	A	79	GLU	N-CA	5.19	1.56	1.46
1	A	65	GLY	N-CA	5.18	1.53	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	148	GLU	CD-OE1	5.18	1.31	1.25
1	A	54	PRO	C-N	-5.17	1.22	1.34
1	A	71	VAL	N-CA	5.16	1.56	1.46
1	A	81	THR	CA-CB	5.16	1.66	1.53
1	A	18	PHE	CD2-CE2	5.16	1.49	1.39
1	A	83	VAL	N-CA	5.15	1.56	1.46
1	A	15	TRP	N-CA	5.15	1.56	1.46
1	A	30	PHE	CA-CB	5.14	1.65	1.53
1	A	10	LEU	CA-C	5.10	1.66	1.52
1	A	5	GLU	CD-OE2	5.10	1.31	1.25
1	A	58	PRO	N-CD	5.10	1.54	1.47
1	A	20	ALA	CA-CB	5.09	1.63	1.52
1	A	68	PHE	CE2-CZ	5.09	1.47	1.37
1	A	108	PRO	C-N	5.09	1.45	1.34
1	A	149	MET	N-CA	5.08	1.56	1.46
1	A	29	PHE	CD1-CE1	-5.08	1.29	1.39
1	A	152	ALA	N-CA	5.08	1.56	1.46
1	A	62	ALA	C-O	5.08	1.32	1.23
1	A	153	ALA	C-OXT	5.06	1.32	1.23
1	A	18	PHE	CD1-CE1	5.05	1.49	1.39
1	A	29	PHE	CD2-CE2	-5.04	1.29	1.39
1	A	18	PHE	C-O	5.04	1.32	1.23
1	A	68	PHE	CG-CD1	5.03	1.46	1.38
1	A	117	THR	CB-OG1	5.03	1.53	1.43
1	A	67	VAL	CA-C	5.01	1.66	1.52

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	16	GLU	OE1-CD-OE2	-10.20	111.06	123.30
1	A	112	GLU	OE1-CD-OE2	-9.99	111.32	123.30
1	A	73	GLU	OE1-CD-OE2	-9.26	112.19	123.30
1	A	28	ARG	NE-CZ-NH2	-9.26	115.67	120.30
1	A	72	TYR	CB-CG-CD1	-8.68	115.80	121.00
1	A	128	GLU	OE1-CD-OE2	-8.15	113.52	123.30
1	A	15	TRP	CG-CD2-CE3	-8.11	126.60	133.90
1	A	5	GLU	OE1-CD-OE2	-8.11	113.57	123.30
1	A	46	PHE	CB-CG-CD2	8.08	126.46	120.80
1	A	138	TYR	CB-CG-CD2	7.91	125.75	121.00
1	A	108	PRO	N-CA-CB	7.54	112.35	103.30
1	A	29	PHE	CB-CG-CD1	-6.94	115.94	120.80
1	A	54	PRO	N-CA-CB	6.84	111.51	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	29	PHE	CD1-CG-CD2	6.70	127.01	118.30
1	A	134	TRP	CG-CD1-NE1	-6.52	103.58	110.10
1	A	126	TRP	CE2-CD2-CG	-6.46	102.14	107.30
1	A	30	PHE	CB-CG-CD2	-6.39	116.33	120.80
1	A	120	GLU	OE1-CD-OE2	-6.30	115.74	123.30
1	A	87	ASP	CB-CG-OD2	-6.28	112.65	118.30
1	A	68	PHE	CB-CG-CD1	-6.24	116.44	120.80
1	A	17	GLU	OE1-CD-OE2	-6.20	115.86	123.30
1	A	138	TYR	CD1-CE1-CZ	6.18	125.36	119.80
1	A	23	PRO	N-CA-CB	6.16	110.69	103.30
1	A	131	ASN	O-C-N	6.15	132.54	122.70
1	A	124	ALA	CB-CA-C	-6.14	100.89	110.10
1	A	15	TRP	CH2-CZ2-CE2	-6.12	111.28	117.40
1	A	48	LYS	CB-CA-C	-5.93	98.54	110.40
1	A	59	GLU	OE1-CD-OE2	-5.78	116.37	123.30
1	A	15	TRP	CD2-CE3-CZ3	-5.77	111.30	118.80
1	A	142	ALA	O-C-N	5.77	131.93	122.70
1	A	72	TYR	CG-CD1-CE1	-5.75	116.70	121.30
1	A	138	TYR	CG-CD2-CE2	5.65	125.82	121.30
1	A	8	ALA	O-C-N	5.61	131.67	122.70
1	A	15	TRP	CD1-CG-CD2	-5.59	101.83	106.30
1	A	31	ILE	CB-CA-C	-5.46	100.67	111.60
1	A	29	PHE	CB-CG-CD2	-5.42	117.01	120.80
1	A	126	TRP	CD1-CG-CD2	5.41	110.63	106.30
1	A	56	ASN	CB-CA-C	-5.31	99.78	110.40
1	A	15	TRP	NE1-CE2-CZ2	-5.25	124.62	130.40
1	A	134	TRP	CD1-CG-CD2	5.24	110.50	106.30
1	A	138	TYR	O-C-N	5.23	131.07	122.70
1	A	15	TRP	CD1-NE1-CE2	-5.22	104.30	109.00
1	A	126	TRP	NE1-CE2-CD2	5.20	112.50	107.30
1	A	12	LYS	O-C-N	5.17	130.98	122.70
1	A	149	MET	O-C-N	5.15	130.94	122.70
1	A	46	PHE	CG-CD2-CE2	5.09	126.40	120.80
1	A	146	LYS	O-C-N	5.07	130.82	122.70
1	A	83	VAL	CB-CA-C	-5.05	101.81	111.40
1	A	99	SER	O-C-N	5.04	130.77	122.70

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	120	GLU	Sidechain

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Mol	Chain	Res	Type	Group
1	A	17	GLU	Sidechain
1	A	42	ASP	Sidechain
1	A	56	ASN	Sidechain
1	A	57	ASN	Sidechain
1	A	59	GLU	Sidechain
1	A	61	GLN	Sidechain
1	A	7	GLN	Sidechain
1	A	87	ASP	Sidechain

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	1180	0	1200	20	264
2	A	43	0	30	2	0
3	A	9	0	4	2	0
4	A	65	0	0	0	36
All	All	1297	0	1234	21	265

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 9.

All (21) 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:A:95:SER:HA	1:A:152:ALA:HB1	1.77	0.67
1:A:77:GLN:NE2	1:A:85:VAL:H	2.00	0.59
1:A:26:THR:HB	1:A:64:ALA:HB3	1.83	0.59
1:A:21:ASN:C	1:A:21:ASN:HD22	2.08	0.56
1:A:102:VAL:HG13	2:A:154:HEM:HAC	1.90	0.54
1:A:18:PHE:CE1	1:A:25:HIS:HB3	2.44	0.53
1:A:86:THR:HA	1:A:90:LEU:HD12	1.91	0.52
1:A:92:ASN:O	1:A:96:VAL:HG12	2.11	0.51
1:A:103:ALA:O	1:A:106:HIS:HB2	2.13	0.49
1:A:63:HIS:HB3	3:A:155:NIO:O1	2.12	0.49
1:A:29:PHE:O	1:A:33:VAL:HG23	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:LEU:HA	1:A:93:LEU:HD23	1.62	0.47
1:A:116:LYS:O	1:A:120:GLU:HG3	2.15	0.47
1:A:87:ASP:O	1:A:91:LYS:HG3	2.15	0.47
1:A:21:ASN:C	1:A:21:ASN:ND2	2.71	0.44
1:A:139:ASP:O	1:A:143:ILE:HG13	2.18	0.43
1:A:57:ASN:OD1	1:A:59:GLU:HB2	2.20	0.42
1:A:117:THR:O	1:A:121:VAL:HG23	2.19	0.42
1:A:1:GLY:HA3	1:A:7:GLN:HE22	1.84	0.42
2:A:154:HEM:C1A	3:A:155:NIO:H1	2.55	0.40

All (265) 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:9:ALA:N	1:A:13:SER:N[2_675]	0.52	1.68
1:A:126:TRP:C	1:A:131:ASN:O[2_675]	0.55	1.65
1:A:130:LEU:CA	1:A:130:LEU:CG[2_675]	0.60	1.60
1:A:118:ILE:CG2	1:A:129:GLU:CB[2_675]	0.61	1.59
1:A:126:TRP:CD1	1:A:128:GLU:O[2_675]	0.62	1.58
1:A:10:LEU:C	1:A:10:LEU:C[2_675]	0.68	1.52
1:A:4:THR:N	1:A:17:GLU:CG[2_675]	0.71	1.49
1:A:128:GLU:N	4:A:210:HOH:O[2_675]	0.78	1.42
1:A:8:ALA:N	1:A:13:SER:C[2_675]	0.81	1.39
1:A:6:SER:C	1:A:15:TRP:N[2_675]	0.85	1.35
1:A:4:THR:CB	1:A:17:GLU:CA[2_675]	0.85	1.35
1:A:7:GLN:CA	1:A:14:SER:CA[2_675]	0.87	1.33
1:A:6:SER:C	1:A:14:SER:C[2_675]	0.89	1.31
1:A:122:VAL:CG2	1:A:132[A]:SER:OG[2_675]	0.89	1.31
1:A:9:ALA:CA	1:A:12:LYS:C[2_675]	0.91	1.29
1:A:56:ASN:OD1	4:A:170:HOH:O[1_545]	0.92	1.28
1:A:7:GLN:NE2	1:A:122:VAL:CA[2_675]	0.94	1.26
1:A:134:TRP:CA	4:A:217:HOH:O[2_675]	0.94	1.26
1:A:6:SER:N	1:A:16:GLU:N[2_675]	0.95	1.25
1:A:9:ALA:C	1:A:12:LYS:N[2_675]	0.96	1.24
1:A:8:ALA:CA	1:A:13:SER:CB[2_675]	0.97	1.23
1:A:118:ILE:O	1:A:129:GLU:OE2[2_675]	0.97	1.23
1:A:5:GLU:C	1:A:16:GLU:N[2_675]	0.97	1.23
1:A:126:TRP:C	1:A:131:ASN:C[2_675]	0.98	1.22
1:A:10:LEU:CA	1:A:10:LEU:C[2_675]	1.00	1.20
1:A:8:ALA:C	1:A:13:SER:CA[2_675]	1.00	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:ALA:CA	1:A:12:LYS:CA[2_675]	1.00	1.20
1:A:8:ALA:CA	1:A:13:SER:CA[2_675]	1.04	1.16
1:A:10:LEU:CA	1:A:11:VAL:N[2_675]	1.04	1.16
1:A:130:LEU:CA	1:A:130:LEU:CD2[2_675]	1.05	1.15
1:A:5:GLU:N	1:A:16:GLU:C[2_675]	1.05	1.15
1:A:9:ALA:N	1:A:12:LYS:C[2_675]	1.06	1.14
1:A:9:ALA:CB	1:A:12:LYS:CA[2_675]	1.06	1.14
1:A:5:GLU:CA	1:A:16:GLU:CB[2_675]	1.06	1.14
1:A:19:ASN:N	4:A:220:HOH:O[2_675]	1.07	1.13
1:A:5:GLU:C	1:A:16:GLU:CA[2_675]	1.09	1.11
1:A:6:SER:CA	1:A:15:TRP:CA[2_675]	1.11	1.09
1:A:8:ALA:C	1:A:13:SER:N[2_675]	1.12	1.08
1:A:7:GLN:N	1:A:14:SER:C[2_675]	1.12	1.08
1:A:127:SER:N	1:A:131:ASN:CA[2_675]	1.12	1.08
1:A:4:THR:CB	1:A:17:GLU:C[2_675]	1.13	1.07
1:A:119:LYS:C	4:A:181:HOH:O[2_675]	1.13	1.07
1:A:126:TRP:CA	1:A:131:ASN:C[2_675]	1.14	1.06
1:A:5:GLU:CA	1:A:16:GLU:CA[2_675]	1.15	1.05
1:A:7:GLN:C	1:A:14:SER:N[2_675]	1.15	1.05
1:A:3:LEU:N	1:A:17:GLU:OE1[2_675]	1.15	1.05
1:A:4:THR:CA	1:A:17:GLU:CA[2_675]	1.16	1.04
1:A:119:LYS:CA	4:A:181:HOH:O[2_675]	1.17	1.03
1:A:10:LEU:CA	1:A:10:LEU:O[2_675]	1.20	1.00
1:A:130:LEU:CB	1:A:130:LEU:CG[2_675]	1.21	0.99
1:A:7:GLN:N	1:A:14:SER:CA[2_675]	1.22	0.98
1:A:125:LYS:CG	1:A:136:ILE:CB[2_675]	1.24	0.96
1:A:4:THR:C	1:A:17:GLU:N[2_675]	1.25	0.95
1:A:130:LEU:CB	1:A:130:LEU:CB[2_675]	1.26	0.94
1:A:6:SER:CA	1:A:15:TRP:C[2_675]	1.27	0.93
1:A:126:TRP:O	1:A:131:ASN:O[2_675]	1.27	0.93
1:A:126:TRP:CE3	1:A:131:ASN:OD1[2_675]	1.28	0.92
1:A:6:SER:O	1:A:15:TRP:N[2_675]	1.29	0.91
1:A:9:ALA:N	1:A:13:SER:CA[2_675]	1.31	0.89
1:A:10:LEU:CD1	1:A:134:TRP:NE1[2_675]	1.31	0.89
1:A:127:SER:N	1:A:131:ASN:C[2_675]	1.32	0.88
1:A:4:THR:OG1	1:A:17:GLU:CA[2_675]	1.32	0.88
1:A:6:SER:OG	1:A:14:SER:O[2_675]	1.33	0.87
1:A:7:GLN:OE1	1:A:17:GLU:OE2[2_675]	1.33	0.87
1:A:8:ALA:CA	1:A:13:SER:OG[2_675]	1.34	0.86
1:A:135:THR:OG1	4:A:159:HOH:O[2_675]	1.34	0.86
1:A:9:ALA:CA	1:A:13:SER:N[2_675]	1.35	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:6:SER:N	1:A:15:TRP:C[2_675]	1.36	0.84
1:A:3:LEU:C	1:A:17:GLU:CG[2_675]	1.36	0.84
1:A:130:LEU:N	1:A:130:LEU:CD2[2_675]	1.36	0.84
1:A:6:SER:CB	1:A:15:TRP:CA[2_675]	1.37	0.83
1:A:6:SER:CA	1:A:15:TRP:N[2_675]	1.38	0.82
1:A:9:ALA:CB	1:A:12:LYS:C[2_675]	1.40	0.80
1:A:9:ALA:O	1:A:12:LYS:N[2_675]	1.40	0.80
1:A:124:ALA:O	1:A:135:THR:CB[2_675]	1.41	0.79
1:A:5:GLU:N	1:A:17:GLU:N[2_675]	1.41	0.79
1:A:118:ILE:CG2	1:A:129:GLU:CG[2_675]	1.43	0.77
1:A:126:TRP:NE1	1:A:128:GLU:O[2_675]	1.43	0.77
1:A:8:ALA:C	1:A:13:SER:CB[2_675]	1.44	0.76
1:A:8:ALA:N	1:A:13:SER:O[2_675]	1.44	0.76
1:A:3:LEU:CA	1:A:17:GLU:CD[2_675]	1.45	0.75
1:A:127:SER:N	1:A:131:ASN:O[2_675]	1.46	0.74
1:A:7:GLN:NE2	1:A:122:VAL:CB[2_675]	1.47	0.73
1:A:125:LYS:O	1:A:134:TRP:N[2_675]	1.48	0.72
1:A:4:THR:N	1:A:17:GLU:CB[2_675]	1.50	0.70
1:A:124:ALA:O	1:A:135:THR:CG2[2_675]	1.51	0.69
1:A:122:VAL:O	1:A:136:ILE:CD1[2_675]	1.52	0.68
1:A:126:TRP:NE1	1:A:128:GLU:C[2_675]	1.52	0.68
1:A:119:LYS:O	4:A:181:HOH:O[2_675]	1.54	0.66
1:A:7:GLN:CG	1:A:122:VAL:CG1[2_675]	1.54	0.66
1:A:79:GLU:CG	4:A:204:HOH:O[2_675]	1.55	0.65
1:A:7:GLN:C	1:A:13:SER:C[2_675]	1.55	0.65
1:A:10:LEU:O	1:A:10:LEU:CB[2_675]	1.56	0.64
1:A:5:GLU:CA	1:A:16:GLU:C[2_675]	1.58	0.62
1:A:10:LEU:C	1:A:11:VAL:N[2_675]	1.58	0.62
1:A:4:THR:OG1	1:A:17:GLU:CB[2_675]	1.59	0.61
1:A:10:LEU:CA	1:A:11:VAL:CA[2_675]	1.60	0.60
1:A:126:TRP:NE1	1:A:128:GLU:CA[2_675]	1.60	0.60
1:A:5:GLU:CB	1:A:16:GLU:CA[2_675]	1.61	0.59
1:A:5:GLU:C	1:A:16:GLU:CB[2_675]	1.61	0.59
1:A:8:ALA:N	1:A:13:SER:CA[2_675]	1.61	0.59
1:A:10:LEU:CG	1:A:14:SER:OG[2_675]	1.62	0.58
1:A:10:LEU:CD1	1:A:14:SER:OG[2_675]	1.62	0.58
1:A:6:SER:CA	1:A:16:GLU:N[2_675]	1.62	0.58
1:A:3:LEU:CG	1:A:125:LYS:CE[2_675]	1.63	0.57
1:A:9:ALA:CB	1:A:12:LYS:O[2_675]	1.63	0.57
1:A:128:GLU:CA	4:A:210:HOH:O[2_675]	1.63	0.57
1:A:122:VAL:C	1:A:132[C]:SER:OG[2_675]	1.63	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:LEU:CA	1:A:130:LEU:CB[2_675]	1.64	0.56
1:A:130:LEU:C	1:A:130:LEU:CB[2_675]	1.65	0.55
1:A:6:SER:N	1:A:16:GLU:CA[2_675]	1.67	0.53
1:A:7:GLN:CA	1:A:14:SER:N[2_675]	1.67	0.53
1:A:8:ALA:N	1:A:14:SER:N[2_675]	1.67	0.53
1:A:1:GLY:CA	1:A:121:VAL:O[2_675]	1.67	0.53
1:A:7:GLN:OE1	1:A:17:GLU:CD[2_675]	1.67	0.53
1:A:18:PHE:C	4:A:220:HOH:O[2_675]	1.67	0.53
1:A:56:ASN:CG	4:A:170:HOH:O[1_545]	1.68	0.52
1:A:4:THR:CA	1:A:17:GLU:CB[2_675]	1.68	0.52
1:A:134:TRP:N	4:A:217:HOH:O[2_675]	1.68	0.52
1:A:10:LEU:N	1:A:11:VAL:C[2_675]	1.68	0.52
1:A:7:GLN:CD	1:A:17:GLU:OE2[2_675]	1.68	0.52
1:A:10:LEU:N	1:A:10:LEU:O[2_675]	1.68	0.52
1:A:4:THR:OG1	1:A:17:GLU:C[2_675]	1.69	0.51
1:A:126:TRP:CD1	1:A:128:GLU:C[2_675]	1.69	0.51
1:A:5:GLU:O	1:A:16:GLU:N[2_675]	1.70	0.50
1:A:129:GLU:O	1:A:130:LEU:CD2[2_675]	1.70	0.50
1:A:4:THR:CB	1:A:17:GLU:CB[2_675]	1.72	0.48
1:A:126:TRP:CA	1:A:131:ASN:O[2_675]	1.72	0.48
1:A:3:LEU:N	1:A:17:GLU:CD[2_675]	1.73	0.47
1:A:126:TRP:O	1:A:135:THR:OG1[2_675]	1.74	0.46
1:A:118:ILE:C	1:A:129:GLU:OE2[2_675]	1.74	0.46
1:A:125:LYS:O	1:A:133:ALA:C[2_675]	1.74	0.46
1:A:7:GLN:NE2	1:A:122:VAL:CG1[2_675]	1.74	0.46
1:A:4:THR:C	1:A:17:GLU:CA[2_675]	1.74	0.46
1:A:126:TRP:CD2	1:A:131:ASN:CB[2_675]	1.75	0.45
1:A:126:TRP:CE3	1:A:131:ASN:CG[2_675]	1.75	0.45
1:A:9:ALA:CA	1:A:12:LYS:N[2_675]	1.75	0.45
1:A:129:GLU:C	1:A:130:LEU:CD2[2_675]	1.75	0.45
1:A:8:ALA:O	1:A:9:ALA:O[2_675]	1.76	0.44
1:A:5:GLU:O	1:A:12:LYS:O[2_675]	1.77	0.43
1:A:6:SER:C	1:A:14:SER:CA[2_675]	1.78	0.42
1:A:127:SER:C	4:A:210:HOH:O[2_675]	1.78	0.42
1:A:6:SER:O	1:A:14:SER:C[2_675]	1.79	0.41
1:A:7:GLN:N	1:A:14:SER:O[2_675]	1.80	0.40
1:A:134:TRP:N	4:A:190:HOH:O[2_675]	1.80	0.40
1:A:126:TRP:CD2	4:A:189:HOH:O[2_675]	1.80	0.40
1:A:10:LEU:C	1:A:10:LEU:O[2_675]	1.80	0.40
1:A:4:THR:O	1:A:13:SER:O[2_675]	1.80	0.40
1:A:6:SER:CB	1:A:15:TRP:C[2_675]	1.80	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:ALA:O	1:A:13:SER:CB[2_675]	1.80	0.40
1:A:118:ILE:CB	1:A:129:GLU:CB[2_675]	1.80	0.40
1:A:9:ALA:C	1:A:12:LYS:CA[2_675]	1.81	0.39
1:A:123:GLY:N	1:A:132[C]:SER:OG[2_675]	1.82	0.38
1:A:126:TRP:CG	1:A:128:GLU:O[2_675]	1.83	0.37
1:A:6:SER:N	1:A:17:GLU:N[2_675]	1.83	0.37
1:A:10:LEU:N	1:A:12:LYS:N[2_675]	1.83	0.37
1:A:130:LEU:N	1:A:130:LEU:CG[2_675]	1.83	0.37
4:A:159:HOH:O	4:A:176:HOH:O[2_675]	1.84	0.36
1:A:130:LEU:C	1:A:130:LEU:CD2[2_675]	1.84	0.36
1:A:5:GLU:N	1:A:16:GLU:O[2_675]	1.84	0.36
1:A:15:TRP:CB	4:A:219:HOH:O[2_675]	1.84	0.36
1:A:7:GLN:CA	1:A:14:SER:CB[2_675]	1.84	0.36
1:A:9:ALA:C	1:A:11:VAL:C[2_675]	1.84	0.36
1:A:7:GLN:CD	1:A:122:VAL:CG1[2_675]	1.84	0.36
1:A:5:GLU:O	1:A:16:GLU:CB[2_675]	1.85	0.35
1:A:9:ALA:CA	1:A:12:LYS:CB[2_675]	1.85	0.35
1:A:7:GLN:NE2	1:A:122:VAL:N[2_675]	1.86	0.34
1:A:127:SER:CA	1:A:131:ASN:ND2[2_675]	1.86	0.34
1:A:3:LEU:CA	1:A:17:GLU:OE1[2_675]	1.87	0.33
1:A:6:SER:N	1:A:16:GLU:C[2_675]	1.87	0.33
1:A:8:ALA:CB	1:A:13:SER:OG[2_675]	1.87	0.33
1:A:6:SER:O	1:A:14:SER:N[2_675]	1.88	0.32
1:A:125:LYS:CA	1:A:136:ILE:N[2_675]	1.88	0.32
1:A:4:THR:OG1	1:A:18:PHE:N[2_675]	1.88	0.32
1:A:119:LYS:CE	1:A:128:GLU:CG[2_675]	1.90	0.30
1:A:7:GLN:OE1	1:A:17:GLU:OE1[2_675]	1.90	0.30
1:A:126:TRP:C	1:A:131:ASN:CA[2_675]	1.90	0.30
1:A:56:ASN:CB	4:A:187:HOH:O[1_545]	1.91	0.29
1:A:4:THR:CB	1:A:17:GLU:O[2_675]	1.91	0.29
1:A:6:SER:O	1:A:14:SER:CA[2_675]	1.91	0.29
1:A:5:GLU:CG	1:A:16:GLU:CG[2_675]	1.92	0.28
1:A:125:LYS:CB	1:A:133:ALA:O[2_675]	1.92	0.28
1:A:5:GLU:CB	1:A:16:GLU:CB[2_675]	1.92	0.28
1:A:122:VAL:CG2	1:A:129:GLU:O[2_675]	1.93	0.27
1:A:6:SER:CA	1:A:14:SER:C[2_675]	1.94	0.26
1:A:119:LYS:N	4:A:181:HOH:O[2_675]	1.94	0.26
1:A:4:THR:OG1	1:A:17:GLU:N[2_675]	1.95	0.25
1:A:135:THR:CG2	4:A:159:HOH:O[2_675]	1.95	0.25
1:A:3:LEU:CD2	4:A:201:HOH:O[2_675]	1.95	0.25
1:A:3:LEU:CD1	1:A:125:LYS:CD[2_675]	1.96	0.24

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4:THR:CG2	1:A:17:GLU:C[2_675]	1.96	0.24
1:A:9:ALA:N	1:A:12:LYS:O[2_675]	1.97	0.23
1:A:6:SER:O	1:A:11:VAL:O[2_675]	1.97	0.23
1:A:130:LEU:O	4:A:190:HOH:O[2_675]	1.97	0.23
1:A:118:ILE:O	1:A:129:GLU:CD[2_675]	1.97	0.23
1:A:7:GLN:O	1:A:14:SER:N[2_675]	1.98	0.22
1:A:18:PHE:N	4:A:220:HOH:O[2_675]	1.98	0.22
1:A:135:THR:CB	4:A:159:HOH:O[2_675]	1.99	0.21
1:A:6:SER:C	1:A:14:SER:O[2_675]	1.99	0.21
1:A:3:LEU:CD1	1:A:125:LYS:CE[2_675]	1.99	0.21
1:A:4:THR:N	1:A:17:GLU:CD[2_675]	1.99	0.21
1:A:18:PHE:CA	4:A:220:HOH:O[2_675]	2.00	0.20
1:A:8:ALA:CA	1:A:13:SER:C[2_675]	2.00	0.20
1:A:9:ALA:C	1:A:13:SER:N[2_675]	2.01	0.19
1:A:8:ALA:CB	1:A:13:SER:CA[2_675]	2.01	0.19
1:A:5:GLU:N	1:A:16:GLU:CA[2_675]	2.01	0.19
1:A:16:GLU:OE1	1:A:79:GLU:OE1[2_675]	2.01	0.19
1:A:3:LEU:C	1:A:17:GLU:CD[2_675]	2.02	0.18
1:A:4:THR:CA	1:A:17:GLU:N[2_675]	2.02	0.18
1:A:7:GLN:C	1:A:14:SER:CA[2_675]	2.02	0.18
1:A:5:GLU:C	1:A:16:GLU:C[2_675]	2.02	0.18
1:A:134:TRP:C	4:A:217:HOH:O[2_675]	2.03	0.17
1:A:127:SER:O	1:A:131:ASN:CA[2_675]	2.03	0.17
1:A:4:THR:CG2	1:A:17:GLU:O[2_675]	2.04	0.16
1:A:124:ALA:O	1:A:135:THR:C[2_675]	2.04	0.16
1:A:4:THR:CA	1:A:17:GLU:CG[2_675]	2.04	0.16
1:A:125:LYS:N	1:A:136:ILE:CG1[2_675]	2.04	0.16
1:A:126:TRP:CG	4:A:189:HOH:O[2_675]	2.05	0.15
1:A:7:GLN:N	1:A:15:TRP:N[2_675]	2.05	0.15
1:A:10:LEU:N	1:A:10:LEU:C[2_675]	2.05	0.15
1:A:130:LEU:C	1:A:130:LEU:CG[2_675]	2.06	0.14
1:A:4:THR:C	1:A:16:GLU:C[2_675]	2.06	0.14
1:A:130:LEU:CA	1:A:130:LEU:CD1[2_675]	2.07	0.13
1:A:6:SER:CB	1:A:14:SER:O[2_675]	2.07	0.13
1:A:118:ILE:O	4:A:181:HOH:O[2_675]	2.07	0.13
1:A:122:VAL:CG2	1:A:132[C]:SER:OG[2_675]	2.07	0.13
1:A:8:ALA:O	1:A:13:SER:N[2_675]	2.07	0.13
1:A:1:GLY:C	1:A:121:VAL:O[2_675]	2.08	0.12
1:A:126:TRP:CE3	1:A:131:ASN:CB[2_675]	2.08	0.12
1:A:10:LEU:C	1:A:10:LEU:CB[2_675]	2.09	0.11
1:A:1:GLY:O	1:A:121:VAL:O[2_675]	2.09	0.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:ALA:O	1:A:135:THR:CA[2_675]	2.09	0.11
1:A:3:LEU:CA	1:A:17:GLU:CG[2_675]	2.10	0.10
1:A:6:SER:CB	1:A:15:TRP:O[2_675]	2.10	0.10
1:A:126:TRP:CZ3	1:A:131:ASN:OD1[2_675]	2.11	0.09
1:A:118:ILE:CG2	1:A:129:GLU:CA[2_675]	2.11	0.09
1:A:4:THR:O	1:A:17:GLU:N[2_675]	2.11	0.09
1:A:7:GLN:O	1:A:10:LEU:O[2_675]	2.12	0.08
1:A:129:GLU:N	4:A:210:HOH:O[2_675]	2.13	0.07
1:A:124:ALA:CB	4:A:188:HOH:O[2_675]	2.13	0.07
1:A:127:SER:C	1:A:131:ASN:ND2[2_675]	2.13	0.07
1:A:7:GLN:N	1:A:14:SER:N[2_675]	2.14	0.06
1:A:2:ALA:C	1:A:17:GLU:OE1[2_675]	2.14	0.06
1:A:7:GLN:CB	4:A:201:HOH:O[2_675]	2.14	0.06
1:A:56:ASN:CB	4:A:170:HOH:O[1_545]	2.15	0.05
1:A:6:SER:CA	1:A:14:SER:O[2_675]	2.15	0.05
1:A:10:LEU:CG	1:A:134:TRP:NE1[2_675]	2.15	0.05
1:A:4:THR:CB	1:A:18:PHE:N[2_675]	2.15	0.05
1:A:5:GLU:CB	1:A:16:GLU:C[2_675]	2.16	0.04
1:A:125:LYS:O	1:A:133:ALA:N[2_675]	2.16	0.04
1:A:125:LYS:C	1:A:133:ALA:N[2_675]	2.16	0.04
1:A:8:ALA:CB	1:A:13:SER:CB[2_675]	2.16	0.04
1:A:7:GLN:CB	1:A:17:GLU:OE2[2_675]	2.16	0.04
1:A:125:LYS:CB	1:A:133:ALA:C[2_675]	2.17	0.03
1:A:12:LYS:CB	4:A:203:HOH:O[2_675]	2.17	0.03
1:A:5:GLU:O	1:A:16:GLU:CG[2_675]	2.17	0.03
1:A:56:ASN:OD1	4:A:171:HOH:O[1_545]	2.18	0.02
1:A:128:GLU:C	4:A:210:HOH:O[2_675]	2.18	0.02
1:A:5:GLU:O	1:A:16:GLU:CA[2_675]	2.18	0.02
1:A:122:VAL:CB	1:A:132[A]:SER:OG[2_675]	2.18	0.02
1:A:5:GLU:CG	1:A:16:GLU:CB[2_675]	2.18	0.02
1:A:127:SER:CA	1:A:131:ASN:CA[2_675]	2.18	0.02
1:A:126:TRP:CB	1:A:131:ASN:C[2_675]	2.19	0.01
1:A:9:ALA:CA	1:A:12:LYS:O[2_675]	2.19	0.01
1:A:125:LYS:CG	1:A:136:ILE:CG2[2_675]	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	153/153 (100%)	149 (97%)	3 (2%)	1 (1%)	26 19

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	LEU

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	127/125 (102%)	124 (98%)	3 (2%)	57 58

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	ASN
1	A	34	LEU
1	A	96	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	ASN
1	A	25	HIS
1	A	61	GLN
1	A	77	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

2 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	154	1,3	30,50,50	4.60	24 (80%)	24,82,82	2.76	10 (41%)
3	NIO	A	155	2	6,9,9	2.84	4 (66%)	8,11,11	2.93	5 (62%)

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	154	1,3	-	0/10/54/54	0/0/8/8
3	NIO	A	155	2	-	0/0/4/4	0/1/1/1

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	154	HEM	C2D-C3D	-6.08	1.36	1.54
3	A	155	NIO	C1-C2	-5.07	1.29	1.39
2	A	154	HEM	C2C-C1C	-3.08	1.46	1.52
3	A	155	NIO	C4-C5	-2.71	1.29	1.37
2	A	154	HEM	CAD-CBD	-2.03	1.43	1.52
2	A	154	HEM	C2D-C1D	2.33	1.59	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	154	HEM	C2B-C1B	2.47	1.60	1.51
3	A	155	NIO	C4-C3	2.51	1.44	1.38
2	A	154	HEM	CMA-C3A	2.82	1.57	1.51
3	A	155	NIO	C1-N	2.92	1.40	1.34
2	A	154	HEM	CMB-C2B	3.17	1.60	1.53
2	A	154	HEM	CMD-C2D	3.22	1.60	1.53
2	A	154	HEM	C3C-CAC	3.27	1.57	1.51
2	A	154	HEM	CMC-C2C	3.36	1.61	1.53
2	A	154	HEM	C1A-CHA	3.66	1.49	1.39
2	A	154	HEM	C2A-C3A	3.95	1.49	1.37
2	A	154	HEM	C3D-C4D	4.14	1.56	1.51
2	A	154	HEM	C4A-CHB	4.63	1.52	1.39
2	A	154	HEM	CAD-C3D	5.27	1.64	1.54
2	A	154	HEM	FE-ND	5.32	2.25	1.97
2	A	154	HEM	FE-NB	5.39	2.26	1.97
2	A	154	HEM	CHC-C1C	5.74	1.49	1.36
2	A	154	HEM	CAA-C2A	6.03	1.62	1.52
2	A	154	HEM	C4C-NC	6.47	1.44	1.36
2	A	154	HEM	CHD-C4C	6.53	1.51	1.36
2	A	154	HEM	C3B-C4B	7.41	1.58	1.51
2	A	154	HEM	C3B-CAB	7.79	1.65	1.51
2	A	154	HEM	C1C-NC	9.56	1.47	1.36

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	154	HEM	CMA-C3A-C4A	-5.42	119.40	128.36
2	A	154	HEM	CAA-C2A-C1A	-4.60	122.01	127.01
2	A	154	HEM	C2C-C1C-NC	-2.69	105.67	110.21
3	A	155	NIO	C4-C5-N	-2.37	115.68	122.51
2	A	154	HEM	C3C-CAC-CBC	-2.30	120.93	124.46
3	A	155	NIO	C1-C2-C6	-2.02	118.74	121.21
2	A	154	HEM	CMA-C3A-C2A	2.24	129.91	125.24
2	A	154	HEM	CMD-C2D-C3D	2.42	125.05	114.35
3	A	155	NIO	C4-C3-C2	3.21	124.80	120.56
2	A	154	HEM	CMB-C2B-C3B	3.61	125.54	116.53
3	A	155	NIO	C3-C2-C6	4.55	126.58	120.45
2	A	154	HEM	CAD-C3D-C4D	4.56	128.56	112.47
2	A	154	HEM	CAD-C3D-C2D	4.64	126.55	113.22
3	A	155	NIO	C5-N-C1	5.15	126.32	116.84
2	A	154	HEM	CMC-C2C-C3C	5.44	130.12	116.53

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	154	HEM	2	0
3	A	155	NIO	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	153/153 (100%)	4.62	131 (85%) 0 0	6, 17, 50, 67	18 (11%)

All (131) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	ALA	24.0
1	A	45	SER	23.9
1	A	51	SER	18.0
1	A	153	ALA	16.9
1	A	101	GLY	12.9
1	A	1	GLY	12.2
1	A	124	ALA	11.3
1	A	49	GLY	11.3
1	A	46	PHE	10.6
1	A	80	VAL	10.2
1	A	88	ALA	8.9
1	A	60	LEU	8.6
1	A	47	LEU	8.3
1	A	130	LEU	8.3
1	A	144	VAL	8.1
1	A	90	LEU	7.6
1	A	40	ALA	7.5
1	A	19	ASN	7.4
1	A	100	LYS	7.1
1	A	89	THR	7.1
1	A	108	PRO	6.9
1	A	41	LYS	6.8
1	A	150	ASP	6.7
1	A	99	SER	6.7
1	A	50	THR	6.6
1	A	44	PHE	6.5
1	A	43	LEU	6.4

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Mol	Chain	Res	Type	RSRZ
1	A	151	ASP	6.3
1	A	152	ALA	6.3
1	A	133	ALA	6.2
1	A	48	LYS	6.1
1	A	62	ALA	6.0
1	A	138	TYR	5.9
1	A	105	ALA	5.9
1	A	95	SER	5.8
1	A	143	ILE	5.8
1	A	10	LEU	5.8
1	A	58	PRO	5.7
1	A	136	ILE	5.6
1	A	69	LYS	5.5
1	A	116	LYS	5.5
1	A	31	ILE	5.5
1	A	107	PHE	5.4
1	A	109	VAL	5.4
1	A	3	LEU	5.4
1	A	70	LEU	5.4
1	A	123	GLY	5.3
1	A	42	ASP	5.2
1	A	87	ASP	4.8
1	A	63	HIS	4.8
1	A	127	SER	4.8
1	A	145	ILE	4.7
1	A	5	GLU	4.7
1	A	93	LEU	4.6
1	A	18	PHE	4.6
1	A	72	TYR	4.5
1	A	20	ALA	4.5
1	A	15	TRP	4.5
1	A	126	TRP	4.4
1	A	121	VAL	4.4
1	A	26	THR	4.4
1	A	115	LEU	4.3
1	A	129	GLU	4.3
1	A	148	GLU	4.3
1	A	11	VAL	4.3
1	A	135	THR	4.1
1	A	7	GLN	4.1
1	A	38	PRO	4.1
1	A	28	ARG	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	27	HIS	4.0
1	A	22	ILE	4.0
1	A	71	VAL	4.0
1	A	67	VAL	3.9
1	A	21	ASN	3.9
1	A	147	LYS	3.9
1	A	117	THR	3.8
1	A	54	PRO	3.8
1	A	92	ASN	3.8
1	A	75	ALA	3.8
1	A	98	VAL	3.8
1	A	33	VAL	3.7
1	A	137	ALA	3.7
1	A	122	VAL	3.6
1	A	55	GLN	3.5
1	A	131	ASN	3.5
1	A	29	PHE	3.5
1	A	73	GLU	3.4
1	A	96	VAL	3.4
1	A	149	MET	3.4
1	A	86	THR	3.4
1	A	32	LEU	3.3
1	A	110	VAL	3.3
1	A	36	ILE	3.3
1	A	82	GLY	3.3
1	A	66	LYS	3.2
1	A	94	GLY	3.1
1	A	132[A]	SER	3.0
1	A	140	GLU	2.9
1	A	16	GLU	2.9
1	A	56	ASN	2.9
1	A	119	LYS	2.8
1	A	12	LYS	2.8
1	A	128	GLU	2.8
1	A	76	ILE	2.8
1	A	68	PHE	2.8
1	A	74	ALA	2.8
1	A	83	VAL	2.7
1	A	102	VAL	2.7
1	A	141	LEU	2.7
1	A	78	LEU	2.6
1	A	118	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	61	GLN	2.5
1	A	64	ALA	2.5
1	A	139	ASP	2.5
1	A	34	LEU	2.4
1	A	57	ASN	2.4
1	A	120	GLU	2.4
1	A	77	GLN	2.4
1	A	142	ALA	2.4
1	A	104	ASP	2.3
1	A	4	THR	2.2
1	A	23	PRO	2.2
1	A	53	VAL	2.2
1	A	125	LYS	2.2
1	A	146	LYS	2.2
1	A	52	GLU	2.1
1	A	91	LYS	2.1
1	A	79	GLU	2.1
1	A	97	HIS	2.1
1	A	103	ALA	2.1
1	A	111	LYS	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
3	NIO	A	155	9/9	0.66	0.33	-0.11	7,12,19,21	0
2	HEM	A	154	43/43	0.76	0.30	-0.41	0,17,44,50	3

6.5 Other polymers [i](#)

There are no such residues in this entry.