



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 04:33 AM GMT

PDB ID : 1A2G
Title : PROBING THE STRENGTH AND CHARACTER OF AN ASP-HIS-X HYDROGEN BOND BY INTRODUCING BURIED CHARGES
Authors : Cao, Y.; Goodin, D.B.; Mcree, D.E.
Deposited on : 1998-01-02
Resolution : 2.10 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

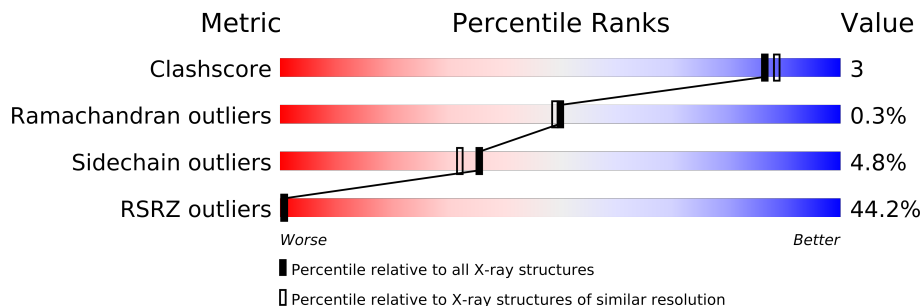
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.10 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	79885	3649 (2.10-2.10)
Ramachandran outliers	78287	3610 (2.10-2.10)
Sidechain outliers	78261	3611 (2.10-2.10)
RSRZ outliers	66119	3013 (2.10-2.10)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	291	

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 3016 atoms, of which 514 are hydrogens and 0 are deuterium.

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.

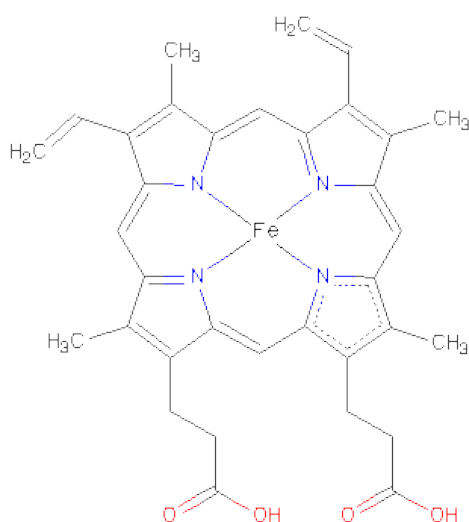
- Molecule 1 is a protein called CYTOCHROME C PEROXIDASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	291	2866	1502	514	394	451	5	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	53	ILE	THR	SUBSTITUTION	UNP P00431
A	152	GLY	ASP	SUBSTITUTION	UNP P00431
A	231	HIS	MET	SUBSTITUTION	UNP P00431

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

- Molecule 3 is water.

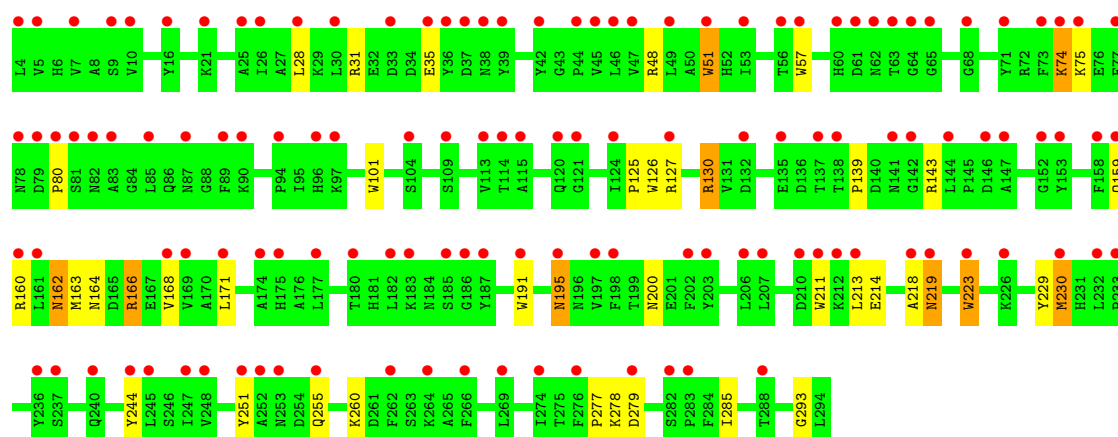
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	107	Total 107	O 107	0	0

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: CYTOCHROME C PEROXIDASE

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.60Å 74.00Å 45.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	5.00 – 2.10 42.71 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (5.00-2.10) 84.4 (42.71-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.15 (at 2.00Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.184 , (Not available) 0.376 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	19.7	Xtriage
Anisotropy	0.569	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 22.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 20674 reflections	Xtriage
F_o, F_c correlation	0.80	EDS
Total number of atoms	3016	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 6.26% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.85	0/2419	1.55	40/3275 (1.2%)

There are no bond length outliers.

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	31	ARG	NE-CZ-NH2	-11.43	114.58	120.30
1	A	127	ARG	NE-CZ-NH2	-11.19	114.71	120.30
1	A	127	ARG	NE-CZ-NH1	9.34	124.97	120.30
1	A	223	TRP	CD1-CG-CD2	8.73	113.28	106.30
1	A	163	MET	CG-SD-CE	-8.72	86.25	100.20
1	A	51	TRP	CD1-CG-CD2	8.04	112.73	106.30
1	A	101	TRP	CD1-CG-CD2	7.80	112.54	106.30
1	A	143	ARG	NE-CZ-NH1	7.73	124.16	120.30
1	A	223	TRP	CE2-CD2-CG	-7.47	101.33	107.30
1	A	143	ARG	NE-CZ-NH2	-7.17	116.71	120.30
1	A	229	TYR	CB-CG-CD2	-7.16	116.70	121.00
1	A	211	TRP	CD1-CG-CD2	7.16	112.03	106.30
1	A	51	TRP	CE2-CD2-CG	-7.07	101.64	107.30
1	A	57	TRP	CD1-CG-CD2	7.03	111.92	106.30
1	A	31	ARG	NE-CZ-NH1	7.01	123.81	120.30
1	A	126	TRP	CD1-CG-CD2	6.94	111.86	106.30
1	A	101	TRP	CE2-CD2-CG	-6.91	101.77	107.30
1	A	191	TRP	CB-CG-CD1	-6.86	118.08	127.00
1	A	191	TRP	CE2-CD2-CG	-6.70	101.94	107.30
1	A	160	ARG	NE-CZ-NH2	-6.64	116.98	120.30
1	A	57	TRP	CE2-CD2-CG	-6.60	102.02	107.30
1	A	211	TRP	CE2-CD2-CG	-6.49	102.10	107.30
1	A	48	ARG	NE-CZ-NH1	6.45	123.53	120.30
1	A	244	TYR	CB-CG-CD2	-6.35	117.19	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	162	ASN	CA-C-N	-6.17	103.62	117.20
1	A	126	TRP	CE2-CD2-CG	-6.11	102.41	107.30
1	A	51	TRP	CB-CG-CD1	-5.89	119.34	127.00
1	A	191	TRP	CD1-CG-CD2	5.86	110.99	106.30
1	A	130	ARG	CG-CD-NE	-5.73	99.76	111.80
1	A	223	TRP	CG-CD1-NE1	-5.66	104.44	110.10
1	A	51	TRP	CG-CD1-NE1	-5.55	104.55	110.10
1	A	230	MET	CG-SD-CE	-5.50	91.40	100.20
1	A	166	ARG	NE-CZ-NH2	-5.36	117.62	120.30
1	A	101	TRP	CG-CD1-NE1	-5.29	104.81	110.10
1	A	277	PRO	CA-C-N	5.28	128.82	117.20
1	A	278	LYS	CA-CB-CG	-5.20	101.95	113.40
1	A	251	TYR	CB-CG-CD2	-5.19	117.89	121.00
1	A	191	TRP	CG-CD2-CE3	5.08	138.47	133.90
1	A	162	ASN	CA-C-O	5.08	130.76	120.10
1	A	57	TRP	CG-CD1-NE1	-5.01	105.09	110.10

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2352	514	1713	12	2
2	A	43	0	30	0	0
3	A	107	0	0	3	2
All	All	2502	514	1743	12	2

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 3.

All (12) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:125:PRO:HG3	1:A:285:ILE:HD11	1.85	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:74:LYS:H	1:A:74:LYS:HD2	1.69	0.56
1:A:200:ASN:H	1:A:255:GLN:HE22	1.55	0.54
1:A:130:ARG:NE	3:A:326:HOH:O	2.48	0.46
1:A:125:PRO:HG3	1:A:285:ILE:CD1	2.47	0.44
1:A:75:LYS:HE3	1:A:139:PRO:O	2.18	0.44
1:A:164:ASN:O	1:A:168:VAL:HG23	2.19	0.42
1:A:130:ARG:NH2	3:A:326:HOH:O	2.51	0.42
1:A:213:LEU:HD13	1:A:223:TRP:CE2	2.54	0.42
1:A:195:ASN:HB3	3:A:308:HOH:O	2.21	0.41
1:A:218:ALA:O	1:A:219:ASN:HB2	2.21	0.41
1:A:230:MET:SD	1:A:230:MET:C	3.00	0.40

All (2) 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	Distance(Å)	Clash(Å)
1:A:214:GLU:OE2	3:A:374:HOH:O[4_4610]	1.92	0.28
1:A:293:GLY:O	3:A:330:HOH:O[3_549]	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	289/291 (99%)	276 (96%)	12 (4%)	1 (0%)	50	49

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	162	ASN

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	249/249 (100%)	237 (95%)	12 (5%)	35	32

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LEU
1	A	35	GLU
1	A	51	TRP
1	A	74	LYS
1	A	80	PRO
1	A	159	GLN
1	A	166	ARG
1	A	171	LEU
1	A	195	ASN
1	A	219	ASN
1	A	260	LYS
1	A	279	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	24	ASN
1	A	87	ASN
1	A	195	ASN
1	A	208	ASN
1	A	220	ASN
1	A	231	HIS
1	A	255	GLN
1	A	292	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

1 ligand is 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	1	1,3	49,50,50	5.32	24 (48%)	46,82,82	1.42	6 (13%)

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	1	1,3	-	0/14/114/114	0/0/8/8

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	HEM	C3D-C4D	-21.97	1.39	1.44
2	A	1	HEM	C2D-C1D	-20.65	1.39	1.44
2	A	1	HEM	C2B-C1B	-17.32	1.40	1.44
2	A	1	HEM	C4C-NC	-3.96	1.32	1.38
2	A	1	HEM	CHA-C4D	3.35	1.40	1.35
2	A	1	HEM	CHB-C1B	3.29	1.40	1.35
2	A	1	HEM	C3B-C4B	-3.28	1.40	1.44
2	A	1	HEM	C1A-C2A	-3.22	1.38	1.43
2	A	1	HEM	FE-NA	3.08	2.05	1.92
2	A	1	HEM	C1B-NB	-3.02	1.33	1.39
2	A	1	HEM	CBB-CAB	2.67	1.44	1.28
2	A	1	HEM	C1C-NC	-2.53	1.34	1.38
2	A	1	HEM	FE-NB	2.48	2.06	1.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	HEM	C4D-ND	-2.47	1.34	1.39
2	A	1	HEM	FE-ND	2.46	2.06	1.97
2	A	1	HEM	CHD-C4C	2.41	1.40	1.36
2	A	1	HEM	CBC-CAC	2.34	1.42	1.28
2	A	1	HEM	C3D-C2D	-2.24	1.39	1.43
2	A	1	HEM	C4B-NB	-2.23	1.32	1.37
2	A	1	HEM	C3B-C2B	-2.23	1.39	1.43
2	A	1	HEM	O2A-CGA	-2.22	1.22	1.30
2	A	1	HEM	CHC-C1C	2.13	1.40	1.36
2	A	1	HEM	CMC-C2C	2.11	1.54	1.47
2	A	1	HEM	CMB-C2B	2.02	1.53	1.47

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	HEM	C3B-C4B-NB	-3.98	111.15	114.00
2	A	1	HEM	CHC-C1C-NC	-2.61	122.47	124.73
2	A	1	HEM	C3A-C4A-NA	2.49	111.29	109.41
2	A	1	HEM	CMB-C2B-C3B	2.27	131.51	126.16
2	A	1	HEM	CMA-C3A-C4A	-2.15	125.31	128.62
2	A	1	HEM	CMA-C3A-C2A	2.04	128.78	124.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	291/291 (100%)	2.02	128 (43%) ⓘ ⓘ	10, 22, 38, 50	0

All (128) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	89	PHE	5.4
1	A	223	TRP	5.0
1	A	74	LYS	4.8
1	A	73	PHE	4.7
1	A	83	ALA	4.6
1	A	39	TYR	4.6
1	A	7	VAL	4.5
1	A	182	LEU	4.5
1	A	38	ASN	4.4
1	A	142	GLY	4.2
1	A	141	ASN	4.2
1	A	226	LYS	4.2
1	A	171	LEU	4.2
1	A	252	ALA	4.0
1	A	233	PRO	3.9
1	A	138	THR	3.8
1	A	187	TYR	3.8
1	A	53	ILE	3.7
1	A	253	ASN	3.7
1	A	218	ALA	3.6
1	A	245	LEU	3.6
1	A	45	VAL	3.6
1	A	183	LYS	3.4
1	A	244	TYR	3.4
1	A	63	THR	3.4
1	A	5	VAL	3.4
1	A	169	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	36	TYR	3.3
1	A	78	ASN	3.3
1	A	219	ASN	3.3
1	A	71	TYR	3.3
1	A	60	HIS	3.2
1	A	4	LEU	3.2
1	A	35	GLU	3.2
1	A	274	ILE	3.2
1	A	153	TYR	3.2
1	A	161	LEU	3.2
1	A	168	VAL	3.1
1	A	37	ASP	3.1
1	A	124	ILE	3.1
1	A	269	LEU	3.1
1	A	191	TRP	3.1
1	A	16	TYR	3.1
1	A	174	ALA	3.0
1	A	147	ALA	3.0
1	A	186	GLY	3.0
1	A	236	TYR	3.0
1	A	251	TYR	2.9
1	A	9	SER	2.9
1	A	96	HIS	2.9
1	A	152	GLY	2.8
1	A	85	LEU	2.8
1	A	240	GLN	2.8
1	A	198	PHE	2.8
1	A	213	LEU	2.8
1	A	115	ALA	2.8
1	A	127	ARG	2.8
1	A	262	PHE	2.7
1	A	247	ILE	2.7
1	A	266	PHE	2.7
1	A	160	ARG	2.7
1	A	42	TYR	2.7
1	A	276	PHE	2.7
1	A	175	HIS	2.7
1	A	90	LYS	2.6
1	A	97	LYS	2.6
1	A	80	PRO	2.6
1	A	207	LEU	2.6
1	A	33	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	10	VAL	2.6
1	A	212	LYS	2.6
1	A	81	SER	2.6
1	A	57	TRP	2.6
1	A	109	SER	2.6
1	A	49	LEU	2.6
1	A	283	PRO	2.5
1	A	279	ASP	2.5
1	A	159	GLN	2.5
1	A	25	ALA	2.5
1	A	79	ASP	2.5
1	A	202	PHE	2.5
1	A	21	LYS	2.4
1	A	195	ASN	2.4
1	A	61	ASP	2.4
1	A	197	VAL	2.4
1	A	132	ASP	2.4
1	A	211	TRP	2.4
1	A	210	ASP	2.4
1	A	230	MET	2.4
1	A	104	SER	2.3
1	A	237	SER	2.3
1	A	64	GLY	2.3
1	A	30	LEU	2.3
1	A	282	SER	2.3
1	A	75	LYS	2.3
1	A	114	THR	2.3
1	A	65	GLY	2.3
1	A	68	GLY	2.3
1	A	113	VAL	2.3
1	A	46	LEU	2.2
1	A	77	PHE	2.2
1	A	137	THR	2.2
1	A	180	THR	2.2
1	A	185	SER	2.2
1	A	44	PRO	2.2
1	A	47	VAL	2.2
1	A	51	TRP	2.2
1	A	82	ASN	2.2
1	A	94	PRO	2.2
1	A	144	LEU	2.1
1	A	248	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	120	GLN	2.1
1	A	206	LEU	2.1
1	A	26	ILE	2.1
1	A	56	THR	2.1
1	A	146	ASP	2.1
1	A	121	GLY	2.1
1	A	135	GLU	2.1
1	A	158	PHE	2.1
1	A	62	ASN	2.0
1	A	28	LEU	2.0
1	A	87	ASN	2.0
1	A	288	THR	2.0
1	A	264	LYS	2.0
1	A	255	GLN	2.0
1	A	203	TYR	2.0
1	A	177	LEU	2.0
1	A	232	LEU	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	HEM	A	1	43/43	0.26	0.05	7,15,18,29	0

6.5 Other polymers ⓘ

There are no such residues in this entry.