



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 10:28 AM GMT

PDB ID : 1A2F
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>

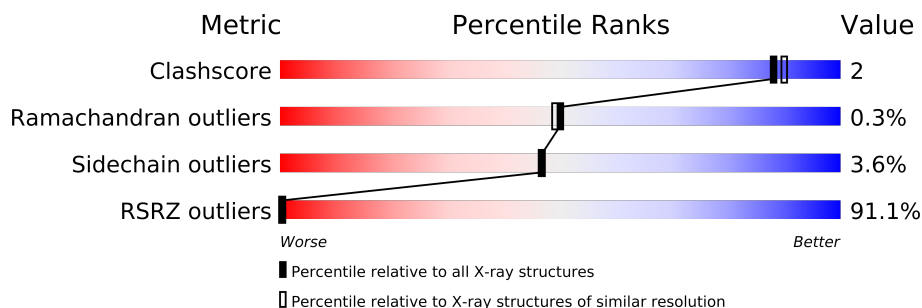
The following versions of software and data (see [references](#)) were used in the production of this report:

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 515 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
1	A	291	Total	C	H	N	O	S	0	0	0
			2866	1502	515	393	451	5			

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

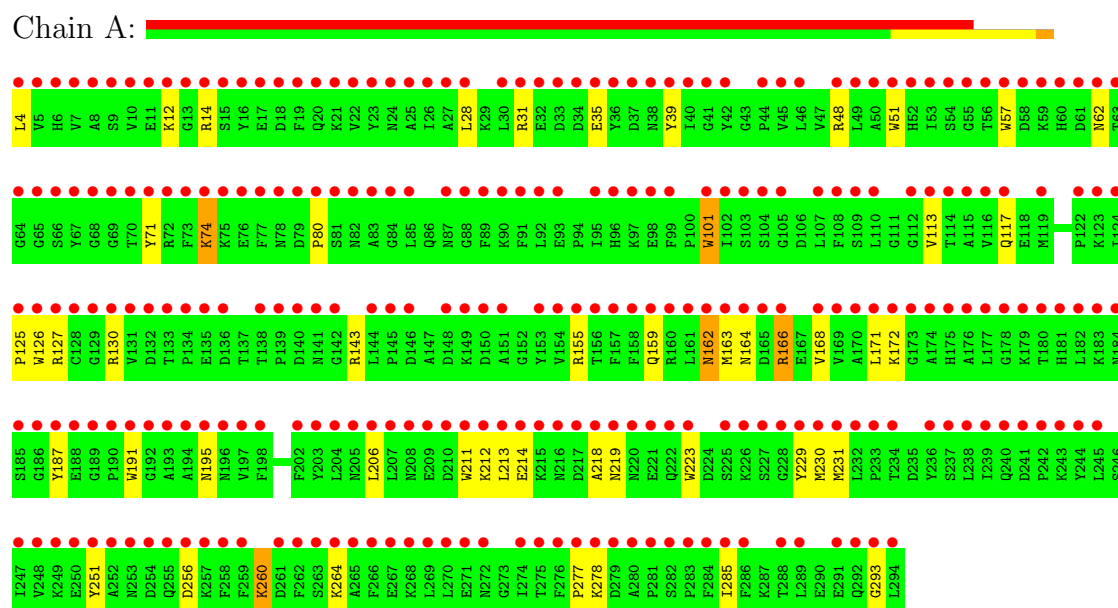
- Molecule 3 is water.

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 ($RSRZ > 2$). 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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	103.80Å 73.50Å 44.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	5.00 – 2.10 14.92 – 1.91	Depositor EDS
% Data completeness (in resolution range)	(Not available) (5.00-2.10) 79.0 (14.92-1.91)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.58 (at 1.91Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.184 , (Not available) 0.486 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	20.2	Xtriage
Anisotropy	0.644	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 25.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	2 of 21478 reflections (0.009%)	Xtriage
F_o, F_c correlation	0.62	EDS
Total number of atoms	3016	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.28% 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	0.86	0/2417	1.58	40/3271 (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	-12.81	113.89	120.30
1	A	51	TRP	CD1-CG-CD2	9.44	113.85	106.30
1	A	31	ARG	NE-CZ-NH1	8.96	124.78	120.30
1	A	51	TRP	CE2-CD2-CG	-8.24	100.71	107.30
1	A	191	TRP	CE2-CD2-CG	-8.17	100.77	107.30
1	A	101	TRP	CD1-CG-CD2	8.02	112.72	106.30
1	A	143	ARG	NE-CZ-NH1	7.75	124.18	120.30
1	A	191	TRP	CD1-CG-CD2	7.70	112.46	106.30
1	A	211	TRP	CD1-CG-CD2	7.46	112.27	106.30
1	A	223	TRP	CD1-CG-CD2	7.46	112.27	106.30
1	A	126	TRP	CD1-CG-CD2	7.27	112.11	106.30
1	A	51	TRP	CB-CG-CD1	-7.24	117.59	127.00
1	A	101	TRP	CE2-CD2-CG	-7.17	101.56	107.30
1	A	127	ARG	NE-CZ-NH2	-7.10	116.75	120.30
1	A	57	TRP	CD1-CG-CD2	6.83	111.76	106.30
1	A	223	TRP	CE2-CD2-CG	-6.81	101.85	107.30
1	A	48	ARG	NE-CZ-NH1	6.67	123.64	120.30
1	A	51	TRP	CG-CD2-CE3	6.62	139.86	133.90
1	A	211	TRP	CE2-CD2-CG	-6.60	102.02	107.30
1	A	51	TRP	CG-CD1-NE1	-6.52	103.58	110.10
1	A	229	TYR	CB-CG-CD2	-6.47	117.12	121.00
1	A	57	TRP	CE2-CD2-CG	-6.46	102.13	107.30
1	A	127	ARG	NE-CZ-NH1	6.33	123.47	120.30
1	A	126	TRP	CE2-CD2-CG	-6.24	102.31	107.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	278	LYS	CA-CB-CG	-6.16	99.84	113.40
1	A	162	ASN	CA-C-N	-5.99	104.03	117.20
1	A	251	TYR	CB-CG-CD2	-5.84	117.49	121.00
1	A	101	TRP	CG-CD1-NE1	-5.78	104.32	110.10
1	A	187	TYR	CB-CG-CD2	-5.77	117.54	121.00
1	A	155	ARG	NE-CZ-NH2	-5.71	117.44	120.30
1	A	230	MET	CA-CB-CG	5.70	122.99	113.30
1	A	163	MET	CG-SD-CE	-5.55	91.31	100.20
1	A	71	TYR	CB-CG-CD2	-5.49	117.70	121.00
1	A	277	PRO	CA-C-N	5.42	129.12	117.20
1	A	166	ARG	NE-CZ-NH2	-5.25	117.68	120.30
1	A	191	TRP	CB-CG-CD1	-5.24	120.19	127.00
1	A	39	TYR	CB-CG-CD2	-5.22	117.87	121.00
1	A	101	TRP	CG-CD2-CE3	5.16	138.55	133.90
1	A	230	MET	CG-SD-CE	-5.09	92.06	100.20
1	A	101	TRP	CB-CG-CD1	-5.08	120.39	127.00

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	2351	515	1718	11	17
2	A	43	0	30	0	0
3	A	107	0	0	2	11
All	All	2501	515	1748	11	17

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 2.

All (11) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:168:VAL:O	1:A:172:LYS:HG2	1.98	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:206:LEU:HD13	1:A:231:MET:SD	2.38	0.62
1:A:74:LYS:HD2	1:A:74:LYS:H	1.74	0.52
1:A:130:ARG:NE	3:A:326:HOH:O	2.43	0.51
1:A:256:ASP:O	1:A:260:LYS:HD2	2.17	0.44
1:A:164:ASN:O	1:A:168:VAL:HG23	2.17	0.44
1:A:218:ALA:O	1:A:219:ASN:HB2	2.18	0.44
1:A:125:PRO:HG3	1:A:285:ILE:HD11	2.01	0.42
1:A:113:VAL:O	1:A:117:GLN:HG3	2.20	0.41
1:A:4:LEU:HB2	1:A:62:ASN:HB3	2.02	0.41
1:A:130:ARG:CZ	3:A:326:HOH:O	2.69	0.40

All (17) 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:212:LYS:CG	3:A:372:HOH:O[4_4610]	1.70	0.50
1:A:212:LYS:NZ	3:A:374:HOH:O[4_4610]	1.70	0.50
1:A:212:LYS:CD	3:A:372:HOH:O[4_4610]	1.74	0.46
1:A:14:ARG:NH2	1:A:213:LEU:C[4_5610]	1.81	0.39
1:A:264:LYS:NZ	3:A:389:HOH:O[3_559]	1.83	0.37
1:A:14:ARG:NH2	1:A:213:LEU:O[4_5610]	1.86	0.34
1:A:212:LYS:CE	3:A:374:HOH:O[4_4610]	1.86	0.34
1:A:12:LYS:CB	1:A:214:GLU:OE2[4_5610]	1.87	0.33
1:A:214:GLU:OE2	3:A:374:HOH:O[4_4610]	1.89	0.31
1:A:212:LYS:CE	3:A:372:HOH:O[4_4610]	1.97	0.23
1:A:14:ARG:NH2	1:A:214:GLU:N[4_5610]	2.02	0.18
1:A:214:GLU:CG	3:A:373:HOH:O[4_4610]	2.05	0.15
1:A:101:TRP:CB	1:A:213:LEU:O[4_5610]	2.07	0.13
1:A:12:LYS:N	1:A:214:GLU:OE2[4_5610]	2.15	0.05
1:A:214:GLU:CB	3:A:373:HOH:O[4_4610]	2.17	0.03
1:A:213:LEU:O	3:A:373:HOH:O[4_4610]	2.18	0.02
1:A:293:GLY:O	3:A:330:HOH:O[3_549]	2.18	0.02

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%)	282 (98%)	6 (2%)	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%)	240 (96%)	9 (4%)	47 46

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LEU
1	A	35	GLU
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	260	LYS

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	240	GLN
1	A	255	GLN

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Mol	Chain	Res	Type
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	6.24	25 (51%)	46,82,82	1.34	5 (10%)

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 (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	HEM	C2D-C1D	-25.67	1.38	1.44
2	A	1	HEM	C3D-C4D	-24.52	1.38	1.44
2	A	1	HEM	C2B-C1B	-21.35	1.39	1.44
2	A	1	HEM	C3B-C4B	-4.49	1.39	1.44
2	A	1	HEM	C4C-NC	-3.37	1.33	1.38
2	A	1	HEM	CHB-C1B	3.35	1.40	1.35
2	A	1	HEM	C1A-C2A	-3.30	1.37	1.43
2	A	1	HEM	C4D-ND	-3.12	1.33	1.39
2	A	1	HEM	FE-ND	3.06	2.09	1.97
2	A	1	HEM	CBC-CAC	3.06	1.46	1.28
2	A	1	HEM	CHA-C4D	2.76	1.39	1.35
2	A	1	HEM	FE-NA	2.67	2.03	1.92
2	A	1	HEM	C3B-C2B	-2.60	1.39	1.43
2	A	1	HEM	CHD-C4C	2.54	1.40	1.36
2	A	1	HEM	CHC-C1C	2.49	1.40	1.36
2	A	1	HEM	CBB-CAB	2.47	1.43	1.28
2	A	1	HEM	C3D-C2D	-2.46	1.39	1.43
2	A	1	HEM	C1B-NB	-2.41	1.34	1.39
2	A	1	HEM	CMC-C2C	2.40	1.54	1.47
2	A	1	HEM	C1C-NC	-2.33	1.34	1.38
2	A	1	HEM	FE-NB	2.22	2.05	1.97
2	A	1	HEM	C4A-C3A	-2.16	1.37	1.40
2	A	1	HEM	C3C-C2C	-2.12	1.40	1.43
2	A	1	HEM	CMD-C2D	2.09	1.53	1.47
2	A	1	HEM	FE-NC	2.01	2.05	1.97

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	HEM	C3B-C4B-NB	-4.12	111.05	114.00
2	A	1	HEM	CHD-C4C-NC	-2.45	122.60	124.73
2	A	1	HEM	CMB-C2B-C3B	2.21	131.37	126.16
2	A	1	HEM	CHC-C1C-NC	-2.19	122.83	124.73
2	A	1	HEM	C3A-C4A-NA	2.17	111.05	109.41

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%)	3.87	265 (91%) 0 0	10, 20, 35, 45	0

All (265) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	138	THR	13.1
1	A	171	LEU	12.1
1	A	79	ASP	8.1
1	A	22	VAL	7.9
1	A	73	PHE	7.7
1	A	223	TRP	7.5
1	A	25	ALA	7.5
1	A	4	LEU	7.3
1	A	53	ILE	7.3
1	A	5	VAL	7.2
1	A	211	TRP	7.1
1	A	64	GLY	7.1
1	A	10	VAL	7.0
1	A	38	ASN	7.0
1	A	251	TYR	6.7
1	A	77	PHE	6.6
1	A	57	TRP	6.5
1	A	213	LEU	6.5
1	A	294	LEU	6.5
1	A	36	TYR	6.5
1	A	71	TYR	6.4
1	A	277	PRO	6.4
1	A	228	GLY	6.4
1	A	156	THR	6.4
1	A	276	PHE	6.4
1	A	8	ALA	6.3
1	A	124	ILE	6.3

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Mol	Chain	Res	Type	RSRZ
1	A	16	TYR	6.2
1	A	206	LEU	6.1
1	A	275	THR	6.0
1	A	42	TYR	6.0
1	A	46	LEU	6.0
1	A	187	TYR	6.0
1	A	63	THR	5.9
1	A	160	ARG	5.9
1	A	75	LYS	5.9
1	A	266	PHE	5.8
1	A	169	VAL	5.7
1	A	269	LEU	5.7
1	A	174	ALA	5.7
1	A	282	SER	5.7
1	A	134	PRO	5.7
1	A	30	LEU	5.7
1	A	231	MET	5.6
1	A	127	ARG	5.6
1	A	12	LYS	5.6
1	A	202	PHE	5.6
1	A	90	LYS	5.5
1	A	67	TYR	5.5
1	A	92	LEU	5.5
1	A	255	GLN	5.5
1	A	131	VAL	5.4
1	A	272	ASN	5.4
1	A	39	TYR	5.3
1	A	89	PHE	5.3
1	A	85	LEU	5.3
1	A	78	ASN	5.3
1	A	286	PHE	5.2
1	A	191	TRP	5.2
1	A	203	TYR	5.2
1	A	254	ASP	5.2
1	A	60	HIS	5.2
1	A	244	TYR	5.1
1	A	9	SER	5.1
1	A	182	LEU	5.1
1	A	262	PHE	5.1
1	A	109	SER	5.1
1	A	265	ALA	5.0
1	A	258	PHE	5.0

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Mol	Chain	Res	Type	RSRZ
1	A	207	LEU	4.9
1	A	26	ILE	4.9
1	A	230	MET	4.9
1	A	219	ASN	4.9
1	A	145	PRO	4.8
1	A	49	LEU	4.8
1	A	245	LEU	4.8
1	A	139	PRO	4.7
1	A	270	LEU	4.7
1	A	153	TYR	4.7
1	A	136	ASP	4.7
1	A	68	GLY	4.7
1	A	229	TYR	4.7
1	A	14	ARG	4.6
1	A	128	CYS	4.6
1	A	133	THR	4.6
1	A	239	ILE	4.5
1	A	233	PRO	4.5
1	A	242	PRO	4.5
1	A	241	ASP	4.5
1	A	225	SER	4.4
1	A	283	PRO	4.4
1	A	65	GLY	4.4
1	A	236	TYR	4.4
1	A	102	ILE	4.4
1	A	93	GLU	4.4
1	A	248	VAL	4.4
1	A	72	ARG	4.3
1	A	74	LYS	4.3
1	A	97	LYS	4.3
1	A	218	ALA	4.3
1	A	52	HIS	4.3
1	A	198	PHE	4.3
1	A	125	PRO	4.3
1	A	104	SER	4.2
1	A	154	VAL	4.2
1	A	81	SER	4.2
1	A	61	ASP	4.2
1	A	51	TRP	4.1
1	A	161	LEU	4.1
1	A	101	TRP	4.1
1	A	28	LEU	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	274	ILE	4.1
1	A	7	VAL	4.1
1	A	95	ILE	4.0
1	A	205	ASN	4.0
1	A	163	MET	4.0
1	A	141	ASN	4.0
1	A	45	VAL	4.0
1	A	80	PRO	4.0
1	A	288	THR	4.0
1	A	278	LYS	4.0
1	A	226	LYS	4.0
1	A	193	ALA	3.9
1	A	62	ASN	3.9
1	A	35	GLU	3.9
1	A	41	GLY	3.9
1	A	204	LEU	3.9
1	A	44	PRO	3.9
1	A	113	VAL	3.9
1	A	99	PHE	3.9
1	A	238	LEU	3.9
1	A	279	ASP	3.9
1	A	96	HIS	3.8
1	A	116	VAL	3.8
1	A	144	LEU	3.8
1	A	249	LYS	3.8
1	A	108	PHE	3.8
1	A	165	ASP	3.8
1	A	150	ASP	3.7
1	A	13	GLY	3.7
1	A	189	GLY	3.7
1	A	264	LYS	3.7
1	A	23	TYR	3.6
1	A	54	SER	3.6
1	A	183	LYS	3.6
1	A	126	TRP	3.6
1	A	105	GLY	3.6
1	A	34	ASP	3.6
1	A	48	ARG	3.5
1	A	33	ASP	3.5
1	A	180	THR	3.5
1	A	289	LEU	3.5
1	A	234	THR	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	177	LEU	3.5
1	A	196	ASN	3.5
1	A	6	HIS	3.5
1	A	214	GLU	3.5
1	A	56	THR	3.4
1	A	140	ASP	3.4
1	A	55	GLY	3.4
1	A	155	ARG	3.4
1	A	168	VAL	3.3
1	A	115	ALA	3.3
1	A	240	GLN	3.3
1	A	257	LYS	3.3
1	A	291	GLU	3.3
1	A	142	GLY	3.2
1	A	149	LYS	3.2
1	A	292	GLN	3.2
1	A	19	PHE	3.2
1	A	285	ILE	3.2
1	A	263	SER	3.2
1	A	31	ARG	3.2
1	A	252	ALA	3.2
1	A	32	GLU	3.1
1	A	173	GLY	3.1
1	A	17	GLU	3.1
1	A	21	LYS	3.1
1	A	220	ASN	3.1
1	A	253	ASN	3.1
1	A	268	LYS	3.0
1	A	119	MET	3.0
1	A	159	GLN	3.0
1	A	237	SER	3.0
1	A	247	ILE	3.0
1	A	87	ASN	2.9
1	A	162	ASN	2.9
1	A	11	GLU	2.9
1	A	190	PRO	2.9
1	A	117	GLN	2.9
1	A	175	HIS	2.9
1	A	107	LEU	2.9
1	A	197	VAL	2.9
1	A	212	LYS	2.9
1	A	83	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	91	PHE	2.9
1	A	209	GLU	2.9
1	A	24	ASN	2.9
1	A	210	ASP	2.8
1	A	129	GLY	2.8
1	A	123	LYS	2.8
1	A	259	PHE	2.8
1	A	76	GLU	2.8
1	A	208	ASN	2.8
1	A	170	ALA	2.8
1	A	132	ASP	2.8
1	A	146	ASP	2.8
1	A	110	LEU	2.8
1	A	66	SER	2.8
1	A	166	ARG	2.8
1	A	188	GLU	2.8
1	A	221	GLU	2.8
1	A	130	ARG	2.7
1	A	179	LYS	2.7
1	A	151	ALA	2.7
1	A	216	ASN	2.7
1	A	157	PHE	2.7
1	A	82	ASN	2.7
1	A	58	ASP	2.7
1	A	217	ASP	2.7
1	A	280	ALA	2.6
1	A	227	SER	2.6
1	A	184	ASN	2.6
1	A	222	GLN	2.6
1	A	37	ASP	2.6
1	A	215	LYS	2.6
1	A	284	PHE	2.6
1	A	27	ALA	2.6
1	A	70	THR	2.6
1	A	243	LYS	2.6
1	A	181	HIS	2.5
1	A	158	PHE	2.5
1	A	88	GLY	2.5
1	A	232	LEU	2.4
1	A	281	PRO	2.4
1	A	271	GLU	2.4
1	A	69	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	50	ALA	2.4
1	A	186	GLY	2.4
1	A	172	LYS	2.4
1	A	103	SER	2.4
1	A	18	ASP	2.3
1	A	122	PRO	2.3
1	A	185	SER	2.3
1	A	40	ILE	2.3
1	A	176	ALA	2.2
1	A	112	GLY	2.2
1	A	256	ASP	2.2
1	A	250	GLU	2.2
1	A	261	ASP	2.2
1	A	293	GLY	2.2
1	A	114	THR	2.2
1	A	15	SER	2.2
1	A	98	GLU	2.2
1	A	59	LYS	2.2
1	A	164	ASN	2.2
1	A	195	ASN	2.1
1	A	84	GLY	2.1
1	A	135	GLU	2.1
1	A	194	ALA	2.1
1	A	20	GLN	2.1
1	A	267	GLU	2.1
1	A	178	GLY	2.1
1	A	192	GLY	2.0
1	A	148	ASP	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	0.32	-0.27	10,14,18,23	0

6.5 Other polymers ⓘ

There are no such residues in this entry.