WORLDWIDE PDB
PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Feb 12, 2017 – 08:23 pm GMT

PDB ID	:	2EU7
Title	:	Crystal structure of D1A mutant of nitrophorin 2 complexed with ammonia
Authors	:	Weichsel, A.; Montfort, W.R.
Deposited on	:	2005-10-28
Resolution	:	1.20 Å(reported)

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

|		
MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.
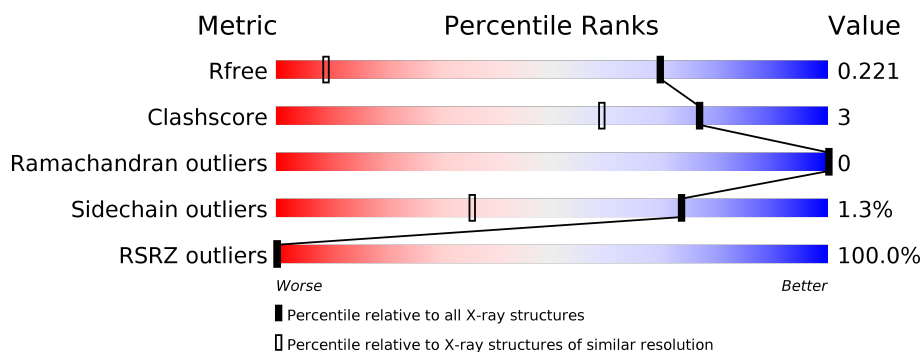
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	1131 (1.24-1.16)
Clashscore	112137	1201 (1.24-1.16)
Ramachandran outliers	110173	1148 (1.24-1.16)
Sidechain outliers	110143	1147 (1.24-1.16)
RSRZ outliers	101464	1132 (1.24-1.16)

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 <=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	X	179	100% 91% 8% •

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 1706 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 Nitrophorin 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	X	179	Total	C	N	O	S	0	4	0
			1424	892	234	290	8			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	1	ALA	ASP	ENGINEERED	UNP Q26241

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).

HEM

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	X	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is AMMONIA (three-letter code: NH3) (formula: H_3N).

NH3

NH_3N
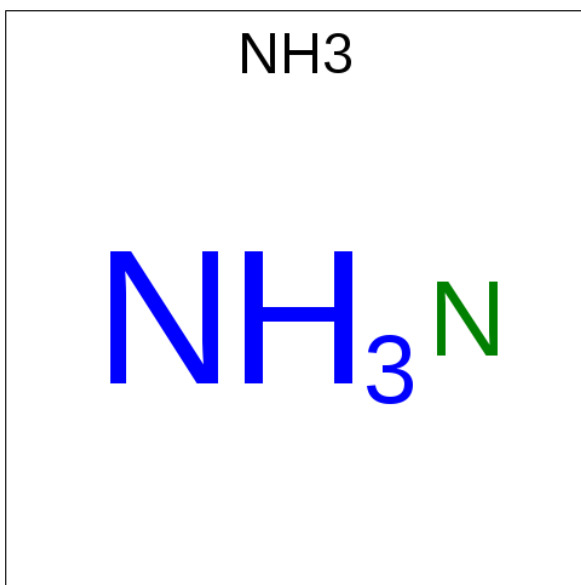
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	X	1	Total 1	N 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	X	238	Total 238	O 238	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 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: Nitrophorin 2
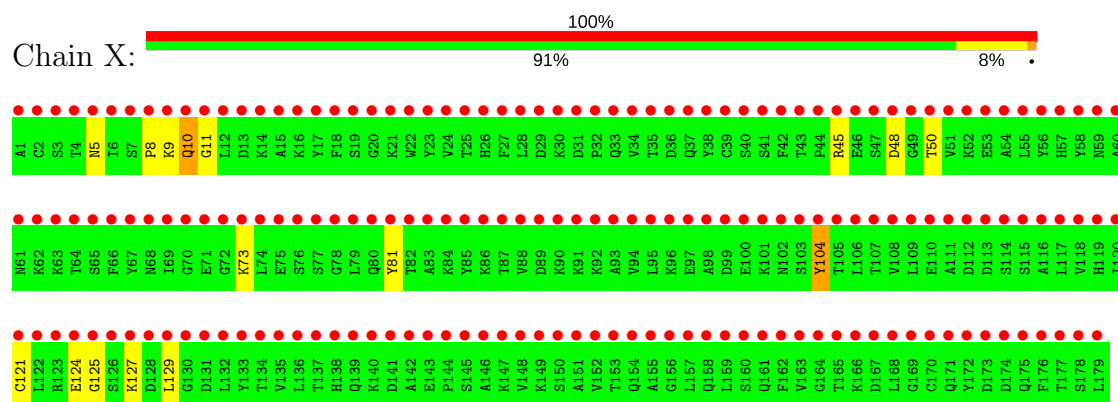
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	39.77Å 125.30Å 34.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 1.20 5.99 – 1.20	Depositor EDS
% Data completeness (in resolution range)	88.3 (6.00-1.20) 88.3 (5.99-1.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$< I/\sigma(I) >$ [1]	2.76 (at 1.20Å)	Xtriage
Refinement program	REFMAC 5.2.0003	Depositor
R, R_{free}	0.177 , 0.215 0.183 , 0.221	Depositor DCC
R_{free} test set	2426 reflections (5.38%)	DCC
Wilson B-factor (Å^2)	10.8	Xtriage
Anisotropy	0.182	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< |L| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	1706	wwPDB-VP
Average B, all atoms (Å^2)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 41.89 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.2104e-04.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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, NH3

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	X	0.95	1/1450 (0.1%)	1.00	3/1955 (0.2%)

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	X	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	X	104	TYR	CD1-CE1	-6.48	1.29	1.39

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	45	ARG	NE-CZ-NH2	-6.94	116.83	120.30
1	X	48	ASP	CB-CG-OD2	5.29	123.06	118.30
1	X	81	TYR	CB-CG-CD1	5.09	124.06	121.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	X	125	GLY	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	X	1424	0	1379	9	0
2	X	43	0	30	1	0
3	X	1	0	0	0	0
4	X	238	0	0	2	0
All	All	1706	0	1409	10	0

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 3.

All (10) 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:X:8:PRO:HB2	4:X:413:HOH:O	1.75	0.85
1:X:10:GLN:HE21	1:X:10:GLN:HA	1.51	0.75
1:X:124:GLU:HB3	1:X:129:LEU:HD11	1.72	0.70
2:X:201:HEM:HMC2	2:X:201:HEM:HBC2	1.82	0.60
1:X:50:THR:OG1	1:X:73:LYS:NZ	2.41	0.54
1:X:9:LYS:NZ	4:X:397:HOH:O	2.43	0.52
1:X:10:GLN:NE2	1:X:10:GLN:HA	2.26	0.48
1:X:10:GLN:HE21	1:X:11:GLY:H	1.62	0.46
1:X:5:ASN:N	1:X:5:ASN:OD1	2.49	0.44
1:X:104:TYR:HA	1:X:121[B]:CYS:O	2.19	0.43

There are no symmetry-related clashes.

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	X	181/179 (101%)	180 (99%)	1 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	X	159/155 (103%)	157 (99%)	2 (1%)	73	35

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	X	10	GLN
1	X	127	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	X	10	GLN
1	X	80	GLN
1	X	102	ASN
1	X	171	GLN
1	X	175	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)

Of 2 ligands modelled in this entry, 1 is modelled with single atom - leaving 1 for Mogul analysis.

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	X	201	1,3	28,50,50	1.87	6 (21%)	17,82,82	1.99	6 (35%)

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	X	201	1,3	-	0/6/54/54	0/0/8/8

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	X	201	HEM	C3C-C2C	-6.27	1.32	1.40
2	X	201	HEM	C3B-C2B	-4.71	1.34	1.40
2	X	201	HEM	C2A-C3A	-2.05	1.31	1.37
2	X	201	HEM	C1B-NB	2.15	1.39	1.36
2	X	201	HEM	C3D-C2D	2.16	1.44	1.37
2	X	201	HEM	CMB-C2B	2.25	1.56	1.51

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	X	201	HEM	CMA-C3A-C4A	-3.08	123.73	128.46
2	X	201	HEM	CBD-CAD-C3D	-2.30	108.08	112.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	X	201	HEM	CMC-C2C-C3C	2.03	128.66	124.89
2	X	201	HEM	CMA-C3A-C2A	2.11	128.92	124.94
2	X	201	HEM	CMB-C2B-C3B	3.04	130.53	124.89
2	X	201	HEM	C4C-C3C-C2C	4.76	110.22	106.90

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	X	201	HEM	1	0

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	X	179/179 (100%)	5.15	179 (100%)	0	0	7, 14, 29, 38	0

All (179) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	X	125	GLY	10.0
1	X	170[A]	CYS	9.8
1	X	129	LEU	9.5
1	X	126	SER	9.4
1	X	121[A]	CYS	9.4
1	X	6	ILE	8.9
1	X	4	THR	8.8
1	X	2[A]	CYS	8.6
1	X	1	ALA	8.5
1	X	34	VAL	8.3
1	X	39[A]	CYS	8.1
1	X	58	TYR	7.9
1	X	55	LEU	7.8
1	X	74	LEU	7.6
1	X	38	TYR	7.6
1	X	179	LEU	7.5
1	X	81	TYR	7.5
1	X	120	ILE	7.4
1	X	66	PHE	7.3
1	X	79	LEU	7.3
1	X	104	TYR	7.2
1	X	12	LEU	7.2
1	X	22	TRP	7.1
1	X	109	LEU	7.1
1	X	67	TYR	7.0
1	X	18	PHE	6.9
1	X	136	LEU	6.9

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Mol	Chain	Res	Type	RSRZ
1	X	127	LYS	6.8
1	X	85	TYR	6.7
1	X	135	VAL	6.7
1	X	95	LEU	6.7
1	X	23	TYR	6.7
1	X	56	TYR	6.7
1	X	122	LEU	6.7
1	X	69	ILE	6.6
1	X	132	LEU	6.6
1	X	157	LEU	6.6
1	X	51	VAL	6.6
1	X	168	LEU	6.6
1	X	162	PHE	6.5
1	X	176	PHE	6.5
1	X	24	VAL	6.5
1	X	163	VAL	6.5
1	X	172	TYR	6.5
1	X	77	SER	6.5
1	X	106	LEU	6.5
1	X	50	THR	6.5
1	X	128	ASP	6.5
1	X	118	VAL	6.5
1	X	88	VAL	6.4
1	X	117	LEU	6.4
1	X	28	LEU	6.3
1	X	133	TYR	6.3
1	X	42	PHE	6.3
1	X	130	GLY	6.2
1	X	94	VAL	6.1
1	X	152	VAL	6.1
1	X	17	TYR	6.0
1	X	148	VAL	5.9
1	X	3	SER	5.9
1	X	15	ALA	5.9
1	X	124	GLU	5.9
1	X	27	PHE	5.9
1	X	108	VAL	5.8
1	X	8	PRO	5.8
1	X	107	THR	5.7
1	X	25	THR	5.7
1	X	5	ASN	5.6
1	X	105	THR	5.6

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Mol	Chain	Res	Type	RSRZ
1	X	134	THR	5.6
1	X	159	LEU	5.5
1	X	49	GLY	5.5
1	X	72	GLY	5.5
1	X	64	THR	5.4
1	X	137	THR	5.4
1	X	93	ALA	5.3
1	X	32	PRO	5.3
1	X	35	THR	5.2
1	X	151	ALA	5.1
1	X	43	THR	5.1
1	X	165	THR	5.1
1	X	146	ALA	5.1
1	X	78	GLY	5.0
1	X	142	ALA	5.0
1	X	54	ALA	5.0
1	X	87	THR	4.9
1	X	111	ALA	4.9
1	X	116	ALA	4.9
1	X	164	GLY	4.8
1	X	177	THR	4.8
1	X	60	ALA	4.8
1	X	61	ASN	4.8
1	X	153	THR	4.7
1	X	82	THR	4.7
1	X	44	PRO	4.7
1	X	83	ALA	4.7
1	X	98	ALA	4.7
1	X	155	ALA	4.7
1	X	57	HIS	4.6
1	X	119	HIS	4.6
1	X	11	GLY	4.6
1	X	36	ASP	4.6
1	X	70	GLY	4.5
1	X	102	ASN	4.5
1	X	91	LYS	4.5
1	X	144	PRO	4.4
1	X	29	ASP	4.3
1	X	59	ASN	4.3
1	X	150	SER	4.2
1	X	7	SER	4.2
1	X	73	LYS	4.1

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Mol	Chain	Res	Type	RSRZ
1	X	19	SER	4.0
1	X	169	GLY	4.0
1	X	123	ARG	4.0
1	X	10	GLN	4.0
1	X	37	GLN	4.0
1	X	48	ASP	4.0
1	X	103	SER	4.0
1	X	16	LYS	4.0
1	X	47	SER	4.0
1	X	76	SER	4.0
1	X	41	SER	3.9
1	X	26	HIS	3.9
1	X	178	SER	3.9
1	X	156	GLY	3.9
1	X	80	GLN	3.8
1	X	115	SER	3.8
1	X	139	GLN	3.8
1	X	171	GLN	3.8
1	X	143	GLU	3.8
1	X	174	ASP	3.7
1	X	86	LYS	3.7
1	X	166	LYS	3.7
1	X	68	ASN	3.7
1	X	20	GLY	3.7
1	X	114	SER	3.7
1	X	99	ASP	3.7
1	X	45	ARG	3.7
1	X	30	LYS	3.6
1	X	52	LYS	3.6
1	X	31	ASP	3.6
1	X	40	SER	3.6
1	X	145	SER	3.6
1	X	167	ASP	3.5
1	X	138	HIS	3.5
1	X	13	ASP	3.5
1	X	89	ASP	3.5
1	X	62	LYS	3.5
1	X	113	ASP	3.5
1	X	175	GLN	3.5
1	X	131	ASP	3.5
1	X	84	LYS	3.4
1	X	65	SER	3.4

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Mol	Chain	Res	Type	RSRZ
1	X	90	LYS	3.4
1	X	149	LYS	3.3
1	X	112	ASP	3.3
1	X	71	GLU	3.3
1	X	9	LYS	3.3
1	X	33	GLN	3.3
1	X	154	GLN	3.3
1	X	96	LYS	3.2
1	X	141	ASP	3.2
1	X	63	LYS	3.2
1	X	75	GLU	3.2
1	X	173	ASP	3.2
1	X	140	LYS	3.1
1	X	147	LYS	3.1
1	X	160	SER	3.1
1	X	100	GLU	3.1
1	X	101	LYS	3.1
1	X	158	GLN	3.0
1	X	92	LYS	3.0
1	X	97	GLU	3.0
1	X	14	LYS	2.9
1	X	46	GLU	2.9
1	X	161	GLN	2.8
1	X	110	GLU	2.7
1	X	53	GLU	2.7
1	X	21	LYS	2.5

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	X	201	43/43	0.94	0.29	0.03	8,10,21,29	0
3	NH3	X	202	1/1	0.92	0.53	-	13,13,13,13	0

6.5 Other polymers ⓘ

There are no such residues in this entry.