Full wwPDB X-ray Structure Validation Report (i)

Nov 7, 2023 – 01:23 PM JST

PDB ID	:	4XNB
Title	:	Crystal Structure of E. coli Aminopeptidase N in complex with L-Beta Homophenylalanine
Authors	:	Addlagatta, A.; Gumpena, R.
Deposited on	:	2015-01-15
Resolution	:	1.95 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

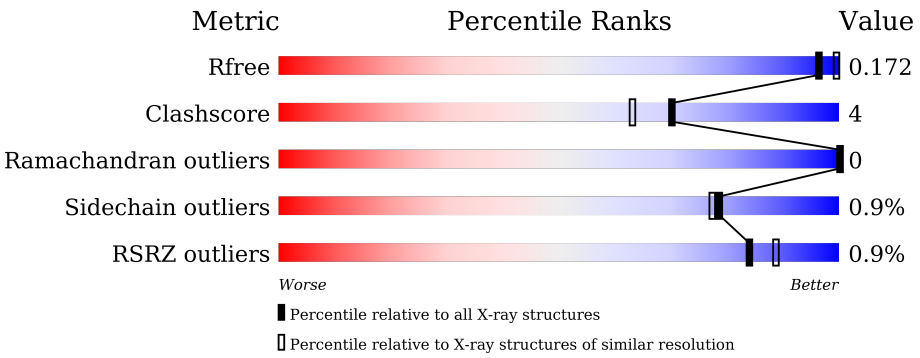
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

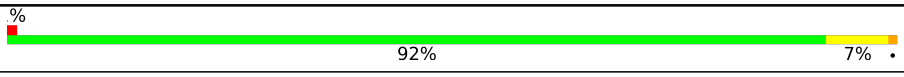
The reported resolution of this entry is 1.95 Å.

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}	130704	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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	A	866	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	GOL	A	917	-	X	-	-
5	GOL	A	928	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	MLI	A	936	-	X	-	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 8371 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.

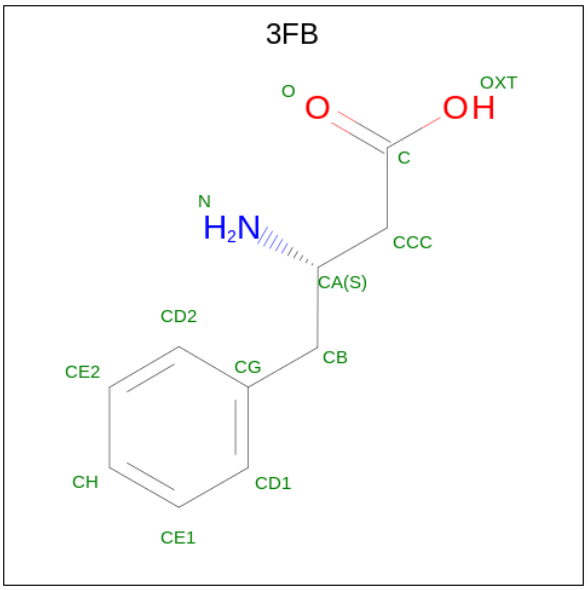
- Molecule 1 is a protein called Aminopeptidase N.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	866	7115	4512	1221	1354	28	0	32	0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
2	A	1	1	1	0	0

- Molecule 3 is (3S)-3-AMINO-4-PHENYLBUTANOIC ACID (three-letter code: 3FB) (formula: $C_{10}H_{13}NO_2$).

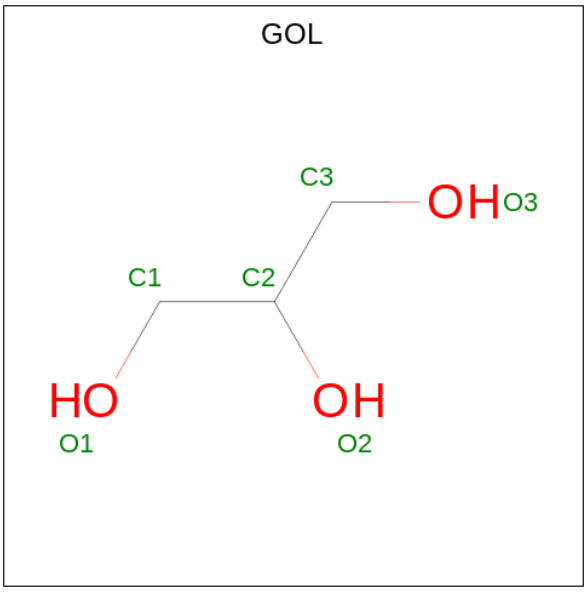


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	13	10	1	2	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
4	A	8	8	8	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	A	1	6	3	3	0	0
			Total	C	O		
5	A	1	6	3	3	0	0
			Total	C	O		
5	A	1	6	3	3	0	0
			Total	C	O		
5	A	1	6	3	3	0	0
			Total	C	O		
5	A	1	6	3	3	0	0
			Total	C	O		
5	A	1	6	3	3	0	0
			Total	C	O		
5	A	1	6	3	3	0	0
			Total	C	O		
5	A	1	6	3	3	0	0
			Total	C	O		
5	A	1	6	3	3	0	0
			Total	C	O		
5	A	1	12	6	6	0	1

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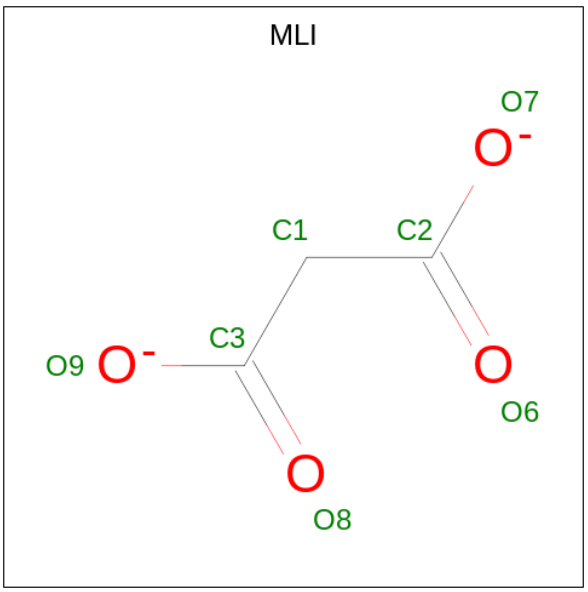
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O			
5	A	1	6	3	3		0	0
5	A	1	6	3	3		0	0
5	A	1	6	3	3		0	0
5	A	1	6	3	3		0	0
5	A	1	6	3	3		0	0
5	A	1	6	3	3		0	0
5	A	1	6	3	3		0	0
5	A	1	6	3	3		0	0
5	A	1	6	3	3		0	0
5	A	1	6	3	3		0	0
5	A	1	6	3	3		0	0
5	A	1	6	3	3		0	0

- Molecule 6 is MALONATE ION (three-letter code: MLI) (formula: $C_3H_2O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
6	A	1	14	6	8	0	1
			Total	C	O		
6	A	1	7	3	4	0	0
			Total	C	O		
6	A	1	7	3	4	0	0
			Total	C	O		
6	A	1	7	3	4	0	0

- Molecule 7 is water.

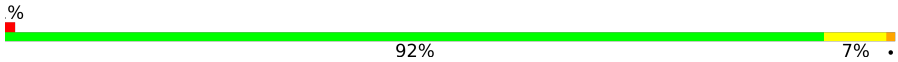
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	1061	1061	1061	0	0

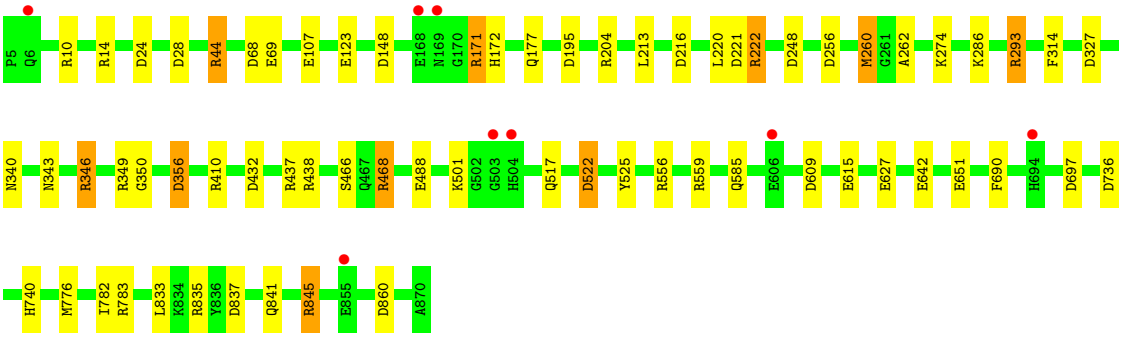
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Aminopeptidase N

Chain A:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	120.19Å 120.19Å 169.92Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.16 – 1.95 19.16 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.4 (19.16-1.95) 99.6 (19.16-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$< I/\sigma(I) >$ [1]	3.25 (at 1.96Å)	Xtriage
Refinement program	REFMAC 5.8.0107	Depositor
R, R_{free}	0.132 , 0.165 0.145 , 0.172	Depositor DCC
R_{free} test set	5141 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	21.9	Xtriage
Anisotropy	0.024	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.42 , 56.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.52$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	0.010 for -h,-k,l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	8371	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.75% of the height of the origin peak. No significant pseudotranslation is detected.*

[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: 3FB, NA, ZN, MLI, GOL

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	1.06	9/7367 (0.1%)	1.08	47/9998 (0.5%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	585	GLN	CG-CD	7.54	1.68	1.51
1	A	466[A]	SER	CB-OG	-6.94	1.33	1.42
1	A	466[B]	SER	CB-OG	-6.94	1.33	1.42
1	A	349	ARG	CD-NE	-5.87	1.36	1.46
1	A	346[A]	ARG	CZ-NH1	5.58	1.40	1.33
1	A	346[B]	ARG	CZ-NH1	5.58	1.40	1.33
1	A	69	GLU	CD-OE1	-5.25	1.19	1.25
1	A	123	GLU	CG-CD	5.09	1.59	1.51
1	A	525	TYR	CB-CG	5.08	1.59	1.51

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	349	ARG	NE-CZ-NH2	-13.64	113.48	120.30
1	A	346[A]	ARG	NE-CZ-NH2	-11.68	114.46	120.30
1	A	346[B]	ARG	NE-CZ-NH2	-11.68	114.46	120.30
1	A	346[A]	ARG	NE-CZ-NH1	11.28	125.94	120.30
1	A	346[B]	ARG	NE-CZ-NH1	11.28	125.94	120.30
1	A	171[A]	ARG	NE-CZ-NH1	9.83	125.22	120.30
1	A	171[B]	ARG	NE-CZ-NH1	9.83	125.22	120.30
1	A	221	ASP	CB-CG-OD1	9.72	127.05	118.30
1	A	438	ARG	NE-CZ-NH1	9.13	124.87	120.30
1	A	349	ARG	NE-CZ-NH1	8.79	124.69	120.30
1	A	783	ARG	NE-CZ-NH2	-8.28	116.16	120.30
1	A	556	ARG	NE-CZ-NH1	8.13	124.37	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	437	ARG	NE-CZ-NH1	7.71	124.15	120.30
1	A	256	ASP	CB-CG-OD1	7.60	125.14	118.30
1	A	248	ASP	CB-CG-OD1	-7.34	111.69	118.30
1	A	783	ARG	NE-CZ-NH1	7.29	123.94	120.30
1	A	845	ARG	NE-CZ-NH1	7.08	123.84	120.30
1	A	222	ARG	NE-CZ-NH2	-7.02	116.79	120.30
1	A	736	ASP	CB-CG-OD1	6.98	124.58	118.30
1	A	432	ASP	CB-CG-OD1	6.89	124.50	118.30
1	A	171[A]	ARG	NE-CZ-NH2	-6.87	116.87	120.30
1	A	171[B]	ARG	NE-CZ-NH2	-6.87	116.87	120.30
1	A	522[A]	ASP	CB-CG-OD1	6.66	124.30	118.30
1	A	522[B]	ASP	CB-CG-OD1	6.66	124.30	118.30
1	A	837	ASP	CB-CG-OD1	6.46	124.12	118.30
1	A	44	ARG	NE-CZ-NH1	-6.45	117.08	120.30
1	A	438	ARG	NE-CZ-NH2	-6.26	117.17	120.30
1	A	148[A]	ASP	CB-CG-OD1	-6.23	112.69	118.30
1	A	148[B]	ASP	CB-CG-OD1	-6.23	112.69	118.30
1	A	346[A]	ARG	CD-NE-CZ	5.99	131.98	123.60
1	A	346[B]	ARG	CD-NE-CZ	5.99	131.98	123.60
1	A	356	ASP	CB-CG-OD1	5.97	123.67	118.30
1	A	410	ARG	NE-CZ-NH1	5.81	123.21	120.30
1	A	204	ARG	NE-CZ-NH2	-5.79	117.41	120.30
1	A	609	ASP	CB-CG-OD1	5.74	123.46	118.30
1	A	68	ASP	CB-CG-OD1	5.49	123.24	118.30
1	A	10	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	A	216	ASP	CB-CG-OD1	5.43	123.19	118.30
1	A	468[A]	ARG	NE-CZ-NH2	5.40	123.00	120.30
1	A	468[B]	ARG	NE-CZ-NH2	5.40	123.00	120.30
1	A	213	LEU	CA-CB-CG	5.33	127.56	115.30
1	A	697	ASP	CB-CG-OD1	5.26	123.04	118.30
1	A	609	ASP	CB-CG-OD2	-5.11	113.70	118.30
1	A	293	ARG	NE-CZ-NH1	5.06	122.83	120.30
1	A	256	ASP	CB-CG-OD2	-5.03	113.77	118.30
1	A	835	ARG	NE-CZ-NH1	-5.03	117.78	120.30
1	A	222	ARG	NE-CZ-NH1	5.02	122.81	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7115	0	7007	41	0
2	A	1	0	0	0	0
3	A	13	0	12	2	0
4	A	8	0	0	0	0
5	A	138	0	183	21	0
6	A	35	0	10	0	0
7	A	1061	0	0	29	2
All	All	8371	0	7212	52	2

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 4.

All (52) 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:346[B]:ARG:NH2	1:A:615:GLU:OE1	1.86	1.08
1:A:346[B]:ARG:NE	7:A:1001:HOH:O	2.16	0.77
1:A:642:GLU:OE1	5:A:928:GOL:H31	1.85	0.77
1:A:177:GLN:HG2	7:A:1848:HOH:O	1.84	0.76
1:A:343:ASN:OD1	7:A:1001:HOH:O	2.04	0.76
1:A:222:ARG:HD2	7:A:1522:HOH:O	1.86	0.74
1:A:642:GLU:HB2	5:A:928:GOL:H2	1.73	0.70
1:A:346[B]:ARG:HB3	5:A:920[B]:GOL:H11	1.80	0.63
5:A:916:GOL:H32	7:A:1364:HOH:O	1.97	0.63
1:A:28:ASP:OD1	1:A:171[A]:ARG:NH2	2.32	0.63
5:A:932:GOL:O1	7:A:1002:HOH:O	2.16	0.60
5:A:930:GOL:H2	7:A:1121:HOH:O	2.01	0.59
1:A:642:GLU:OE1	5:A:928:GOL:C3	2.51	0.58
1:A:651:GLU:OE1	7:A:1003:HOH:O	2.16	0.58
1:A:24[B]:ASP:OD2	7:A:1004:HOH:O	2.18	0.57
1:A:222:ARG:CD	7:A:1522:HOH:O	2.48	0.57
1:A:177:GLN:HG2	7:A:1823:HOH:O	2.03	0.57
1:A:627:GLU:HG3	7:A:1183:HOH:O	2.07	0.55
1:A:24[B]:ASP:CG	7:A:1004:HOH:O	2.45	0.54
1:A:14[B]:ARG:NH2	7:A:1028:HOH:O	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:340:ASN:OD1	5:A:932:GOL:H31	2.08	0.54
1:A:346[B]:ARG:CZ	7:A:1001:HOH:O	2.50	0.54
1:A:346[B]:ARG:NH2	7:A:1001:HOH:O	2.42	0.53
1:A:845:ARG:NH1	7:A:1009:HOH:O	2.25	0.52
1:A:350:GLY:C	7:A:1183:HOH:O	2.47	0.51
1:A:501:LYS:HD2	1:A:522[A]:ASP:OD2	2.09	0.51
5:A:915:GOL:C2	7:A:1058:HOH:O	2.59	0.50
1:A:107[A]:GLU:OE2	7:A:1005:HOH:O	2.20	0.50
1:A:274:LYS:HD3	7:A:1073:HOH:O	2.11	0.49
5:A:913:GOL:HO3	5:A:913:GOL:HO1	0.55	0.49
5:A:920[B]:GOL:C1	7:A:1082:HOH:O	2.60	0.49
1:A:642:GLU:CD	5:A:928:GOL:H31	2.33	0.49
5:A:915:GOL:H2	7:A:1058:HOH:O	2.13	0.47
1:A:468[A]:ARG:NH1	7:A:1050:HOH:O	2.48	0.47
1:A:740:HIS:HD2	7:A:1855:HOH:O	1.97	0.47
1:A:262:ALA:O	3:A:902:3FB:HC2	2.15	0.47
1:A:833:LEU:O	1:A:841:GLN:HG2	2.15	0.47
1:A:293:ARG:HD3	5:A:932:GOL:C1	2.45	0.46
1:A:488[B]:GLU:OE1	1:A:559:ARG:HG2	2.16	0.46
5:A:928:GOL:O1	7:A:1006:HOH:O	2.20	0.45
1:A:260:MET:HG3	3:A:902:3FB:CH	2.47	0.45
1:A:195:ASP:HB3	1:A:220:LEU:HG	1.99	0.45
1:A:44:ARG:HH11	1:A:44:ARG:HD3	1.60	0.44
1:A:690:PHE:CE2	5:A:926:GOL:H32	2.53	0.44
1:A:776:MET:O	1:A:782:ILE:HD11	2.18	0.44
5:A:913:GOL:O1	5:A:913:GOL:O3	1.99	0.42
1:A:314:PHE:CE2	5:A:911:GOL:H31	2.55	0.42
1:A:468[B]:ARG:NE	7:A:1059:HOH:O	2.51	0.41
5:A:920[B]:GOL:H12	7:A:1082:HOH:O	2.19	0.41
5:A:923:GOL:H11	7:A:1794:HOH:O	2.21	0.41
1:A:642:GLU:OE1	5:A:928:GOL:H12	2.20	0.40
1:A:488[B]:GLU:OE2	1:A:559:ARG:NH2	2.53	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	Interatomic distance (Å)	Clash overlap (Å)
7:A:1309:HOH:O	7:A:1309:HOH:O[6_554]	1.98	0.22
7:A:1852:HOH:O	7:A:1913:HOH:O[2_545]	2.14	0.06

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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	896/866 (104%)	884 (99%)	12 (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	A	773/741 (104%)	766 (99%)	7 (1%)	78 77

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	172	HIS
1	A	260	MET
1	A	286	LYS
1	A	327	ASP
1	A	356	ASP
1	A	517	GLN
1	A	860	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 38 ligands modelled in this entry, 9 are monoatomic - leaving 29 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	$\#\|Z\| > 2$
5	GOL	A	917	-	5,5,5	2.41	3 (60%)	5,5,5	2.44	2 (40%)
6	MLI	A	933[B]	-	6,6,6	1.26	0	7,7,7	1.20	1 (14%)
6	MLI	A	935	-	6,6,6	1.67	2 (33%)	7,7,7	2.01	2 (28%)
5	GOL	A	914	-	5,5,5	1.60	2 (40%)	5,5,5	1.42	1 (20%)
5	GOL	A	924	-	5,5,5	1.17	0	5,5,5	1.42	1 (20%)
5	GOL	A	920[A]	-	5,5,5	0.53	0	5,5,5	0.43	0
5	GOL	A	912	-	5,5,5	0.71	0	5,5,5	1.04	0
5	GOL	A	918	-	5,5,5	0.46	0	5,5,5	0.59	0
5	GOL	A	922	-	5,5,5	0.73	0	5,5,5	0.91	0
5	GOL	A	931	-	5,5,5	0.44	0	5,5,5	0.46	0
5	GOL	A	920[B]	-	5,5,5	0.43	0	5,5,5	1.38	1 (20%)
5	GOL	A	916	-	5,5,5	0.93	0	5,5,5	1.75	1 (20%)
5	GOL	A	928	-	5,5,5	0.79	0	5,5,5	1.41	1 (20%)
5	GOL	A	911	-	5,5,5	0.81	0	5,5,5	1.58	1 (20%)
5	GOL	A	925	-	5,5,5	0.29	0	5,5,5	1.15	1 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	GOL	A	915	-	5,5,5	0.89	0	5,5,5	1.21	1 (20%)
5	GOL	A	930	-	5,5,5	0.34	0	5,5,5	0.69	0
5	GOL	A	926	-	5,5,5	1.26	0	5,5,5	2.85	3 (60%)
5	GOL	A	932	-	5,5,5	0.54	0	5,5,5	0.93	0
5	GOL	A	927	-	5,5,5	0.32	0	5,5,5	1.09	0
5	GOL	A	921	-	5,5,5	0.67	0	5,5,5	0.42	0
5	GOL	A	923	-	5,5,5	1.04	0	5,5,5	1.44	1 (20%)
5	GOL	A	919	-	5,5,5	0.48	0	5,5,5	0.67	0
5	GOL	A	929	-	5,5,5	0.42	0	5,5,5	0.67	0
6	MLI	A	934	-	6,6,6	1.12	0	7,7,7	2.14	4 (57%)
6	MLI	A	933[A]	-	6,6,6	1.26	0	7,7,7	1.26	1 (14%)
3	3FB	A	902	2	13,13,13	0.79	1 (7%)	12,16,16	1.81	5 (41%)
6	MLI	A	936	-	6,6,6	1.46	1 (16%)	7,7,7	1.38	2 (28%)
5	GOL	A	913	-	5,5,5	0.32	0	5,5,5	0.48	0

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
5	GOL	A	917	-	-	2/4/4/4	-
6	MLI	A	933[B]	-	-	0/4/4/4	-
6	MLI	A	935	-	-	0/4/4/4	-
5	GOL	A	914	-	-	1/4/4/4	-
5	GOL	A	924	-	-	2/4/4/4	-
5	GOL	A	920[A]	-	-	4/4/4/4	-
5	GOL	A	912	-	-	2/4/4/4	-
5	GOL	A	918	-	-	2/4/4/4	-
5	GOL	A	922	-	-	2/4/4/4	-
5	GOL	A	931	-	-	0/4/4/4	-
5	GOL	A	920[B]	-	-	4/4/4/4	-
5	GOL	A	916	-	-	4/4/4/4	-
5	GOL	A	928	-	-	1/4/4/4	-
5	GOL	A	911	-	-	3/4/4/4	-
5	GOL	A	925	-	-	3/4/4/4	-
5	GOL	A	915	-	-	2/4/4/4	-
5	GOL	A	930	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	A	926	-	-	2/4/4/4	-
5	GOL	A	932	-	-	4/4/4/4	-
5	GOL	A	927	-	-	1/4/4/4	-
5	GOL	A	921	-	-	3/4/4/4	-
5	GOL	A	923	-	-	2/4/4/4	-
5	GOL	A	919	-	-	4/4/4/4	-
5	GOL	A	929	-	-	2/4/4/4	-
6	MLI	A	934	-	-	1/4/4/4	-
6	MLI	A	933[A]	-	-	2/4/4/4	-
3	3FB	A	902	2	-	7/8/8/8	0/1/1/1
6	MLI	A	936	-	-	4/4/4/4	-
5	GOL	A	913	-	-	4/4/4/4	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	917	GOL	O3-C3	4.11	1.59	1.42
6	A	935	MLI	C1-C3	-2.70	1.47	1.51
6	A	936	MLI	C1-C3	2.62	1.55	1.51
5	A	914	GOL	O2-C2	2.48	1.50	1.43
5	A	917	GOL	O2-C2	2.33	1.50	1.43
5	A	917	GOL	C3-C2	2.30	1.61	1.51
5	A	914	GOL	O3-C3	2.25	1.51	1.42
3	A	902	3FB	CB-CA	2.16	1.57	1.53
6	A	935	MLI	O6-C2	2.01	1.28	1.22

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	926	GOL	O1-C1-C2	-4.39	89.16	110.20
5	A	917	GOL	O2-C2-C3	3.93	126.44	109.12
6	A	935	MLI	O8-C3-C1	-3.62	111.50	122.08
5	A	917	GOL	O3-C3-C2	3.45	126.74	110.20
6	A	934	MLI	O6-C2-C1	-3.23	112.64	122.08
5	A	926	GOL	O2-C2-C1	3.09	122.75	109.12
5	A	911	GOL	O3-C3-C2	3.01	124.64	110.20
5	A	916	GOL	O3-C3-C2	2.97	124.46	110.20
6	A	934	MLI	O9-C3-C1	2.81	123.51	114.54
3	A	902	3FB	CE1-CD1-CG	-2.78	116.37	120.63
5	A	926	GOL	O3-C3-C2	-2.75	97.00	110.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	914	GOL	O2-C2-C3	2.71	121.05	109.12
3	A	902	3FB	CH-CE1-CD1	2.71	124.31	120.19
6	A	934	MLI	O8-C3-C1	-2.70	114.19	122.08
3	A	902	3FB	CB-CG-CD1	-2.59	115.76	120.91
6	A	933[A]	MLI	O6-C2-C1	-2.53	114.70	122.08
5	A	925	GOL	O1-C1-C2	-2.49	98.28	110.20
6	A	935	MLI	C3-C1-C2	-2.46	104.25	112.87
6	A	936	MLI	O9-C3-O8	-2.27	117.65	123.30
5	A	920[B]	GOL	O3-C3-C2	-2.27	99.34	110.20
5	A	924	GOL	O2-C2-C3	2.24	118.99	109.12
6	A	933[B]	MLI	O6-C2-C1	-2.21	115.63	122.08
5	A	915	GOL	C3-C2-C1	2.16	120.09	111.70
5	A	928	GOL	C3-C2-C1	2.16	120.09	111.70
3	A	902	3FB	OXT-C-O	-2.12	118.01	123.30
6	A	934	MLI	O7-C2-O6	2.12	128.57	123.30
5	A	923	GOL	C3-C2-C1	-2.07	103.64	111.70
6	A	936	MLI	O9-C3-C1	2.07	121.15	114.54
3	A	902	3FB	CG-CB-CA	2.06	117.17	113.24

There are no chirality outliers.

All (70) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	902	3FB	N-CA-CB-CG
3	A	902	3FB	N-CA-CCC-C
3	A	902	3FB	CB-CA-CCC-C
5	A	911	GOL	C1-C2-C3-O3
5	A	911	GOL	O2-C2-C3-O3
5	A	912	GOL	C1-C2-C3-O3
5	A	912	GOL	O2-C2-C3-O3
5	A	913	GOL	O1-C1-C2-C3
5	A	915	GOL	O1-C1-C2-C3
5	A	916	GOL	O1-C1-C2-C3
5	A	917	GOL	O1-C1-C2-C3
5	A	917	GOL	C1-C2-C3-O3
5	A	919	GOL	C1-C2-C3-O3
5	A	920[A]	GOL	O1-C1-C2-C3
5	A	920[A]	GOL	O2-C2-C3-O3
5	A	920[B]	GOL	C1-C2-C3-O3
5	A	921	GOL	O1-C1-C2-C3
5	A	925	GOL	O1-C1-C2-C3
5	A	926	GOL	O1-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
5	A	930	GOL	C1-C2-C3-O3
5	A	932	GOL	O1-C1-C2-C3
3	A	902	3FB	OXT-C-CCC-CA
5	A	913	GOL	O1-C1-C2-O2
5	A	916	GOL	O1-C1-C2-O2
5	A	916	GOL	O2-C2-C3-O3
5	A	932	GOL	O2-C2-C3-O3
5	A	913	GOL	C1-C2-C3-O3
5	A	916	GOL	C1-C2-C3-O3
5	A	918	GOL	O1-C1-C2-C3
5	A	919	GOL	O1-C1-C2-C3
5	A	920[A]	GOL	C1-C2-C3-O3
5	A	920[B]	GOL	O1-C1-C2-C3
5	A	922	GOL	C1-C2-C3-O3
5	A	929	GOL	C1-C2-C3-O3
5	A	932	GOL	C1-C2-C3-O3
3	A	902	3FB	O-C-CCC-CA
5	A	915	GOL	O1-C1-C2-O2
5	A	919	GOL	O2-C2-C3-O3
5	A	920[B]	GOL	O2-C2-C3-O3
5	A	921	GOL	O1-C1-C2-O2
5	A	922	GOL	O2-C2-C3-O3
5	A	925	GOL	O1-C1-C2-O2
5	A	926	GOL	O1-C1-C2-O2
5	A	930	GOL	O2-C2-C3-O3
5	A	932	GOL	O1-C1-C2-O2
5	A	913	GOL	O2-C2-C3-O3
5	A	920[A]	GOL	O1-C1-C2-O2
5	A	920[B]	GOL	O1-C1-C2-O2
3	A	902	3FB	CA-CB-CG-CD2
3	A	902	3FB	CA-CB-CG-CD1
5	A	924	GOL	C1-C2-C3-O3
5	A	925	GOL	C1-C2-C3-O3
5	A	918	GOL	O1-C1-C2-O2
5	A	923	GOL	O2-C2-C3-O3
5	A	928	GOL	O2-C2-C3-O3
6	A	936	MLI	C3-C1-C2-O6
6	A	936	MLI	C3-C1-C2-O7
6	A	936	MLI	C2-C1-C3-O8
5	A	911	GOL	O1-C1-C2-O2
5	A	929	GOL	O2-C2-C3-O3
5	A	914	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
6	A	933[A]	MLI	C2-C1-C3-O8
6	A	933[A]	MLI	C2-C1-C3-O9
5	A	919	GOL	O1-C1-C2-O2
5	A	927	GOL	O2-C2-C3-O3
6	A	936	MLI	C2-C1-C3-O9
5	A	924	GOL	O2-C2-C3-O3
5	A	921	GOL	C1-C2-C3-O3
5	A	923	GOL	O1-C1-C2-C3
6	A	934	MLI	C3-C1-C2-O6

There are no ring outliers.

11 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	920[B]	GOL	3	0
5	A	916	GOL	1	0
5	A	928	GOL	6	0
5	A	911	GOL	1	0
5	A	915	GOL	2	0
5	A	930	GOL	1	0
5	A	926	GOL	1	0
5	A	932	GOL	3	0
5	A	923	GOL	1	0
3	A	902	3FB	2	0
5	A	913	GOL	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 (i)

6.1 Protein, DNA and RNA chains (i)

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	866/866 (100%)	-0.67	8 (0%) 84 89	13, 21, 35, 65	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	504	HIS	3.8
1	A	169	ASN	3.3
1	A	6	GLN	2.8
1	A	606	GLU	2.7
1	A	503	GLY	2.5
1	A	694	HIS	2.4
1	A	855	GLU	2.4
1	A	168	GLU	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 monosaccharides 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. 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	B-factors(Å^2)	Q<0.9
6	MLI	A	936	7/7	0.73	0.31	63,71,79,92	0
5	GOL	A	931	6/6	0.80	0.28	48,70,75,89	0
5	GOL	A	926	6/6	0.80	0.18	30,35,43,44	0
5	GOL	A	917	6/6	0.81	0.20	31,39,54,57	0
5	GOL	A	928	6/6	0.82	0.31	47,54,58,68	0
5	GOL	A	922	6/6	0.85	0.24	55,66,70,81	0
4	NA	A	909	1/1	0.85	0.12	49,49,49,49	0
5	GOL	A	919	6/6	0.85	0.20	64,69,70,73	0
5	GOL	A	920[A]	6/6	0.85	0.32	67,73,88,89	6
5	GOL	A	920[B]	6/6	0.85	0.32	11,12,13,13	6
5	GOL	A	913	6/6	0.86	0.32	61,71,71,85	0
5	GOL	A	932	6/6	0.87	0.19	43,49,55,74	0
4	NA	A	910	1/1	0.88	0.36	60,60,60,60	0
5	GOL	A	923	6/6	0.89	0.11	34,45,50,51	0
6	MLI	A	935	7/7	0.89	0.25	53,57,66,78	0
5	GOL	A	915	6/6	0.89	0.28	32,34,52,55	0
6	MLI	A	934	7/7	0.90	0.19	42,47,53,76	0
4	NA	A	905	1/1	0.90	0.26	55,55,55,55	0
5	GOL	A	924	6/6	0.90	0.14	34,43,48,49	0
4	NA	A	907	1/1	0.91	0.07	52,52,52,52	0
5	GOL	A	925	6/6	0.91	0.15	43,53,64,79	0
5	GOL	A	916	6/6	0.91	0.28	39,51,59,64	0
5	GOL	A	930	6/6	0.92	0.14	35,49,55,65	0
5	GOL	A	927	6/6	0.92	0.20	54,57,60,60	0
5	GOL	A	921	6/6	0.92	0.10	29,44,44,48	0
5	GOL	A	914	6/6	0.93	0.10	24,30,34,36	0
5	GOL	A	912	6/6	0.93	0.09	31,40,45,45	0
4	NA	A	904	1/1	0.93	0.26	45,45,45,45	0
6	MLI	A	933[B]	7/7	0.95	0.16	32,37,47,49	7
5	GOL	A	911	6/6	0.95	0.10	22,41,45,53	0
5	GOL	A	918	6/6	0.95	0.07	25,42,45,45	0
6	MLI	A	933[A]	7/7	0.95	0.16	27,35,43,46	7
3	3FB	A	902	13/13	0.97	0.06	15,19,21,22	0
5	GOL	A	929	6/6	0.97	0.06	31,36,41,42	0
4	NA	A	903	1/1	0.98	0.03	28,28,28,28	0
4	NA	A	906	1/1	0.99	0.14	35,35,35,35	0
4	NA	A	908	1/1	0.99	0.19	25,25,25,25	0
2	ZN	A	901	1/1	1.00	0.03	15,15,15,15	0

6.5 Other polymers (i)

There are no such residues in this entry.