Full wwPDB X-ray Structure Validation Report (i)

Nov 14, 2023 – 09:49 PM JST

PDB ID	:	6ICA
Title	:	The crystal structure of Legionella pneumophila LapA aminopeptidase
Authors	:	Honghua, G.; Nannan, Z.
Deposited on	:	2018-09-05
Resolution	:	2.19 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:

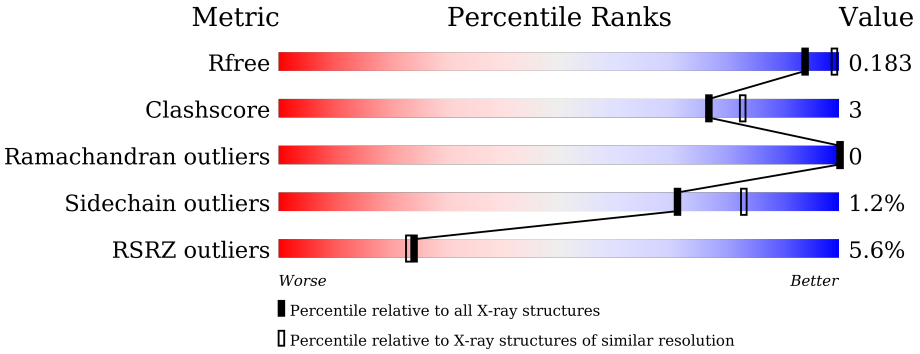
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 2.19 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	430	4% 80% 5% 15%
1	B	430	5% 80% 6% • 14%
1	C	430	6% 84% • 12%

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
2	SO4	A	509	-	-	X	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 9489 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	366	2877	1822	481	560	14	0	1	0
1	B	371	2924	1856	492	562	14	0	1	0
1	C	378	2955	1870	497	574	14	0	1	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	423	LEU	-	expression tag	UNP Q5ZRR6
A	424	GLU	-	expression tag	UNP Q5ZRR6
A	425	HIS	-	expression tag	UNP Q5ZRR6
A	426	HIS	-	expression tag	UNP Q5ZRR6
A	427	HIS	-	expression tag	UNP Q5ZRR6
A	428	HIS	-	expression tag	UNP Q5ZRR6
A	429	HIS	-	expression tag	UNP Q5ZRR6
A	430	HIS	-	expression tag	UNP Q5ZRR6
B	423	LEU	-	expression tag	UNP Q5ZRR6
B	424	GLU	-	expression tag	UNP Q5ZRR6
B	425	HIS	-	expression tag	UNP Q5ZRR6
B	426	HIS	-	expression tag	UNP Q5ZRR6
B	427	HIS	-	expression tag	UNP Q5ZRR6
B	428	HIS	-	expression tag	UNP Q5ZRR6
B	429	HIS	-	expression tag	UNP Q5ZRR6
B	430	HIS	-	expression tag	UNP Q5ZRR6
C	423	LEU	-	expression tag	UNP Q5ZRR6
C	424	GLU	-	expression tag	UNP Q5ZRR6
C	425	HIS	-	expression tag	UNP Q5ZRR6
C	426	HIS	-	expression tag	UNP Q5ZRR6
C	427	HIS	-	expression tag	UNP Q5ZRR6
C	428	HIS	-	expression tag	UNP Q5ZRR6
C	429	HIS	-	expression tag	UNP Q5ZRR6

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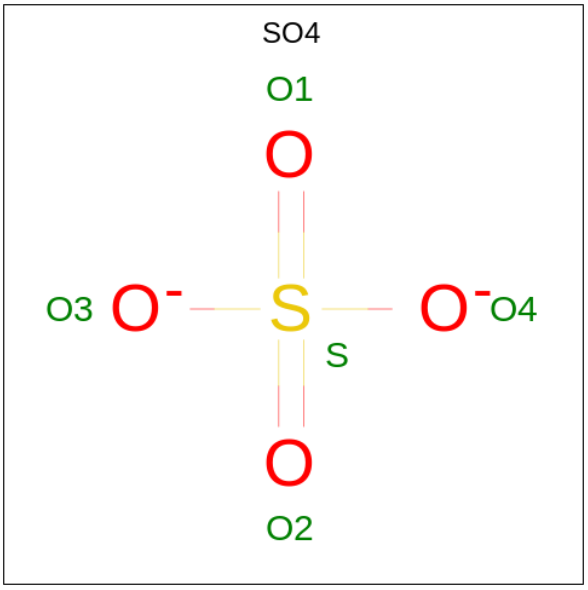
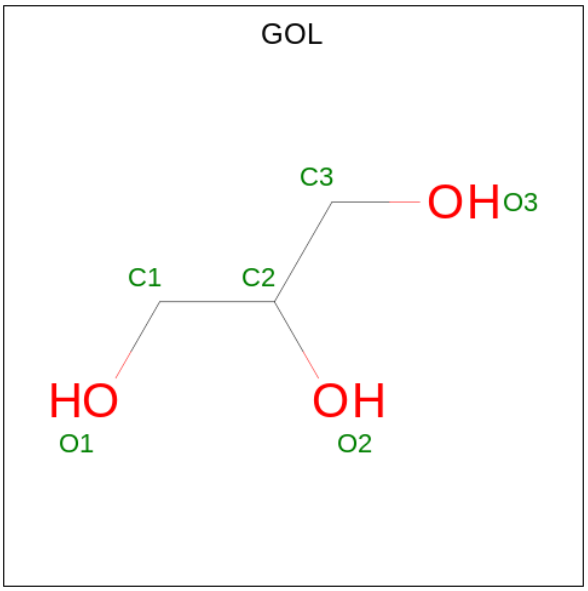
Chain	Residue	Modelled	Actual	Comment	Reference
C	430	HIS	-	expression tag	UNP Q5ZRR6

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	O	S		0	0
			5	4	1			
2	A	1	Total	O	S		0	0
			5	4	1			
2	A	1	Total	O	S		0	0
			5	4	1			
2	B	1	Total	O	S		0	0
			5	4	1			
2	B	1	Total	O	S		0	0
			5	4	1			
2	B	1	Total	O	S		0	0
			5	4	1			
2	B	1	Total	O	S		0	0
			5	4	1			
2	C	1	Total	O	S		0	0
			5	4	1			
2	C	1	Total	O	S		0	0
			5	4	1			

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

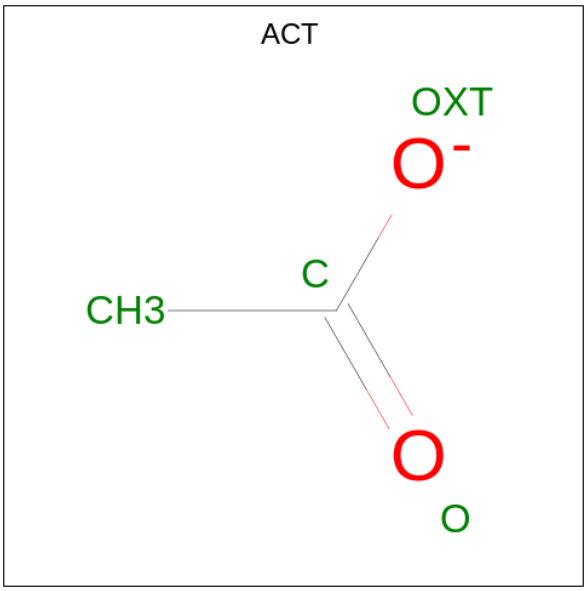


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	6	3	3	0	0
			Total	C	O		
3	A	1	6	3	3	0	0
			Total	C	O		
3	B	1	6	3	3	0	0
			Total	C	O		
3	C	1	6	3	3	0	0
			Total	C	O		
3	C	1	6	3	3	0	0

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
4	A	2	2	2	0	0
			Total	Zn		
4	B	2	2	2	0	0
			Total	Zn		
4	C	2	2	2	0	0

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0

- Molecule 6 is water.

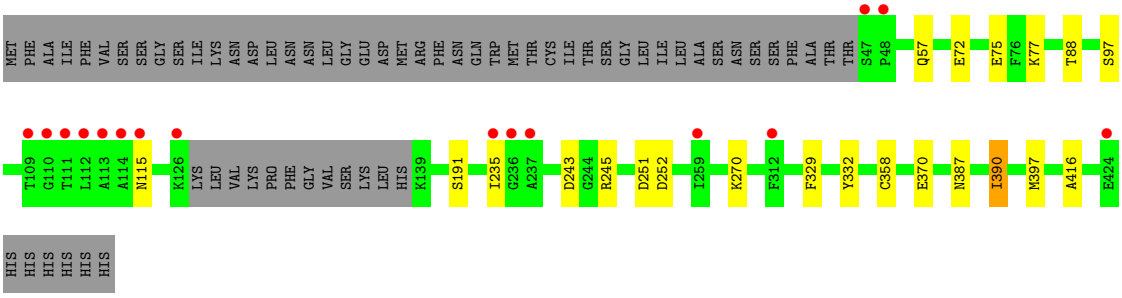
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	225	Total O 225 225	0	0
6	B	206	Total O 206 206	0	0
6	C	213	Total O 213 213	0	0

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.

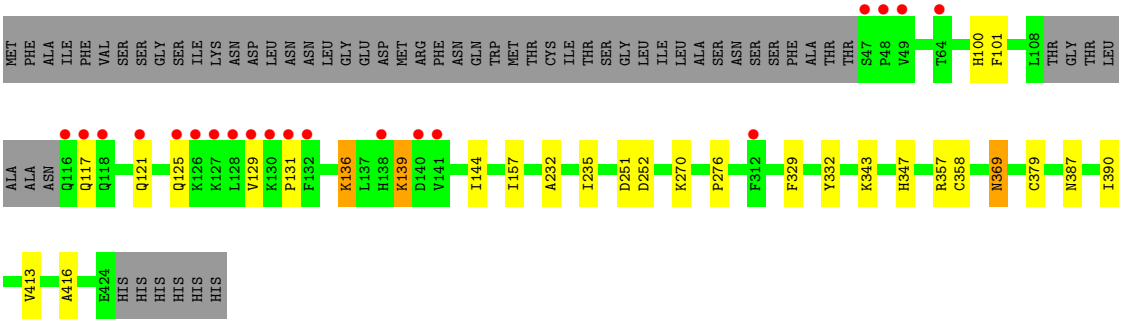
• Molecule 1: Aminopeptidase

Chain A:



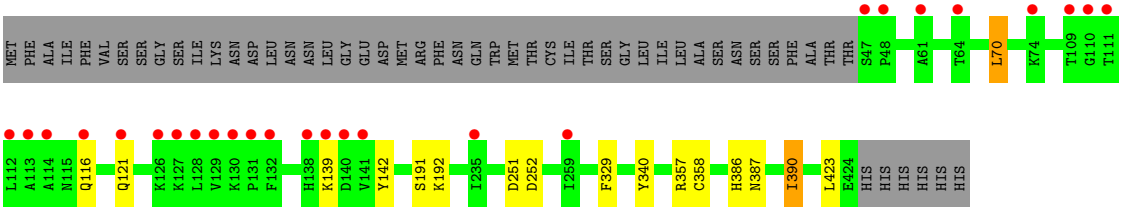
• Molecule 1: Aminopeptidase

Chain B:



• Molecule 1: Aminopeptidase

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	84.42Å 121.91Å 130.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.52 – 2.19 34.52 – 2.19	Depositor EDS
% Data completeness (in resolution range)	99.7 (34.52-2.19) 99.7 (34.52-2.19)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.96 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.143 , 0.183 0.144 , 0.183	Depositor DCC
R_{free} test set	3444 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å^2)	20.3	Xtriage
Anisotropy	0.731	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 55.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	9489	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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: GOL, ACT, ZN, SO4

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	0.42	0/2946	0.54	0/4003
1	B	0.42	0/2996	0.56	0/4068
1	C	0.42	0/3027	0.56	0/4114
All	All	0.42	0/8969	0.55	0/12185

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	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	369	ASN	Sidechain

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	2877	0	2773	15	0
1	B	2924	0	2826	23	0
1	C	2955	0	2844	15	0
2	A	15	0	0	3	0
2	B	20	0	0	0	0
2	C	10	0	0	0	0
3	A	12	0	16	0	0
3	B	6	0	8	0	0
3	C	12	0	16	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
5	A	8	0	6	2	0
6	A	225	0	0	6	0
6	B	206	0	0	0	0
6	C	213	0	0	3	0
All	All	9489	0	8489	52	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 (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:B:357:ARG:HH22	1:C:139:LYS:HE2	1.43	0.84
1:C:121:GLN:NE2	6:C:601:HOH:O	2.12	0.82
1:B:332:TYR:C	1:B:369:ASN:HD22	1.84	0.79
2:A:509:SO4:O3	6:A:601:HOH:O	2.06	0.74
1:B:136:LYS:HD2	1:B:139:LYS:HE2	1.70	0.73
2:A:509:SO4:O2	6:A:602:HOH:O	2.09	0.71
1:C:70:LEU:HD21	1:C:116:GLN:HE21	1.57	0.67
1:A:370:GLU:OE1	6:A:603:HOH:O	2.13	0.66
1:A:245:ARG:NH2	6:A:602:HOH:O	2.27	0.64
1:B:332:TYR:C	1:B:369:ASN:ND2	2.51	0.62
1:B:117:GLN:O	1:B:121:GLN:HG3	2.00	0.61
1:B:357:ARG:HD3	6:C:619:HOH:O	2.00	0.60
1:C:387:ASN:HB3	1:C:390:ILE:HD12	1.83	0.59
1:B:136:LYS:HD2	1:B:139:LYS:CE	2.35	0.56
1:C:329:PHE:CE2	1:C:358:CYS:HB3	2.41	0.55
1:C:70:LEU:HD21	1:C:116:GLN:NE2	2.22	0.55
1:A:332:TYR:H	5:A:506:ACT:H2	1.73	0.54
1:C:387:ASN:HB3	1:C:390:ILE:CD1	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:387:ASN:HB3	1:A:390:ILE:HD13	1.89	0.53
1:C:192:LYS:NZ	6:C:608:HOH:O	2.43	0.51
1:A:235:ILE:HD11	1:A:416:ALA:HB2	1.94	0.50
1:C:70:LEU:CD2	1:C:116:GLN:HE21	2.24	0.49
1:A:88:THR:HG23	6:A:654:HOH:O	2.11	0.49
1:B:136:LYS:HG3	1:C:357:ARG:NH1	2.28	0.48
1:B:136:LYS:HG3	1:C:357:ARG:HH12	1.79	0.48
1:B:235:ILE:HD11	1:B:416:ALA:HB2	1.96	0.48
1:A:72:GLU:HG3	1:A:77:LYS:HG2	1.97	0.46
1:A:75:GLU:OE2	6:A:604:HOH:O	2.21	0.46
1:A:329:PHE:CE2	1:A:358:CYS:HB3	2.50	0.46
1:B:329:PHE:HE1	1:B:379:CYS:HB3	1.81	0.46
1:B:329:PHE:CE2	1:B:358:CYS:HB3	2.51	0.46
1:B:144:ILE:HG21	1:B:347:HIS:ND1	2.31	0.45
1:C:423:LEU:HD23	1:C:423:LEU:HA	1.68	0.45
1:B:232:ALA:HB2	1:B:276:PRO:HG2	2.00	0.44
1:B:387:ASN:O	1:B:390:ILE:HD12	2.19	0.43
1:A:251:ASP:HA	1:A:252:ASP:HA	1.79	0.43
1:B:343:LYS:HE2	1:B:343:LYS:HB3	1.84	0.43
1:C:142:TYR:HB3	1:C:340:TYR:CD1	2.53	0.43
1:A:57:GLN:HE22	1:A:72:GLU:HG3	1.84	0.42
1:A:243:ASP:OD2	5:A:507:ACT:H1	2.19	0.42
1:C:251:ASP:HA	1:C:252:ASP:HA	1.81	0.42
1:A:57:GLN:HE22	1:A:72:GLU:CG	2.33	0.42
1:B:157:ILE:HD11	1:B:413:VAL:HG21	2.02	0.42
1:A:270:LYS:HA	1:A:270:LYS:HD3	1.79	0.42
1:B:136:LYS:HD2	1:B:139:LYS:NZ	2.35	0.42
1:B:329:PHE:CE1	1:B:379:CYS:HB3	2.54	0.42
1:C:142:TYR:HB3	1:C:340:TYR:CG	2.55	0.42
1:B:100:HIS:HB3	1:B:101:PHE:H	1.70	0.41
1:B:270:LYS:HD3	1:B:270:LYS:HA	1.84	0.41
1:B:251:ASP:HA	1:B:252:ASP:HA	1.80	0.41
1:B:129:VAL:O	1:B:131:PRO:HD2	2.20	0.40
1:A:397:MET:HG3	2:A:509:SO4:O4	2.21	0.40

There are no symmetry-related clashes.

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	363/430 (84%)	357 (98%)	6 (2%)	0	100	100
1	B	368/430 (86%)	358 (97%)	10 (3%)	0	100	100
1	C	377/430 (88%)	362 (96%)	15 (4%)	0	100	100
All	All	1108/1290 (86%)	1077 (97%)	31 (3%)	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	315/375 (84%)	311 (99%)	4 (1%)	69	81
1	B	320/375 (85%)	317 (99%)	3 (1%)	78	88
1	C	322/375 (86%)	318 (99%)	4 (1%)	71	83
All	All	957/1125 (85%)	946 (99%)	11 (1%)	71	85

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	97	SER
1	A	115	ASN
1	A	191	SER
1	A	390	ILE
1	B	125	GLN

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Mol	Chain	Res	Type
1	B	136	LYS
1	B	139	LYS
1	C	70	LEU
1	C	191	SER
1	C	386	HIS
1	C	390	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	116	GLN
1	B	369	ASN
1	C	116	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 22 ligands modelled in this entry, 6 are monoatomic - leaving 16 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	$\#\|Z\| > 2$
3	GOL	C	502	-	5,5,5	0.36	0	5,5,5	0.32	0
3	GOL	A	503	-	5,5,5	0.31	0	5,5,5	0.44	0
2	SO4	B	502	-	4,4,4	0.13	0	6,6,6	0.23	0
5	ACT	A	507	-	3,3,3	0.77	0	3,3,3	1.29	0
2	SO4	A	509	-	4,4,4	0.18	0	6,6,6	0.14	0
2	SO4	B	501	-	4,4,4	0.15	0	6,6,6	0.25	0
3	GOL	A	502	-	5,5,5	0.35	0	5,5,5	0.29	0
2	SO4	A	508	-	4,4,4	0.15	0	6,6,6	0.11	0
2	SO4	A	501	-	4,4,4	0.13	0	6,6,6	0.16	0
3	GOL	B	503	-	5,5,5	0.41	0	5,5,5	0.27	0
5	ACT	A	506	-	3,3,3	0.80	0	3,3,3	1.46	0
2	SO4	C	506	-	4,4,4	0.14	0	6,6,6	0.08	0
2	SO4	B	506	-	4,4,4	0.14	0	6,6,6	0.10	0
3	GOL	C	503	-	5,5,5	0.30	0	5,5,5	0.50	0
2	SO4	B	507	-	4,4,4	0.13	0	6,6,6	0.26	0
2	SO4	C	501	-	4,4,4	0.15	0	6,6,6	0.13	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
3	GOL	C	502	-	-	0/4/4/4	-
3	GOL	A	503	-	-	0/4/4/4	-
3	GOL	B	503	-	-	2/4/4/4	-
3	GOL	A	502	-	-	2/4/4/4	-
3	GOL	C	503	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502	GOL	O1-C1-C2-C3
3	B	503	GOL	O1-C1-C2-C3
3	C	503	GOL	O1-C1-C2-C3
3	B	503	GOL	O1-C1-C2-O2
3	C	503	GOL	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
3	A	502	GOL	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	507	ACT	1	0
2	A	509	SO4	3	0
5	A	506	ACT	1	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	366/430 (85%)	-0.04	16 (4%)	34	32	11, 22, 52, 152	0
1	B	371/430 (86%)	0.04	20 (5%)	25	24	11, 22, 66, 145	0
1	C	378/430 (87%)	0.09	26 (6%)	16	15	10, 23, 84, 157	0
All	All	1115/1290 (86%)	0.03	62 (5%)	24	23	10, 22, 67, 157	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	128	LEU	18.1
1	A	112	LEU	17.3
1	A	113	ALA	16.7
1	A	111	THR	15.8
1	C	111	THR	14.4
1	B	131	PRO	12.6
1	C	129	VAL	11.2
1	A	110	GLY	9.6
1	B	128	LEU	9.2
1	B	47	SER	9.2
1	B	132	PHE	8.9
1	C	131	PRO	8.7
1	C	127	LYS	8.4
1	C	47	SER	7.9
1	A	47	SER	7.7
1	B	129	VAL	7.1
1	B	127	LYS	7.0
1	A	114	ALA	6.9
1	B	126	LYS	6.0
1	A	48	PRO	5.3
1	B	118	GLN	5.2
1	C	110	GLY	5.1
1	B	48	PRO	4.9

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Mol	Chain	Res	Type	RSRZ
1	C	130	LYS	4.9
1	A	109	THR	4.3
1	B	130	LYS	4.3
1	C	48	PRO	4.2
1	C	126	LYS	4.2
1	C	114	ALA	4.1
1	B	125	GLN	3.9
1	C	113	ALA	3.9
1	C	109	THR	3.7
1	C	132	PHE	3.6
1	C	141	VAL	3.5
1	C	140	ASP	3.3
1	B	141	VAL	3.2
1	C	139	LYS	3.1
1	B	121	GLN	3.1
1	B	64	THR	3.1
1	C	74	LYS	3.0
1	B	138	HIS	3.0
1	C	138	HIS	3.0
1	A	424	GLU	3.0
1	B	140	ASP	2.9
1	A	115	ASN	2.8
1	B	312	PHE	2.7
1	A	259	ILE	2.6
1	C	112	LEU	2.6
1	B	116	GLN	2.6
1	A	237	ALA	2.5
1	A	312	PHE	2.4
1	B	117	GLN	2.4
1	A	236	GLY	2.2
1	C	235	ILE	2.2
1	C	64	THR	2.1
1	A	126	LYS	2.1
1	C	116	GLN	2.0
1	C	121	GLN	2.0
1	C	259	ILE	2.0
1	A	235	ILE	2.0
1	C	61	ALA	2.0
1	B	49	VAL	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
2	SO4	B	507	5/5	0.82	0.24	88,91,95,103	0
5	ACT	A	507	4/4	0.83	0.17	55,62,63,63	0
5	ACT	A	506	4/4	0.84	0.13	40,48,51,56	0
2	SO4	C	506	5/5	0.85	0.27	101,103,106,107	0
2	SO4	A	508	5/5	0.87	0.24	81,84,88,88	0
2	SO4	A	509	5/5	0.91	0.55	101,102,104,105	0
2	SO4	B	506	5/5	0.92	0.25	77,85,86,94	0
3	GOL	A	503	6/6	0.92	0.14	23,26,35,35	0
2	SO4	C	501	5/5	0.95	0.24	87,89,91,93	0
3	GOL	B	503	6/6	0.96	0.10	21,30,36,36	0
3	GOL	C	502	6/6	0.96	0.09	25,33,41,41	0
3	GOL	A	502	6/6	0.96	0.09	22,23,30,33	0
2	SO4	B	502	5/5	0.96	0.18	57,60,62,63	0
3	GOL	C	503	6/6	0.97	0.07	20,23,31,36	0
4	ZN	B	505	1/1	0.98	0.07	54,54,54,54	0
2	SO4	B	501	5/5	0.98	0.11	39,41,47,49	0
4	ZN	A	505	1/1	0.98	0.04	55,55,55,55	0
4	ZN	C	504	1/1	0.99	0.07	19,19,19,19	0
4	ZN	C	505	1/1	0.99	0.03	53,53,53,53	0
2	SO4	A	501	5/5	0.99	0.07	27,34,43,44	0
4	ZN	A	504	1/1	0.99	0.09	19,19,19,19	0
4	ZN	B	504	1/1	1.00	0.12	19,19,19,19	0

6.5 Other polymers (i)

There are no such residues in this entry.