wwPDB X-ray Structure Validation Summary Report (i)

Jun 12, 2024 – 11:20 PM EDT

PDB ID	:	1K7H
Title	:	CRYSTAL STRUCTURE OF SHRIMP ALKALINE PHOSPHATASE
Authors	:	De Backer, M.E.; Mc Sweeney, S.; Rasmussen, H.B.; Riise, B.W.; Lindley, P.; Hough, E.
Deposited on	:	2001-10-19
Resolution	:	1.92 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

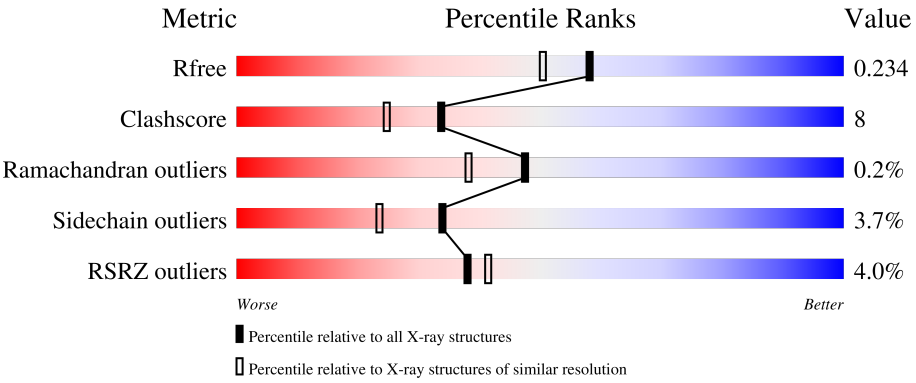
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 1.92 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	7937 (1.94-1.90)
Clashscore	141614	8644 (1.94-1.90)
Ramachandran outliers	138981	8530 (1.94-1.90)
Sidechain outliers	138945	8530 (1.94-1.90)
RSRZ outliers	127900	7793 (1.94-1.90)

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	476	3% 80% 18%
1	B	476	5% 82% 16%

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	MAE	A	487	-	-	-	X

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 8100 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.

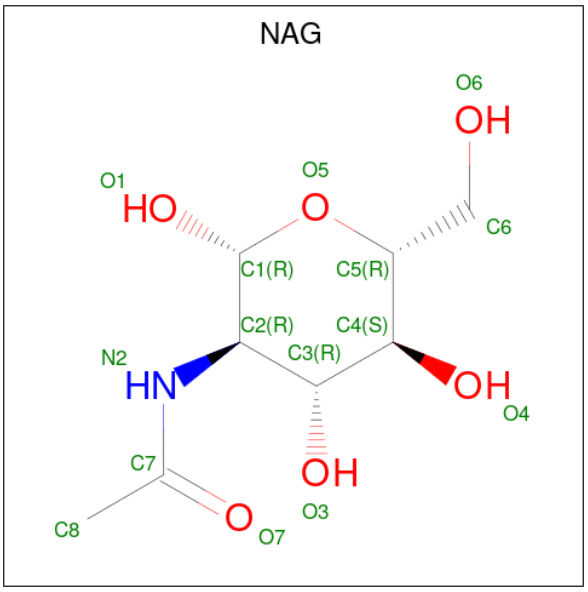
- Molecule 1 is a protein called ALKALINE PHOSPHATASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	476	Total	C	N	O	S	0	0	0
			3732	2333	629	756	14			
1	B	476	Total	C	N	O	S	0	0	0
			3732	2333	629	756	14			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLU	-	cloning artifact	UNP Q9BHT8
A	2	GLU	-	cloning artifact	UNP Q9BHT8
A	3	ASP	-	cloning artifact	UNP Q9BHT8
A	259	ALA	ARG	conflict	UNP Q9BHT8
A	430	ALA	VAL	conflict	UNP Q9BHT8
B	1	GLU	-	cloning artifact	UNP Q9BHT8
B	2	GLU	-	cloning artifact	UNP Q9BHT8
B	3	ASP	-	cloning artifact	UNP Q9BHT8
B	259	ALA	ARG	conflict	UNP Q9BHT8
B	430	ALA	VAL	conflict	UNP Q9BHT8

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

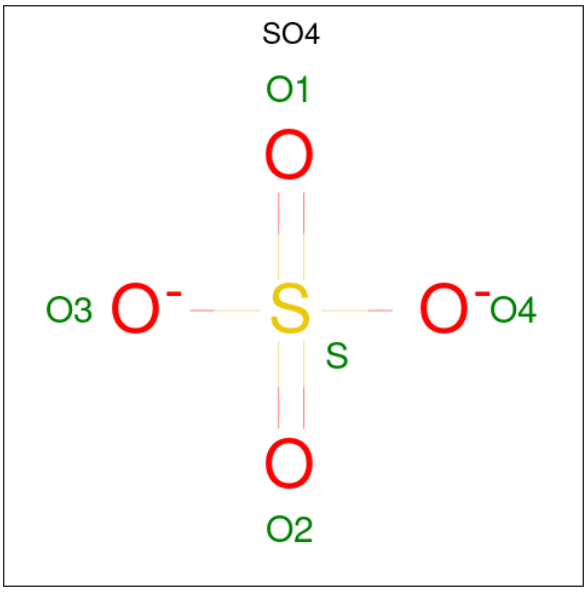


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C N O 14 8 1 5	0	0
2	B	1	Total C N O 14 8 1 5	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

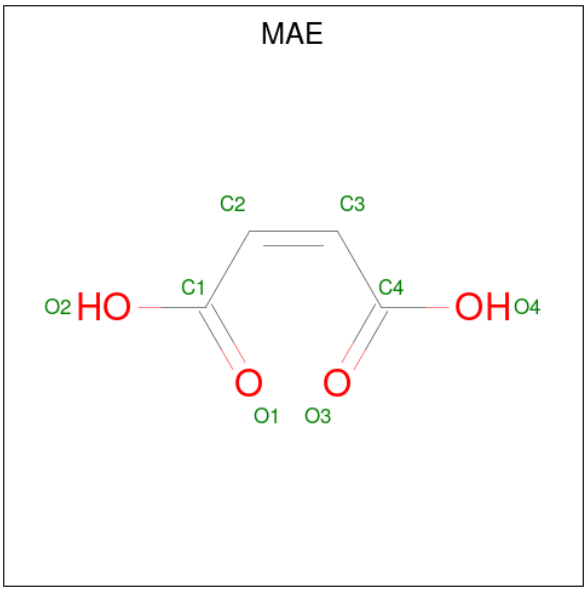
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	3	Total Zn 3 3	0	0
3	B	3	Total Zn 3 3	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 5 is MALEIC ACID (three-letter code: MAE) (formula: $C_4H_4O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 8 4 4	0	0
5	A	1	Total C O 8 4 4	0	0
5	B	1	Total C O 8 4 4	0	0

- Molecule 6 is water.

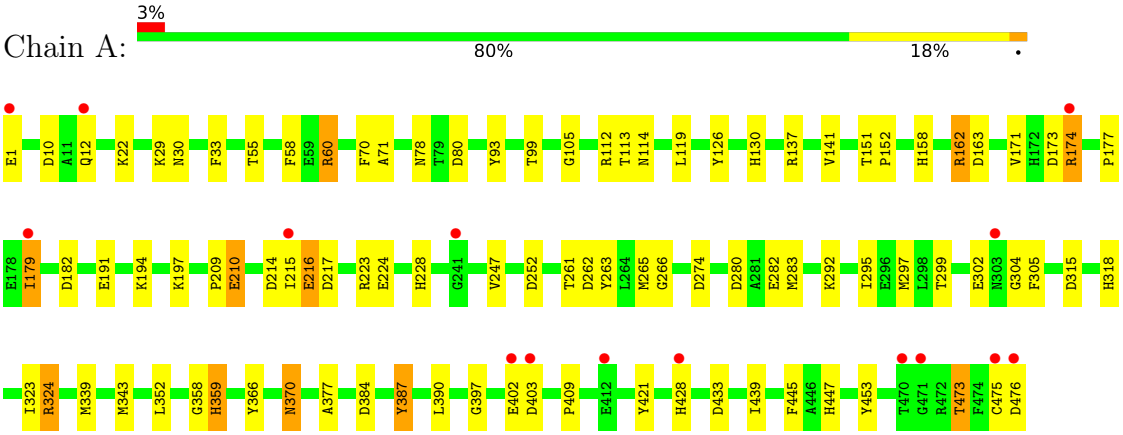
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	294	Total O 294 294	0	0
6	B	254	Total O 254 254	0	0

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.

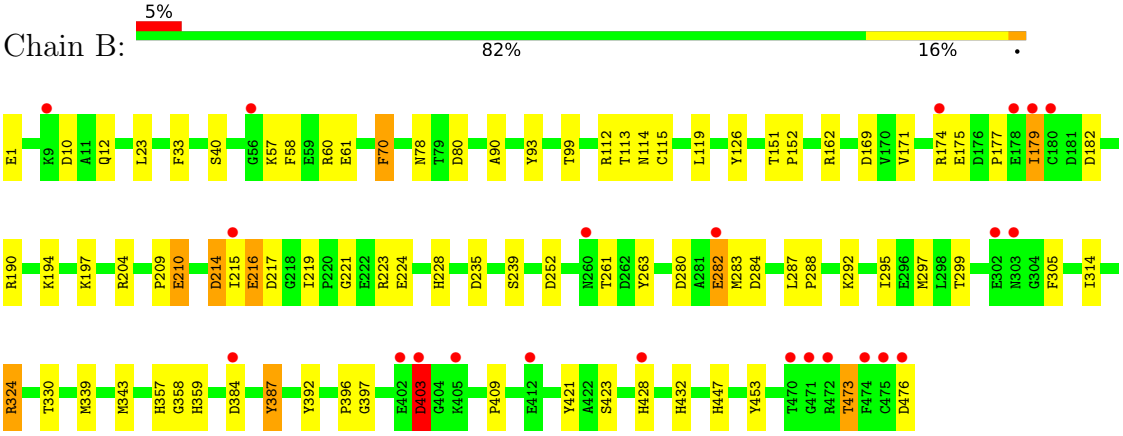
• Molecule 1: ALKALINE PHOSPHATASE

Chain A:



• Molecule 1: ALKALINE PHOSPHATASE

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	171.17Å 171.17Å 84.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	119.50 – 1.92 19.91 – 1.85	Depositor EDS
% Data completeness (in resolution range)	96.9 (119.50-1.92) 97.0 (19.91-1.85)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.18	Depositor
$< I/\sigma(I) >$ [1]	1.74 (at 1.85Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.198 , 0.227 0.207 , 0.234	Depositor DCC
R_{free} test set	5156 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	23.9	Xtriage
Anisotropy	0.481	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.46 , 52.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	8100	wwPDB-VP
Average B, all atoms (Å^2)	29.0	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 27.99 % 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 1.9929e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MAE, SO4, NAG

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	1.35	24/3812 (0.6%)	1.14	25/5174 (0.5%)
1	B	1.39	21/3812 (0.6%)	1.18	29/5174 (0.6%)
All	All	1.37	45/7624 (0.6%)	1.16	54/10348 (0.5%)

The worst 5 of 45 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	453	TYR	CE1-CZ	-18.90	1.14	1.38
1	B	453	TYR	CE2-CZ	-17.23	1.16	1.38
1	A	263	TYR	CE1-CZ	-17.07	1.16	1.38
1	B	453	TYR	CG-CD2	-16.58	1.17	1.39
1	A	387	TYR	CE1-CZ	-16.47	1.17	1.38

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	60	ARG	NE-CZ-NH2	25.17	132.88	120.30
1	A	60	ARG	NE-CZ-NH2	19.80	130.20	120.30
1	B	60	ARG	NH1-CZ-NH2	-10.79	107.53	119.40
1	A	182	ASP	CB-CG-OD2	9.87	127.18	118.30
1	A	60	ARG	NH1-CZ-NH2	-9.71	108.72	119.40

There are no chirality outliers.

There are no planarity outliers.

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	A	3732	0	3522	66	0
1	B	3732	0	3523	55	0
2	A	14	0	13	2	0
2	B	14	0	13	1	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
4	A	15	0	0	1	0
4	B	15	0	0	0	0
5	A	16	0	4	2	0
5	B	8	0	2	1	0
6	A	294	0	0	10	0
6	B	254	0	0	3	0
All	All	8100	0	7077	122	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 8.

The worst 5 of 122 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:114:ASN:HD21	2:A:480:NAG:C1	1.05	1.59
1:B:114:ASN:HD21	2:B:480:NAG:C1	1.29	1.43
5:A:487:MAE:O2	6:A:1018:HOH:O	1.52	1.25
1:A:295:ILE:O	1:A:299:THR:HG23	1.78	0.83
1:A:171:VAL:HG23	1:A:177:PRO:HG3	1.62	0.81

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	474/476 (100%)	460 (97%)	13 (3%)	1 (0%)	47 38
1	B	474/476 (100%)	460 (97%)	13 (3%)	1 (0%)	47 38
All	All	948/952 (100%)	920 (97%)	26 (3%)	2 (0%)	47 38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	216	GLU
1	B	216	GLU

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	394/394 (100%)	379 (96%)	15 (4%)	33 22
1	B	394/394 (100%)	380 (96%)	14 (4%)	35 24
All	All	788/788 (100%)	759 (96%)	29 (4%)	34 23

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	473	THR
1	B	409	PRO
1	B	33	PHE
1	B	384	ASP
1	B	12	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	322	GLN
1	B	447	HIS
1	B	428	HIS
1	A	428	HIS

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Mol	Chain	Res	Type
1	B	303	ASN

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 17 ligands modelled in this entry, 6 are monoatomic - leaving 11 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	MAE	B	488	-	7,7,7	1.97	4 (57%)	8,8,8	2.10	3 (37%)
4	SO4	A	481	-	4,4,4	0.17	0	6,6,6	0.50	0
5	MAE	A	487	-	7,7,7	1.96	4 (57%)	8,8,8	2.10	3 (37%)
4	SO4	A	482	-	4,4,4	0.18	0	6,6,6	0.45	0
2	NAG	B	480	1	14,14,15	0.63	0	17,19,21	1.43	4 (23%)
4	SO4	B	485	-	4,4,4	0.22	0	6,6,6	0.71	0
4	SO4	A	483	-	4,4,4	0.22	0	6,6,6	0.37	0
2	NAG	A	480	1	14,14,15	1.12	1 (7%)	17,19,21	1.99	5 (29%)
4	SO4	B	484	-	4,4,4	0.24	0	6,6,6	0.44	0
5	MAE	A	489	-	7,7,7	1.96	4 (57%)	8,8,8	2.09	3 (37%)
4	SO4	B	486	-	4,4,4	0.28	0	6,6,6	0.26	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	MAE	B	488	-	-	0/5/5/5	-
5	MAE	A	487	-	-	0/5/5/5	-
2	NAG	B	480	1	-	0/6/23/26	0/1/1/1
2	NAG	A	480	1	-	0/6/23/26	0/1/1/1
5	MAE	A	489	-	-	0/5/5/5	-

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	480	NAG	O5-C1	-2.97	1.39	1.43
5	B	488	MAE	O2-C1	-2.59	1.23	1.30
5	A	489	MAE	O2-C1	-2.59	1.23	1.30
5	A	487	MAE	O2-C1	-2.57	1.23	1.30
5	B	488	MAE	C3-C4	-2.52	1.42	1.48

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	480	NAG	O6-C6-C5	4.04	125.14	111.29
2	A	480	NAG	O3-C3-C4	3.70	118.91	110.35
5	A	487	MAE	O2-C1-O1	-3.68	115.03	122.67
5	B	488	MAE	O2-C1-O1	-3.67	115.05	122.67
5	A	489	MAE	O2-C1-O1	-3.65	115.08	122.67

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	488	MAE	1	0
5	A	487	MAE	2	0
4	A	482	SO4	1	0
2	B	480	NAG	1	0
2	A	480	NAG	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

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, 95^{th} 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	476/476 (100%)	0.16	15 (3%)	47	50	19, 27, 40, 59	0
1	B	476/476 (100%)	0.23	23 (4%)	30	34	18, 27, 40, 59	0
All	All	952/952 (100%)	0.19	38 (3%)	38	41	18, 27, 40, 59	0

The worst 5 of 38 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	476	ASP	5.2
1	B	476	ASP	5.1
1	B	302	GLU	4.9
1	B	402	GLU	4.2
1	B	428	HIS	3.9

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 monosaccharides 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. The B-factors column lists the minimum, median, 95^{th} 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	NAG	B	480	14/15	0.71	0.21	46,48,54,57	0
5	MAE	B	488	8/8	0.72	0.40	67,69,74,79	0
5	MAE	A	489	8/8	0.77	0.24	67,69,74,79	0
5	MAE	A	487	8/8	0.78	0.41	67,69,74,79	0
4	SO4	A	483	5/5	0.80	0.23	58,62,64,64	0
2	NAG	A	480	14/15	0.80	0.18	36,41,47,48	0
4	SO4	A	482	5/5	0.84	0.24	51,54,54,55	0
4	SO4	B	484	5/5	0.86	0.23	45,48,54,54	0
4	SO4	B	486	5/5	0.90	0.20	63,64,64,66	0
4	SO4	B	485	5/5	0.92	0.21	50,50,52,54	0
4	SO4	A	481	5/5	0.94	0.17	48,48,52,53	0
3	ZN	A	477	1/1	0.99	0.07	23,23,23,23	0
3	ZN	A	479	1/1	0.99	0.02	27,27,27,27	1
3	ZN	B	477	1/1	0.99	0.06	22,22,22,22	0
3	ZN	A	478	1/1	1.00	0.02	23,23,23,23	0
3	ZN	B	478	1/1	1.00	0.03	22,22,22,22	0
3	ZN	B	479	1/1	1.00	0.06	28,28,28,28	1

6.5 Other polymers (i)

There are no such residues in this entry.