



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:37 PM GMT

PDB ID : 4PFW
Title : Crystal structure of mannohexaose bound oligopeptide ABC transporter, periplasmic oligopeptide-binding protein (TM1226) from THERMOTOGA MARITIMA at 2.2 Å resolution
Authors : Lu, X.; Ghimire-Rijal, S.; Cuneo, M.J.
Deposited on : 2014-04-30
Resolution : 2.20 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

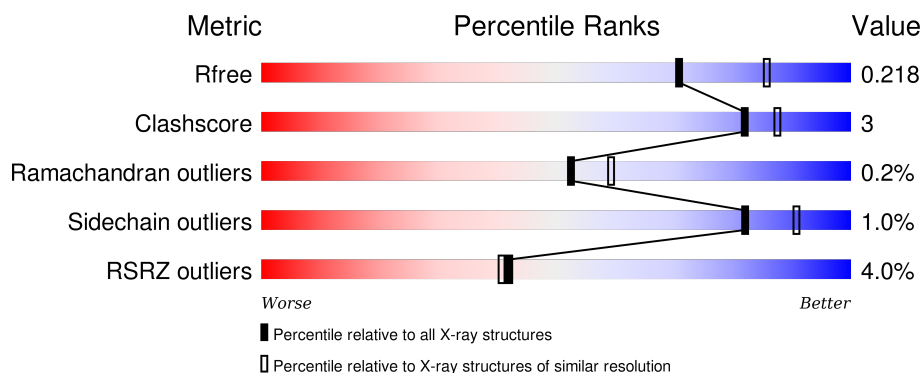
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	91344	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (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 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 $\leq 5\%$. 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	547	<div> <div>5%</div> <div>90%</div> <div>8%</div> </div>
1	B	547	<div> <div>3%</div> <div>89%</div> <div>9%</div> </div>

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
3	MAN	A	602	-	-	-	X
3	BMA	A	607	-	-	-	X
3	BMA	B	604	-	-	-	X
4	SO4	A	611	-	-	-	X
5	GOL	B	610	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9575 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 ABC transporter substrate-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	540	Total	C	N	O	S	0	1	0
			4418	2892	701	809	16			
1	B	540	Total	C	N	O	S	0	4	0
			4450	2912	709	812	17			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	MET	-	initiating methionine	UNP G4FEC0
A	561	HIS	-	expression tag	UNP G4FEC0
A	562	HIS	-	expression tag	UNP G4FEC0
A	563	HIS	-	expression tag	UNP G4FEC0
A	564	HIS	-	expression tag	UNP G4FEC0
A	565	HIS	-	expression tag	UNP G4FEC0
A	566	HIS	-	expression tag	UNP G4FEC0
B	20	MET	-	initiating methionine	UNP G4FEC0
B	561	HIS	-	expression tag	UNP G4FEC0
B	562	HIS	-	expression tag	UNP G4FEC0
B	563	HIS	-	expression tag	UNP G4FEC0
B	564	HIS	-	expression tag	UNP G4FEC0
B	565	HIS	-	expression tag	UNP G4FEC0
B	566	HIS	-	expression tag	UNP G4FEC0

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mg	0	0
			1	1		
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is a polymer of unknown type called SUGAR (6-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	6	Total	C	O	0	0
			67	36	31		
3	B	6	Total	C	O	0	0
			67	36	31		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

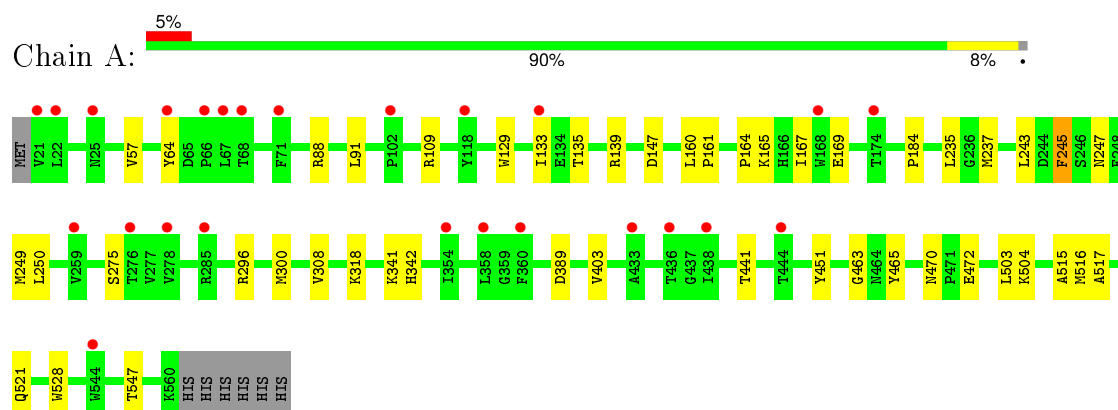
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	239	Total	O	0	0
			239	239		
6	B	289	Total	O	0	0
			289	289		

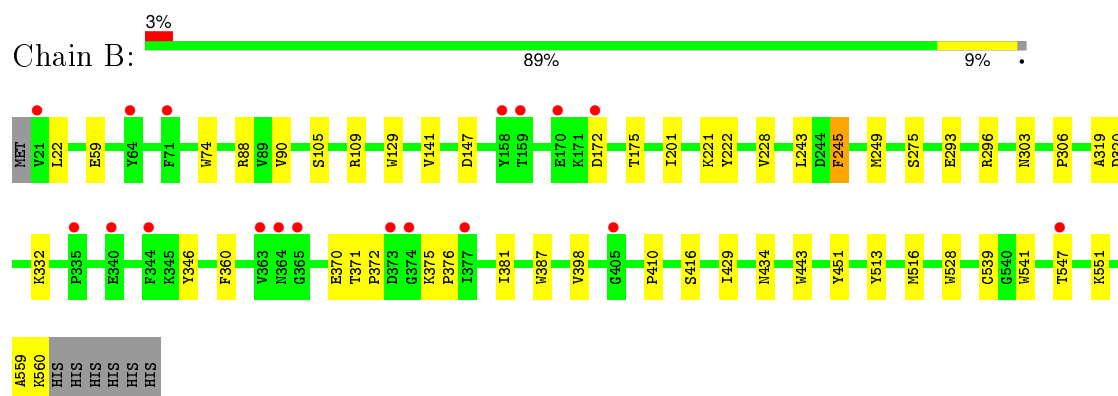
3 Residue-property plots

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: ABC transporter substrate-binding protein



- Molecule 1: ABC transporter substrate-binding protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	99.55Å 194.23Å 159.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.86 – 2.20 44.86 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.0 (44.86-2.20) 97.0 (44.86-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.45 (at 2.20Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.164 , 0.218 0.170 , 0.218	Depositor DCC
R_{free} test set	3849 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	40.0	Xtriage
Anisotropy	0.335	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 76304 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	9575	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.96% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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, MG, BMA, SO4, MAN

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	0.37	0/4576	0.51	0/6266
1	B	0.39	0/4609	0.53	1/6309 (0.0%)
All	All	0.38	0/9185	0.52	1/12575 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	320	ASP	CB-CG-OD1	5.00	122.80	118.30

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	4418	0	4176	25	0
1	B	4450	0	4221	29	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	67	0	57	1	0
3	B	67	0	57	3	0
4	A	20	0	0	0	0
4	B	5	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	18	0	24	4	0
6	A	239	0	0	1	0
6	B	289	0	0	5	0
All	All	9575	0	8535	57	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 (57) 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:434:ASN:HD21	5:B:610:GOL:H31	1.37	0.87
1:B:293:GLU:OE2	1:B:296[B]:ARG:NH1	2.19	0.74
1:B:109:ARG:NH1	4:B:611:SO4:O1	2.27	0.63
1:B:434:ASN:ND2	5:B:610:GOL:H31	2.11	0.63
1:B:443:TRP:HE1	5:B:609:GOL:H11	1.66	0.61
1:B:370:GLU:HG3	1:B:376:PRO:HA	1.87	0.56
1:A:129:TRP:HB2	1:A:147:ASP:O	2.07	0.55
1:A:341:LYS:HG2	1:A:342:HIS:CD2	2.43	0.54
1:B:275:SER:HB3	1:B:516:MET:HB2	1.89	0.54
1:A:341:LYS:HE2	1:A:342:HIS:CE1	2.43	0.53
1:B:88:ARG:HD3	1:B:90:VAL:HG23	1.92	0.52
1:B:360:PHE:CE1	1:B:372:PRO:HD3	2.46	0.51
1:B:172:ASP:OD1	1:B:175:THR:OG1	2.16	0.50
1:A:88:ARG:HD2	6:A:783:HOH:O	2.12	0.50
1:B:346:TYR:OH	6:B:825:HOH:O	2.19	0.48
1:A:109:ARG:NH1	1:A:135:THR:OG1	2.47	0.48
1:A:235:LEU:HD13	1:A:250:LEU:HD13	1.95	0.48
1:A:504:LYS:HA	1:A:504:LYS:HD3	1.68	0.48
1:A:275:SER:HB3	1:A:516:MET:HB2	1.96	0.47
1:A:164:PRO:HG2	1:A:167:ILE:HB	1.96	0.47
1:A:91:LEU:O	1:A:139:ARG:HD2	2.15	0.47
1:A:237:MET:HE2	1:A:243:LEU:HG	1.97	0.47
1:A:249:MET:CE	1:A:515:ALA:HB3	2.45	0.47
1:B:22:LEU:HD11	1:B:201:ILE:HD13	1.96	0.47
3:A:602:MAN:H61	3:A:603:MAN:H2	1.96	0.46
1:A:57:VAL:HG11	1:A:184:PRO:HG2	1.97	0.46
1:A:245:PHE:HB2	1:A:528:TRP:CH2	2.52	0.45
1:B:398:VAL:HG21	1:B:410:PRO:HD3	1.98	0.45
1:B:381:ILE:HA	1:B:429:ILE:O	2.17	0.45
3:B:605:BMA:H2	5:B:610:GOL:O2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:249[B]:MET:HE3	6:B:779:HOH:O	2.17	0.45
1:B:387:TRP:CE3	3:B:607:BMA:H5	2.52	0.44
1:B:332:LYS:NZ	6:B:833:HOH:O	2.45	0.44
1:A:109:ARG:NH2	1:A:133:ILE:O	2.52	0.43
1:B:559:ALA:O	1:B:560:LYS:HB2	2.18	0.43
1:B:371:THR:HG23	1:B:375:LYS:O	2.18	0.43
1:B:59:GLU:HG2	1:B:74:TRP:CZ2	2.53	0.43
1:B:221:LYS:HG2	1:B:222:TYR:CE2	2.53	0.43
1:A:470:ASN:OD1	1:A:472:GLU:HG3	2.19	0.43
1:A:296:ARG:O	1:A:300:MET:HG3	2.19	0.43
1:B:129:TRP:HB2	1:B:147:ASP:O	2.19	0.43
3:B:602:MAN:H1	6:B:914:HOH:O	2.18	0.43
1:B:303:ASN:HB2	1:B:346:TYR:CD1	2.54	0.42
1:B:245:PHE:HB2	1:B:528:TRP:CH2	2.54	0.42
1:B:551:LYS:HG2	6:B:929:HOH:O	2.20	0.42
1:A:308:VAL:HG21	1:A:318:LYS:HB2	2.02	0.42
1:B:105:SER:HB2	1:B:141:VAL:HG22	2.01	0.42
1:A:247:ASN:HA	1:A:517:ALA:O	2.20	0.42
1:A:160:LEU:HD12	1:A:161:PRO:HD2	2.01	0.42
1:B:319:ALA:HA	1:B:513:TYR:CE2	2.56	0.41
1:A:389:ASP:N	1:A:389:ASP:OD1	2.54	0.41
1:A:463:GLY:HA2	1:A:465:TYR:CZ	2.56	0.41
1:A:165:LYS:HE2	1:A:169:GLU:OE2	2.20	0.41
1:A:503:LEU:HD23	1:A:503:LEU:HA	1.88	0.40
1:A:64:TYR:O	1:A:547:THR:HA	2.21	0.40
1:B:539:CYS:SG	1:B:541:TRP:CD2	3.14	0.40
1:B:303:ASN:O	1:B:306:PRO:HD2	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	539/547 (98%)	520 (96%)	18 (3%)	1 (0%)	52	59
1	B	542/547 (99%)	526 (97%)	15 (3%)	1 (0%)	52	59
All	All	1081/1094 (99%)	1046 (97%)	33 (3%)	2 (0%)	52	59

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	451	TYR
1	B	451	TYR

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	470/489 (96%)	466 (99%)	4 (1%)	84	92
1	B	476/489 (97%)	470 (99%)	6 (1%)	76	87
All	All	946/978 (97%)	936 (99%)	10 (1%)	82	89

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	245	PHE
1	A	403	VAL
1	A	441	THR
1	A	521	GLN
1	B	228	VAL
1	B	243	LEU
1	B	245	PHE
1	B	416	SER
1	B	547[A]	THR
1	B	547[B]	THR

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

Mol	Chain	Res	Type
1	B	178	GLN
1	B	392	GLN
1	B	434	ASN

5.3.3 RNA ⓘ

There are no RNA molecules 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 ⓘ

12 carbohydrates are 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	$\# Z > 2$
3	MAN	A	602	3	12,12,12	0.98	1 (8%)	17,17,17	1.60	3 (17%)
3	MAN	A	603	3	11,11,12	0.76	0	14,15,17	0.98	2 (14%)
3	BMA	A	604	3	11,11,12	0.95	0	14,15,17	0.88	1 (7%)
3	BMA	A	605	3	11,11,12	0.95	1 (9%)	14,15,17	0.78	1 (7%)
3	BMA	A	606	3	11,11,12	1.39	1 (9%)	14,15,17	0.73	0
3	BMA	A	607	3	11,11,12	0.88	1 (9%)	14,15,17	0.77	0
3	MAN	B	602	3	12,12,12	0.82	0	17,17,17	1.00	1 (5%)
3	MAN	B	603	3	11,11,12	0.78	0	14,15,17	0.94	0
3	BMA	B	604	3	11,11,12	1.24	1 (9%)	14,15,17	0.88	0
3	BMA	B	605	3	11,11,12	1.10	1 (9%)	14,15,17	0.97	1 (7%)
3	BMA	B	606	3	11,11,12	0.87	0	14,15,17	0.68	0
3	BMA	B	607	3	11,11,12	0.85	0	14,15,17	0.82	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	MAN	A	602	3	-	0/2/22/22	0/1/1/1
3	MAN	A	603	3	-	0/2/19/22	0/1/1/1
3	BMA	A	604	3	-	0/2/19/22	0/1/1/1
3	BMA	A	605	3	-	0/2/19/22	0/1/1/1
3	BMA	A	606	3	-	0/2/19/22	0/1/1/1
3	BMA	A	607	3	-	0/2/19/22	0/1/1/1
3	MAN	B	602	3	-	0/2/22/22	0/1/1/1
3	MAN	B	603	3	-	0/2/19/22	0/1/1/1
3	BMA	B	604	3	-	0/2/19/22	0/1/1/1
3	BMA	B	605	3	-	0/2/19/22	0/1/1/1
3	BMA	B	606	3	-	0/2/19/22	0/1/1/1
3	BMA	B	607	3	-	0/2/19/22	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	604	BMA	O5-C1	-3.78	1.37	1.43
3	A	606	BMA	O5-C1	-2.60	1.39	1.43
3	A	605	BMA	O5-C1	-2.34	1.39	1.43
3	A	607	BMA	O5-C1	-2.33	1.39	1.43
3	B	605	BMA	O5-C1	-2.21	1.40	1.43
3	A	602	MAN	C1-C2	3.11	1.58	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	MAN	C3-C4-C5	-3.45	104.18	110.20
3	B	605	BMA	O2-C2-C3	-2.85	104.39	110.12
3	A	602	MAN	O2-C2-C3	-2.58	104.53	110.34
3	A	603	MAN	O2-C2-C3	-2.17	105.75	110.12
3	A	605	BMA	O2-C2-C3	-2.11	105.89	110.12
3	A	603	MAN	C1-O5-C5	2.26	115.11	112.25
3	A	604	BMA	C1-O5-C5	2.29	115.16	112.25
3	B	602	MAN	O5-C1-C2	2.66	114.04	109.80
3	A	602	MAN	O5-C1-C2	3.31	115.08	109.80

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	602	MAN	1	0
3	A	603	MAN	1	0
3	B	602	MAN	1	0
3	B	605	BMA	1	0
3	B	607	BMA	1	0

5.6 Ligand geometry

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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	$\# Z > 2$
4	SO4	A	608	-	4,4,4	0.15	0	6,6,6	0.18	0
4	SO4	A	609	-	4,4,4	0.16	0	6,6,6	0.12	0
4	SO4	A	610	-	4,4,4	0.22	0	6,6,6	0.18	0
4	SO4	A	611	-	4,4,4	0.21	0	6,6,6	0.12	0
5	GOL	B	608	-	5,5,5	0.38	0	5,5,5	0.42	0
5	GOL	B	609	-	5,5,5	0.32	0	5,5,5	0.37	0
5	GOL	B	610	-	5,5,5	0.41	0	5,5,5	0.40	0
4	SO4	B	611	-	4,4,4	0.21	0	6,6,6	0.19	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
4	SO4	A	608	-	-	0/0/0/0	0/0/0/0
4	SO4	A	609	-	-	0/0/0/0	0/0/0/0
4	SO4	A	610	-	-	0/0/0/0	0/0/0/0
4	SO4	A	611	-	-	0/0/0/0	0/0/0/0
5	GOL	B	608	-	-	0/4/4/4	0/0/0/0
5	GOL	B	609	-	-	0/4/4/4	0/0/0/0
5	GOL	B	610	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SO4	B	611	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	609	GOL	1	0
5	B	610	GOL	3	0
4	B	611	SO4	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

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	540/547 (98%)	0.13	25 (4%) 36 35	30, 48, 72, 96	0
1	B	540/547 (98%)	-0.04	18 (3%) 50 49	27, 42, 67, 102	1 (0%)
All	All	1080/1094 (98%)	0.05	43 (3%) 42 41	27, 45, 72, 102	1 (0%)

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	21	VAL	7.3
1	B	365	GLY	4.3
1	B	363	VAL	4.0
1	A	358	LEU	4.0
1	A	64	TYR	3.5
1	A	22	LEU	3.4
1	B	364	ASN	3.3
1	B	64	TYR	3.2
1	B	344	PHE	3.0
1	A	354	ILE	2.8
1	A	544	TRP	2.8
1	A	360	PHE	2.7
1	B	71	PHE	2.7
1	A	259	VAL	2.6
1	A	118	TYR	2.5
1	A	174	THR	2.5
1	A	433	ALA	2.5
1	A	438	ILE	2.5
1	B	405	GLY	2.4
1	A	168	TRP	2.4
1	B	374	GLY	2.4
1	B	373	ASP	2.3
1	B	21	VAL	2.3
1	B	377	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	276	THR	2.3
1	B	340	GLU	2.3
1	A	25	ASN	2.3
1	A	67	LEU	2.3
1	A	278	VAL	2.3
1	A	66	PRO	2.3
1	B	158	TYR	2.3
1	A	436	THR	2.3
1	B	159	THR	2.3
1	B	172	ASP	2.2
1	A	285	ARG	2.2
1	B	335	PRO	2.2
1	A	444	THR	2.2
1	A	102	PRO	2.1
1	A	68	THR	2.0
1	B	547[A]	THR	2.0
1	B	170	GLU	2.0
1	A	71	PHE	2.0
1	A	133	ILE	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](#)

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
3	MAN	A	602	12/12	0.90	0.18	3.96	65,90,95,98	0
3	BMA	A	607	11/12	0.98	0.16	2.76	31,33,38,40	0
3	BMA	B	604	11/12	0.96	0.21	2.19	44,50,53,60	0
3	MAN	B	603	11/12	0.92	0.22	1.92	66,74,82,91	0
3	MAN	A	603	11/12	0.91	0.15	1.49	71,80,84,85	0
3	MAN	B	602	12/12	0.92	0.16	1.16	68,71,78,79	0
3	BMA	B	606	11/12	0.98	0.12	0.85	30,32,35,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	BMA	A	606	11/12	0.97	0.17	0.48	30,37,42,43	0
3	BMA	B	605	11/12	0.98	0.15	0.30	30,33,37,38	0
3	BMA	A	604	11/12	0.95	0.18	0.04	47,54,61,68	0
3	BMA	A	605	11/12	0.99	0.20	0.03	31,34,42,42	0
3	BMA	B	607	11/12	0.98	0.11	-0.17	28,32,36,36	0

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(\AA^2)	Q<0.9
5	GOL	B	610	6/6	0.75	0.38	9.76	71,73,78,89	0
4	SO4	A	611	5/5	0.86	0.15	2.90	133,137,137,139	0
5	GOL	B	608	6/6	0.88	0.24	1.48	51,56,59,62	0
5	GOL	B	609	6/6	0.95	0.13	0.73	64,76,80,81	0
2	MG	B	601	1/1	0.91	0.12	-1.63	68,68,68,68	0
2	MG	A	601	1/1	0.93	0.07	-1.82	59,59,59,59	0
4	SO4	A	610	5/5	0.91	0.19	-	104,108,111,112	0
4	SO4	B	611	5/5	0.93	0.26	-	70,82,87,91	0
4	SO4	A	608	5/5	0.80	0.20	-	101,118,121,127	0
4	SO4	A	609	5/5	0.90	0.30	-	78,83,90,97	0

6.5 Other polymers [i](#)

There are no such residues in this entry.