



wwPDB X-ray Structure Validation Summary Report

Feb 15, 2017 – 02:32 am GMT

PDB ID : 3RLF
Title : Crystal structure of the maltose-binding protein/maltose transporter complex in an outward-facing conformation bound to MgAMPPNP
Authors : Oldham, M.L.; Chen, J.
Deposited on : 2011-04-19
Resolution : 2.20 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

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

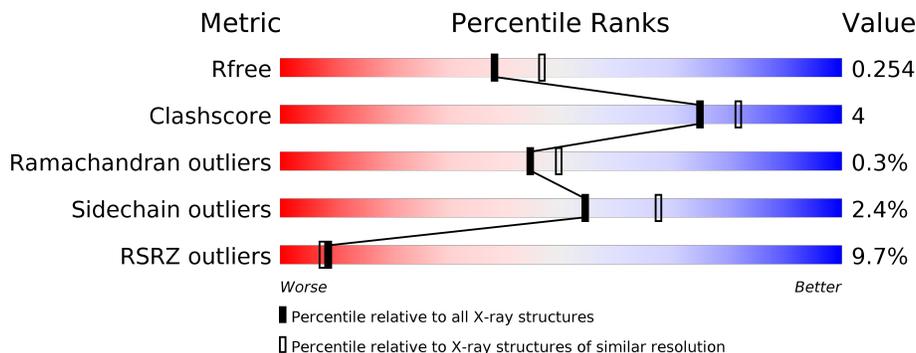
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	100719	4002 (2.20-2.20)
Clashscore	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)
RSRZ outliers	101464	4033 (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	E	380	 12% 89% 9%
2	F	514	 15% 86% 8% 5%
3	G	296	 6% 90% 6%
4	A	381	 4% 86% 11%
4	B	381	 8% 85% 11%

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	UMQ	E	5004	-	-	-	X
7	PGV	G	4009	-	-	-	X

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 15268 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 Maltose-binding periplasmic protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	E	374	2914	1875	476	557	6	0	2	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	371	ALA	-	EXPRESSION TAG	UNP P0AEX9
E	372	SER	-	EXPRESSION TAG	UNP P0AEX9
E	373	ALA	-	EXPRESSION TAG	UNP P0AEX9
E	374	SER	-	EXPRESSION TAG	UNP P0AEX9
E	375	HIS	-	EXPRESSION TAG	UNP P0AEX9
E	376	HIS	-	EXPRESSION TAG	UNP P0AEX9
E	377	HIS	-	EXPRESSION TAG	UNP P0AEX9
E	378	HIS	-	EXPRESSION TAG	UNP P0AEX9
E	379	HIS	-	EXPRESSION TAG	UNP P0AEX9
E	380	HIS	-	EXPRESSION TAG	UNP P0AEX9

- Molecule 2 is a protein called Maltose transport system permease protein malF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	F	490	3832	2517	612	686	17	0	1	0

- Molecule 3 is a protein called Maltose transport system permease protein malG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	G	286	2214	1484	352	370	8	0	2	0

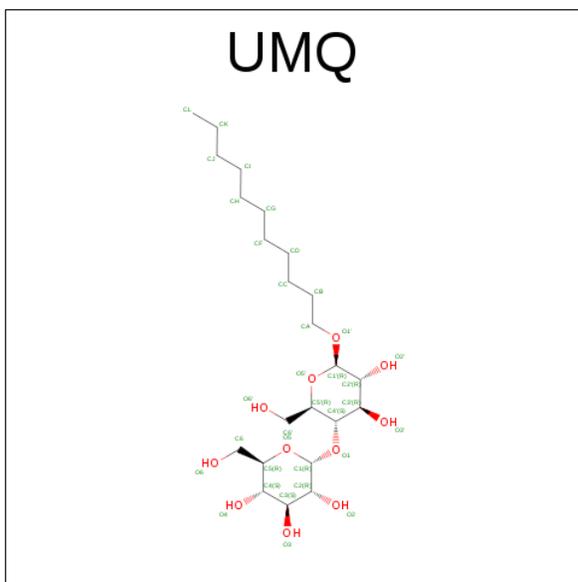
- Molecule 4 is a protein called Maltose/maltodextrin import ATP-binding protein MalK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	371	Total	C	N	O	S	0	0	0
			2876	1819	515	529	13			
4	B	371	Total	C	N	O	S	0	1	0
			2881	1822	515	531	13			

There are 20 discrepancies between the modelled and reference sequences:

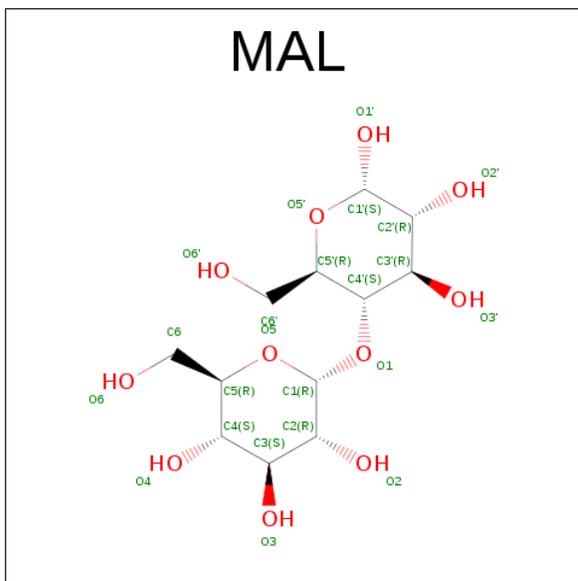
Chain	Residue	Modelled	Actual	Comment	Reference
A	372	ALA	-	EXPRESSION TAG	UNP P68187
A	373	SER	-	EXPRESSION TAG	UNP P68187
A	374	ALA	-	EXPRESSION TAG	UNP P68187
A	375	SER	-	EXPRESSION TAG	UNP P68187
A	376	HIS	-	EXPRESSION TAG	UNP P68187
A	377	HIS	-	EXPRESSION TAG	UNP P68187
A	378	HIS	-	EXPRESSION TAG	UNP P68187
A	379	HIS	-	EXPRESSION TAG	UNP P68187
A	380	HIS	-	EXPRESSION TAG	UNP P68187
A	381	HIS	-	EXPRESSION TAG	UNP P68187
B	372	ALA	-	EXPRESSION TAG	UNP P68187
B	373	SER	-	EXPRESSION TAG	UNP P68187
B	374	ALA	-	EXPRESSION TAG	UNP P68187
B	375	SER	-	EXPRESSION TAG	UNP P68187
B	376	HIS	-	EXPRESSION TAG	UNP P68187
B	377	HIS	-	EXPRESSION TAG	UNP P68187
B	378	HIS	-	EXPRESSION TAG	UNP P68187
B	379	HIS	-	EXPRESSION TAG	UNP P68187
B	380	HIS	-	EXPRESSION TAG	UNP P68187
B	381	HIS	-	EXPRESSION TAG	UNP P68187

- Molecule 5 is UNDECYL-MALTOSIDE (three-letter code: UMQ) (formula: C₂₃H₄₄O₁₁).



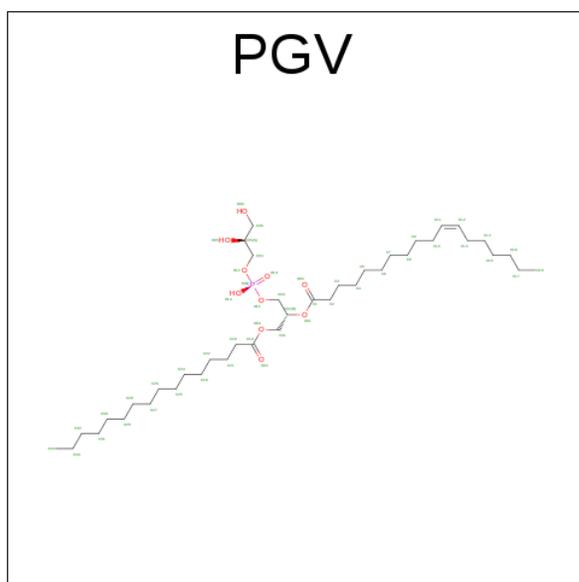
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
5	E	1	Total	C	O	0	0
			34	23	11		

- Molecule 6 is SUGAR (MALTOSE) (three-letter code: MAL) (formula: $C_{12}H_{22}O_{11}$).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
6	F	1	Total	C	O	0	0
			23	12	11		

- Molecule 7 is (1R)-2-[[[(2S)-2,3-DIHYDROXYPROPYL]OXY](HYDROXY)PHOSPHORYL]OXY]-1-[(PALMITOYLOXY)METHYL]ETHYL (11E)-OCTADEC-11-ENOATE (three-letter code: PGV) (formula: $C_{40}H_{77}O_{10}P$).

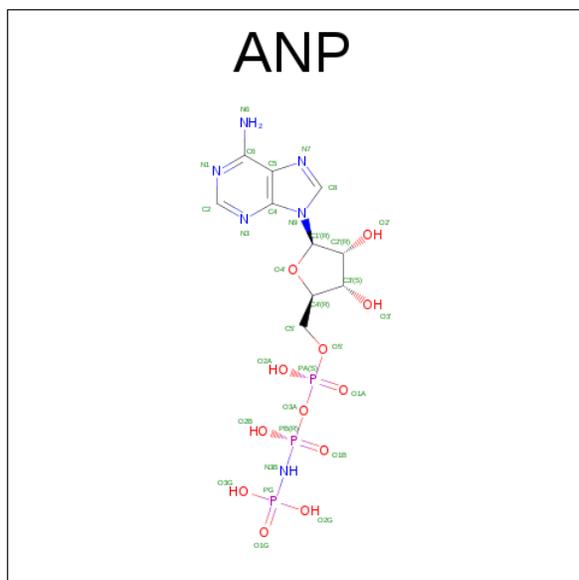


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	F	1	Total C O P 51 40 10 1	0	0
7	F	1	Total C 14 14	0	0
7	G	1	Total C 14 14	0	0
7	G	1	Total C 12 12	0	0

- Molecule 8 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 9 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
9	A	1	31	10	6	12	3	0	0
9	B	1	31	10	6	12	3	0	0

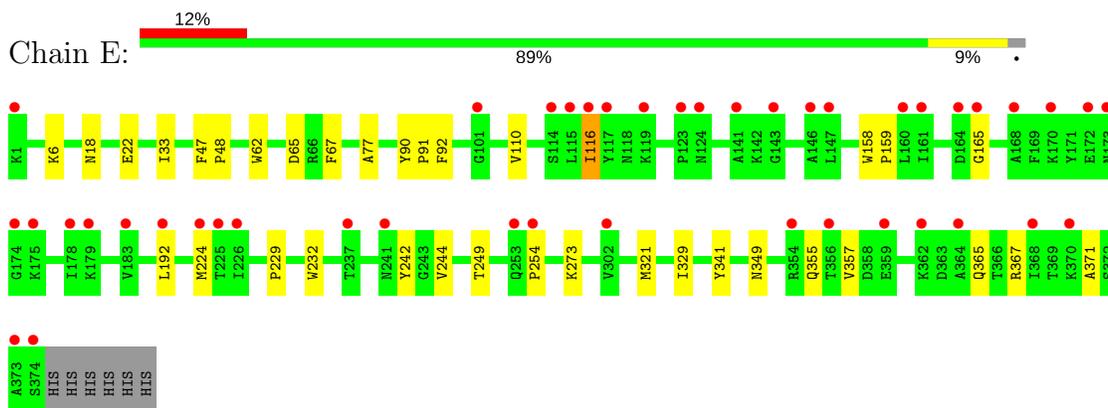
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	E	62	Total	O	0	0
			62	62		
10	F	63	Total	O	0	0
			63	63		
10	G	59	Total	O	0	0
			59	59		
10	A	81	Total	O	0	0
			81	81		
10	B	74	Total	O	0	0
			74	74		

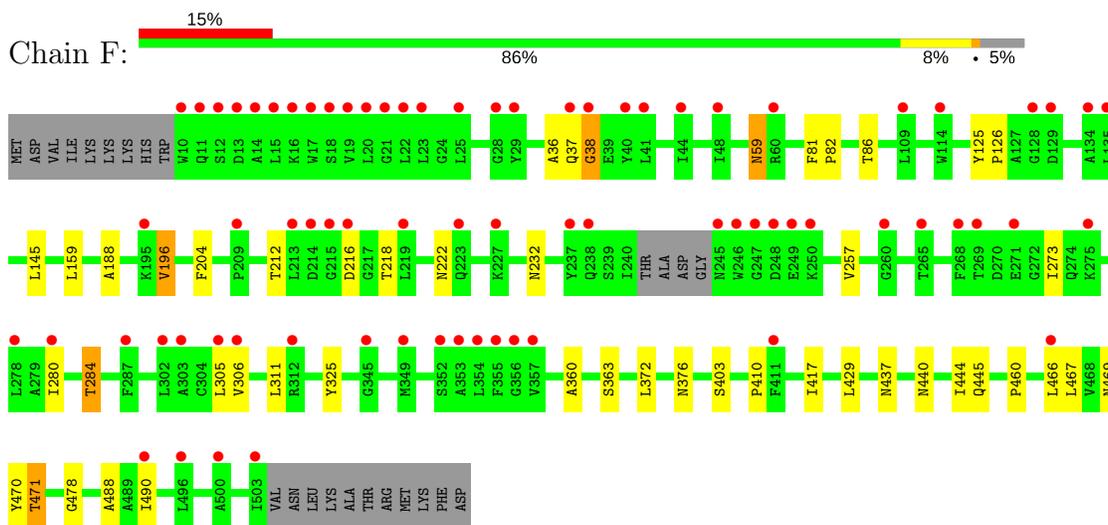
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

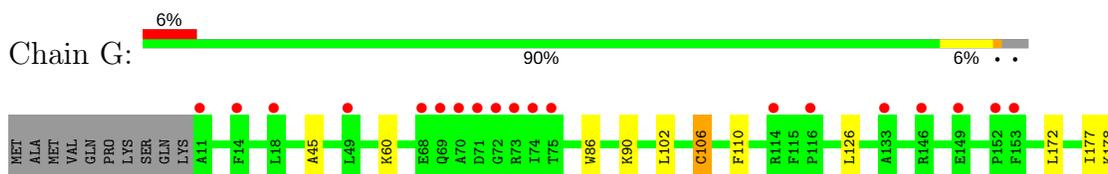
- Molecule 1: Maltose-binding periplasmic protein



- Molecule 2: Maltose transport system permease protein malF

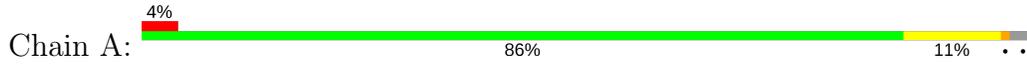


- Molecule 3: Maltose transport system permease protein malG

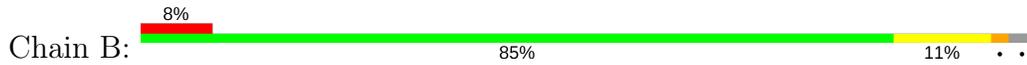




• Molecule 4: Maltose/maltodextrin import ATP-binding protein MalK



• Molecule 4: Maltose/maltodextrin import ATP-binding protein MalK



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	72.10Å 95.81Å 109.98Å 86.70° 82.68° 76.40°	Depositor
Resolution (Å)	20.00 – 2.20 19.97 – 2.20	Depositor EDS
% Data completeness (in resolution range)	86.3 (20.00-2.20) 85.9 (19.97-2.20)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 2.19Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.223 , 0.254 0.223 , 0.254	Depositor DCC
R_{free} test set	6209 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	39.2	Xtrriage
Anisotropy	0.015	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 56.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	15268	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.87% 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, 0.333 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: PGV, ANP, MG, UMQ, MAL

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	E	0.34	0/2983	0.46	0/4048
2	F	0.36	0/3927	0.50	0/5344
3	G	0.37	0/2278	0.49	0/3115
4	A	0.34	0/2926	0.53	1/3968 (0.0%)
4	B	0.35	0/2932	0.53	0/3974
All	All	0.35	0/15046	0.50	1/20449 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	A	347	LEU	CA-CB-CG	5.08	126.98	115.30

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	E	2914	0	2888	19	0
2	F	3832	0	3861	32	0
3	G	2214	0	2302	11	0
4	A	2876	0	2941	26	0
4	B	2881	0	2942	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	34	0	44	0	0
6	F	23	0	22	0	0
7	F	65	0	100	2	0
7	G	26	0	44	1	0
8	A	1	0	0	0	0
8	B	1	0	0	0	0
9	A	31	0	13	2	0
9	B	31	0	13	2	0
10	A	81	0	0	1	0
10	B	74	0	0	2	0
10	E	62	0	0	0	0
10	F	63	0	0	0	0
10	G	59	0	0	0	0
All	All	15268	0	15170	111	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 4.

The worst 5 of 111 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)
2:F:471:THR:HG21	2:F:490:ILE:HG21	1.42	1.01
4:A:39:GLY:H	9:A:2501:ANP:HNB1	1.16	0.94
4:B:39:GLY:H	9:B:2502:ANP:HNB1	1.18	0.88
4:A:223:HIS:CE1	4:A:368:GLU:HG2	2.12	0.85
4:B:344:ALA:CB	4:B:344:ALA:N	2.45	0.80

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	E	374/380 (98%)	364 (97%)	9 (2%)	1 (0%)	44	49
2	F	487/514 (95%)	471 (97%)	14 (3%)	2 (0%)	38	41
3	G	286/296 (97%)	283 (99%)	2 (1%)	1 (0%)	44	49
4	A	369/381 (97%)	360 (98%)	9 (2%)	0	100	100
4	B	369/381 (97%)	360 (98%)	8 (2%)	1 (0%)	44	49
All	All	1885/1952 (97%)	1838 (98%)	42 (2%)	5 (0%)	44	49

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	37	GLN
2	F	38	GLY
1	E	165	GLY
4	B	105	ALA
3	G	230	VAL

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	E	299/305 (98%)	295 (99%)	4 (1%)	73	85
2	F	403/424 (95%)	395 (98%)	8 (2%)	60	74
3	G	230/237 (97%)	226 (98%)	4 (2%)	66	79
4	A	314/323 (97%)	305 (97%)	9 (3%)	48	60
4	B	315/323 (98%)	303 (96%)	12 (4%)	38	47
All	All	1561/1612 (97%)	1524 (98%)	37 (2%)	54	67

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	22	ILE
4	A	270	VAL
4	B	288	GLU

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Mol	Chain	Res	Type
4	A	127	LEU
4	A	219	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	232	ASN
4	B	180	HIS
2	F	440	ASN
2	F	98	ASN
2	F	437	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
9	ANP	A	2501	8	29,33,33	2.07	8 (27%)	28,52,52	2.46	7 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	ANP	B	2502	8	29,33,33	2.03	8 (27%)	28,52,52	2.17	6 (21%)
5	UMQ	E	5004	-	35,35,35	0.44	0	46,46,46	0.89	2 (4%)
6	MAL	F	2000	-	24,24,24	0.46	0	35,35,35	0.92	2 (5%)
7	PGV	F	4001	-	50,50,50	1.08	3 (6%)	51,56,56	1.07	3 (5%)
7	PGV	F	4002	-	13,13,50	0.27	0	12,12,56	0.52	0
7	PGV	G	4006	-	13,13,50	0.26	0	12,12,56	0.53	0
7	PGV	G	4009	-	11,11,50	0.27	0	10,10,56	0.52	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
9	ANP	A	2501	8	-	0/13/38/38	0/3/3/3
9	ANP	B	2502	8	-	1/13/38/38	0/3/3/3
5	UMQ	E	5004	-	-	0/20/60/60	0/2/2/2
6	MAL	F	2000	-	-	0/8/48/48	0/2/2/2
7	PGV	F	4001	-	-	0/55/55/55	0/0/0/0
7	PGV	F	4002	-	-	0/11/11/55	0/0/0/0
7	PGV	G	4006	-	-	0/11/11/55	0/0/0/0
7	PGV	G	4009	-	-	0/9/9/55	0/0/0/0

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	2502	ANP	PG-O3G	-2.32	1.50	1.56
9	A	2501	ANP	PG-O2G	-2.29	1.50	1.56
9	A	2501	ANP	PB-O2B	-2.17	1.50	1.56
9	B	2502	ANP	PG-O2G	-2.06	1.51	1.56
9	B	2502	ANP	C2-N3	2.00	1.35	1.32

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	2501	ANP	O1G-PG-N3B	-7.84	100.06	111.79
9	A	2501	ANP	N3-C2-N1	-6.49	123.21	128.86
9	B	2502	ANP	N3-C2-N1	-6.30	123.38	128.86
9	B	2502	ANP	O1G-PG-N3B	-5.83	103.07	111.79
9	A	2501	ANP	O1B-PB-N3B	-3.57	106.45	111.79

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	B	2502	ANP	O1G-PG-N3B-PB

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	2501	ANP	2	0
9	B	2502	ANP	2	0
7	F	4001	PGV	2	0
7	G	4006	PGV	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	E	374/380 (98%)	0.55	44 (11%) 5 4	30, 66, 111, 133	1 (0%)
2	F	490/514 (95%)	0.83	75 (15%) 2 2	32, 61, 127, 188	0
3	G	286/296 (96%)	0.26	19 (6%) 19 18	28, 44, 81, 108	0
4	A	371/381 (97%)	0.18	15 (4%) 39 37	27, 44, 69, 94	0
4	B	371/381 (97%)	0.25	31 (8%) 12 10	25, 46, 84, 112	0
All	All	1892/1952 (96%)	0.45	184 (9%) 8 7	25, 51, 104, 188	1 (0%)

The worst 5 of 184 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	10	TRP	19.6
2	F	37	GLN	11.0
2	F	38	GLY	8.9
2	F	14	ALA	7.6
2	F	29	TYR	7.4

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron

density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	UMQ	E	5004	34/34	0.77	0.28	3.85	74,80,82,83	0
7	PGV	G	4009	12/51	0.73	0.23	2.15	70,71,74,74	0
7	PGV	F	4001	51/51	0.81	0.23	1.11	75,83,86,91	0
7	PGV	F	4002	14/51	0.72	0.25	0.92	58,60,65,66	0
7	PGV	G	4006	14/51	0.83	0.19	0.82	71,75,82,84	0
8	MG	B	1502	1/1	0.98	0.11	0.26	30,30,30,30	0
9	ANP	B	2502	31/31	0.98	0.10	-0.47	28,35,41,42	0
9	ANP	A	2501	31/31	0.98	0.09	-0.49	25,32,41,41	0
6	MAL	F	2000	23/23	0.95	0.09	-1.03	46,49,51,54	0
8	MG	A	1501	1/1	0.98	0.04	-2.65	28,28,28,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.