



wwPDB X-ray Structure Validation Summary Report

Mar 1, 2014 – 12:18 AM GMT

PDB ID : 1WUU
Title : crystal structure of human galactokinase complexed with MgAMPPNP and galactose
Authors : Thoden, J.B.; Timson, D.J.; Reece, R.J.; Holden, H.M.
Deposited on : 2004-12-08
Resolution : 2.50 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

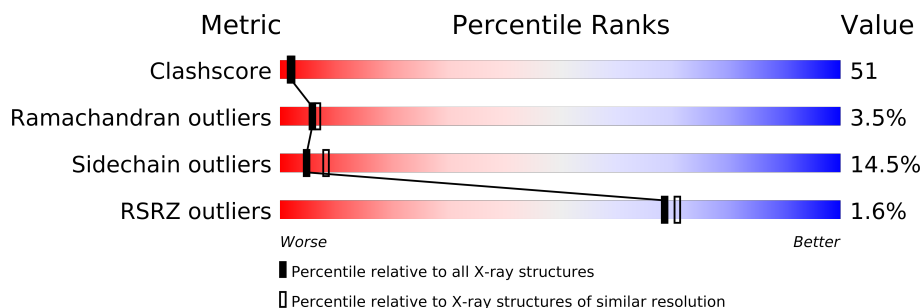
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

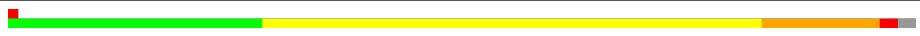



The reported resolution of this entry is 2.50 Å.

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))
Clashscore	79885	3562 (2.50-2.50)
Ramachandran outliers	78287	3480 (2.50-2.50)
Sidechain outliers	78261	3482 (2.50-2.50)
RSRZ outliers	66119	2785 (2.50-2.50)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	399	
1	B	399	
1	C	399	
1	D	399	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	GLA	B	393	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12358 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Galactokinase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	391	Total	C	N	O	S	Se	0	0	0
			2960	1847	538	559	8	8			
1	B	390	Total	C	N	O	S	Se	0	0	0
			2942	1838	530	558	8	8			
1	C	390	Total	C	N	O	S	Se	0	0	0
			2944	1838	532	558	8	8			
1	D	390	Total	C	N	O	S	Se	0	1	0
			2952	1842	535	559	8	8			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MSE	-	EXPRESSION TAG	UNP P51570
A	-5	ALA	-	EXPRESSION TAG	UNP P51570
A	-4	HIS	-	EXPRESSION TAG	UNP P51570
A	-3	HIS	-	EXPRESSION TAG	UNP P51570
A	-2	HIS	-	EXPRESSION TAG	UNP P51570
A	-1	HIS	-	EXPRESSION TAG	UNP P51570
A	0	HIS	-	EXPRESSION TAG	UNP P51570
A	1	HIS	-	EXPRESSION TAG	UNP P51570
A	55	MSE	MET	MODIFIED RESIDUE	UNP P51570
A	60	MSE	MET	MODIFIED RESIDUE	UNP P51570
A	180	MSE	MET	MODIFIED RESIDUE	UNP P51570
A	185	MSE	MET	MODIFIED RESIDUE	UNP P51570
A	192	MSE	MET	MODIFIED RESIDUE	UNP P51570
A	307	MSE	MET	MODIFIED RESIDUE	UNP P51570
A	343	MSE	MET	MODIFIED RESIDUE	UNP P51570
A	365	MSE	MET	MODIFIED RESIDUE	UNP P51570
B	-6	MSE	-	EXPRESSION TAG	UNP P51570
B	-5	ALA	-	EXPRESSION TAG	UNP P51570
B	-4	HIS	-	EXPRESSION TAG	UNP P51570
B	-3	HIS	-	EXPRESSION TAG	UNP P51570
B	-2	HIS	-	EXPRESSION TAG	UNP P51570

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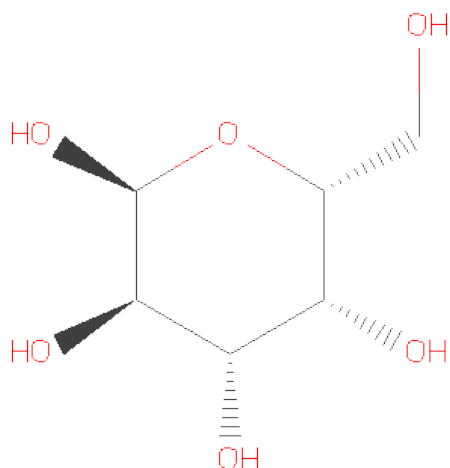
Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	HIS	-	EXPRESSION TAG	UNP P51570
B	0	HIS	-	EXPRESSION TAG	UNP P51570
B	1	HIS	-	EXPRESSION TAG	UNP P51570
B	55	MSE	MET	MODIFIED RESIDUE	UNP P51570
B	60	MSE	MET	MODIFIED RESIDUE	UNP P51570
B	180	MSE	MET	MODIFIED RESIDUE	UNP P51570
B	185	MSE	MET	MODIFIED RESIDUE	UNP P51570
B	192	MSE	MET	MODIFIED RESIDUE	UNP P51570
B	307	MSE	MET	MODIFIED RESIDUE	UNP P51570
B	343	MSE	MET	MODIFIED RESIDUE	UNP P51570
B	365	MSE	MET	MODIFIED RESIDUE	UNP P51570
C	-6	MSE	-	EXPRESSION TAG	UNP P51570
C	-5	ALA	-	EXPRESSION TAG	UNP P51570
C	-4	HIS	-	EXPRESSION TAG	UNP P51570
C	-3	HIS	-	EXPRESSION TAG	UNP P51570
C	-2	HIS	-	EXPRESSION TAG	UNP P51570
C	-1	HIS	-	EXPRESSION TAG	UNP P51570
C	0	HIS	-	EXPRESSION TAG	UNP P51570
C	1	HIS	-	EXPRESSION TAG	UNP P51570
C	55	MSE	MET	MODIFIED RESIDUE	UNP P51570
C	60	MSE	MET	MODIFIED RESIDUE	UNP P51570
C	180	MSE	MET	MODIFIED RESIDUE	UNP P51570
C	185	MSE	MET	MODIFIED RESIDUE	UNP P51570
C	192	MSE	MET	MODIFIED RESIDUE	UNP P51570
C	307	MSE	MET	MODIFIED RESIDUE	UNP P51570
C	343	MSE	MET	MODIFIED RESIDUE	UNP P51570
C	365	MSE	MET	MODIFIED RESIDUE	UNP P51570
D	-6	MSE	-	EXPRESSION TAG	UNP P51570
D	-5	ALA	-	EXPRESSION TAG	UNP P51570
D	-4	HIS	-	EXPRESSION TAG	UNP P51570
D	-3	HIS	-	EXPRESSION TAG	UNP P51570
D	-2	HIS	-	EXPRESSION TAG	UNP P51570
D	-1	HIS	-	EXPRESSION TAG	UNP P51570
D	0	HIS	-	EXPRESSION TAG	UNP P51570
D	1	HIS	-	EXPRESSION TAG	UNP P51570
D	55	MSE	MET	MODIFIED RESIDUE	UNP P51570
D	60	MSE	MET	MODIFIED RESIDUE	UNP P51570
D	180	MSE	MET	MODIFIED RESIDUE	UNP P51570
D	185	MSE	MET	MODIFIED RESIDUE	UNP P51570
D	192	MSE	MET	MODIFIED RESIDUE	UNP P51570
D	307	MSE	MET	MODIFIED RESIDUE	UNP P51570
D	343	MSE	MET	MODIFIED RESIDUE	UNP P51570

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Chain	Residue	Modelled	Actual	Comment	Reference
D	365	MSE	MET	MODIFIED RESIDUE	UNP P51570

- Molecule 2 is SUGAR (D-GALACTOSE) (three-letter code: GLA) (formula: $C_6H_{12}O_6$).

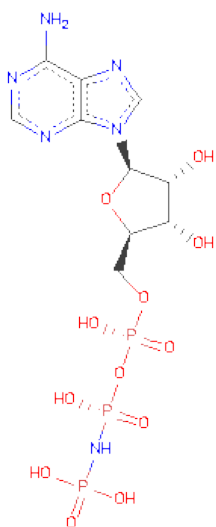


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			12	6	6		
2	B	1	Total	C	O	0	0
			12	6	6		
2	C	1	Total	C	O	0	0
			12	6	6		
2	D	1	Total	C	O	0	0
			12	6	6		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		
3	A	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		

- Molecule 4 is PHOSPHOAMINOPHOSPHONICACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).



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

- Molecule 5 is water.

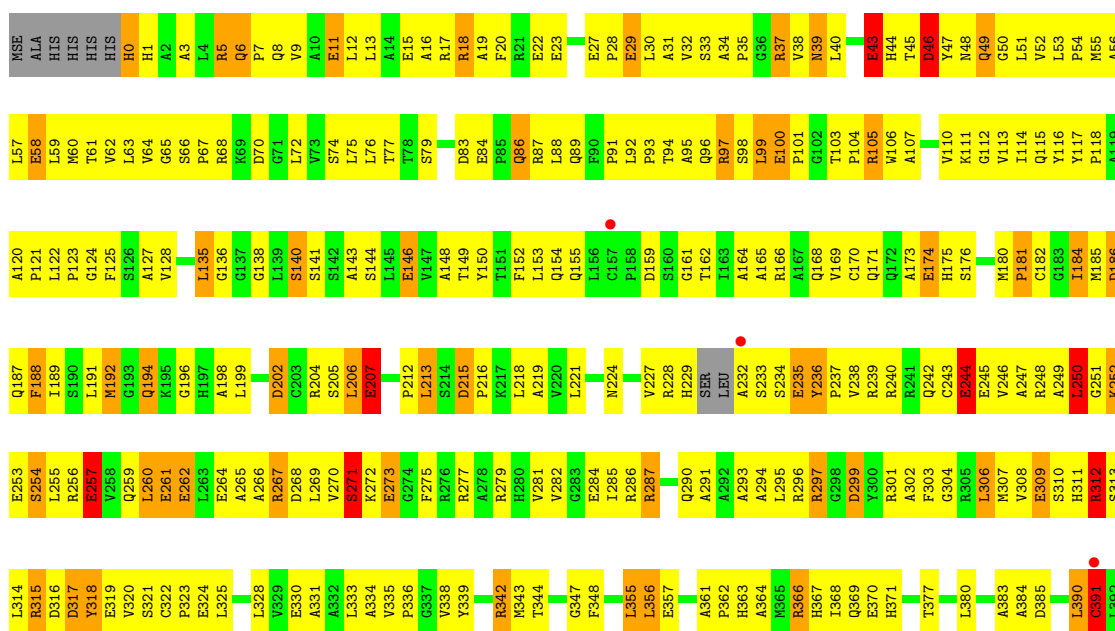
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	94	Total	O	0	0
			94	94		
5	B	89	Total	O	0	0
			89	89		
5	C	105	Total	O	0	0
			105	105		
5	D	96	Total	O	0	0
			96	96		

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.

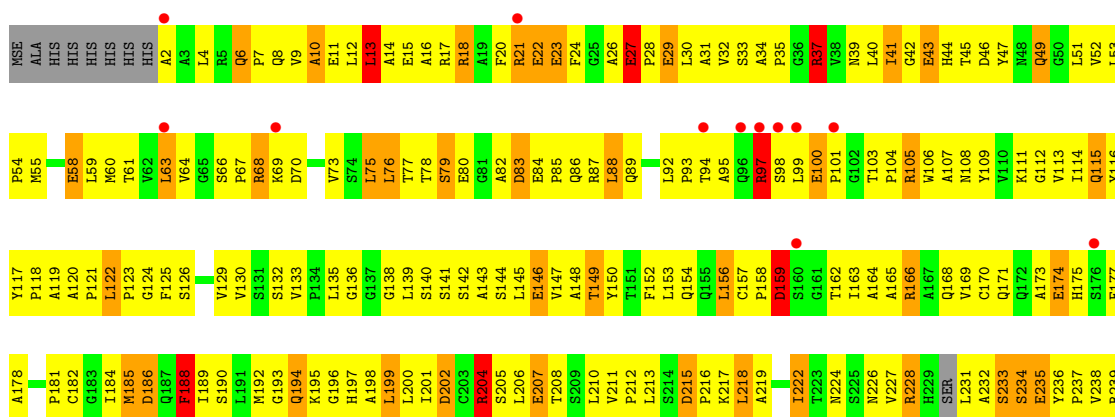
• Molecule 1: Galactokinase

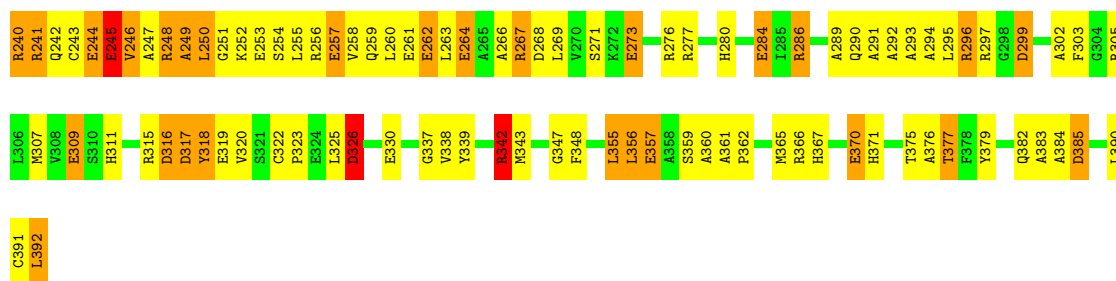
Chain A:



• Molecule 1: Galactokinase

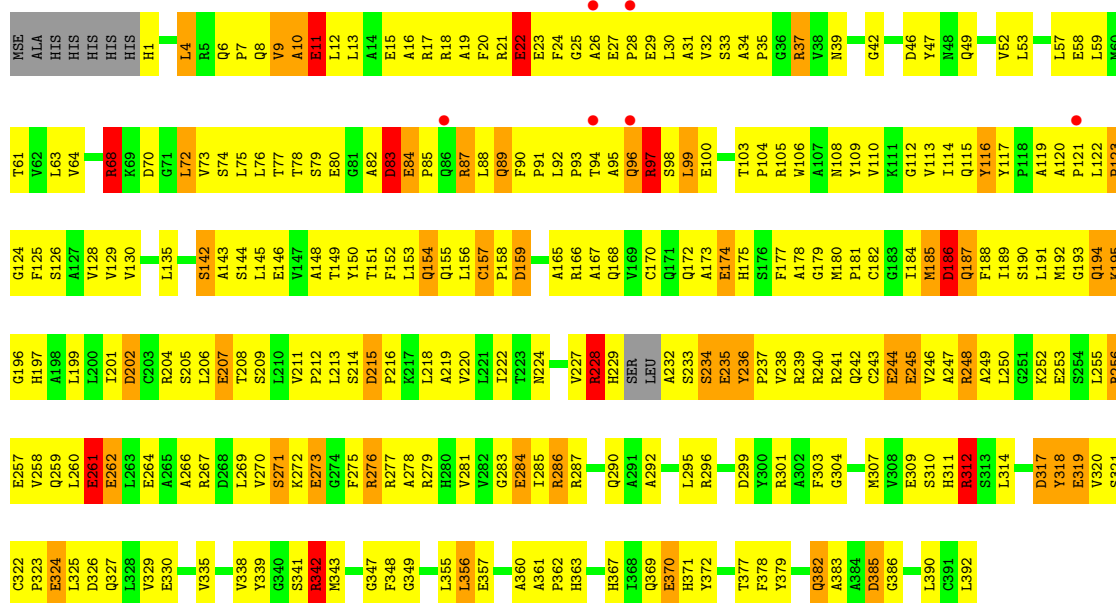
Chain B:





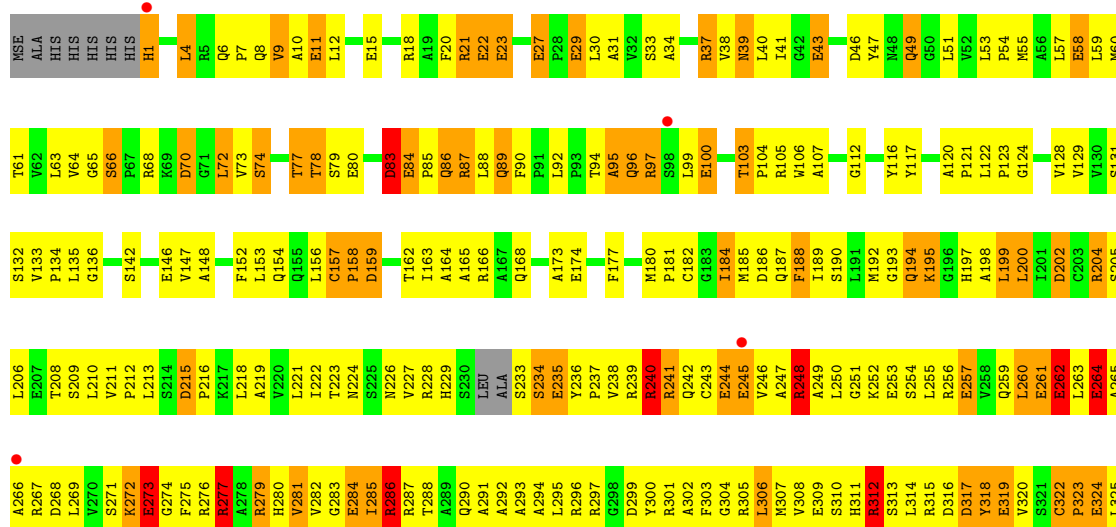
• Molecule 1: Galactokinase

Chain C:



• Molecule 1: Galactokinase

Chain D:



Q326	Q327	L328	Y329	E330	A331	A332	L333	A334	Y335	Y339	G340	S341	R342	M343	T344	G345	G346	G347	F348	G349	G350	C351	T352	T353	T354	L355	L356	E357	A358	S359	A360	A361	F362	H363	A364	M365	R366	H367	L368	Q369	E370	H371	Y372	G373	G374	T375	A376	T377	F378	Y379	L380	S381	Q382	D385	L392
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.20Å 109.60Å 115.80Å 90.00° 95.90° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 19.95 – 2.50	Depositor EDS
% Data completeness (in resolution range)	95.2 (20.00-2.50) 97.9 (19.95-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.02 (at 2.50Å)	Xtriage
Refinement program	TNT	Depositor
R, R_{free}	0.201 , 0.258 0.202 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	41.6	Xtriage
Anisotropy	0.546	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 101.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 61550 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12358	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.59% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GLA, MG, ANP

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	1.05	24/3007 (0.8%)	1.32	28/4062 (0.7%)
1	B	1.02	28/2987 (0.9%)	1.39	38/4036 (0.9%)
1	C	1.05	29/2990 (1.0%)	1.31	31/4040 (0.8%)
1	D	1.05	26/3002 (0.9%)	1.33	32/4055 (0.8%)
All	All	1.04	107/11986 (0.9%)	1.34	129/16193 (0.8%)

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	D	1	0

The worst 5 of 107 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	244	GLU	CD-OE2	7.87	1.34	1.25
1	A	194	GLN	CA-CB	-7.86	1.36	1.53
1	A	84	GLU	CD-OE2	7.60	1.34	1.25
1	C	261	GLU	CD-OE2	7.42	1.33	1.25
1	D	174	GLU	CD-OE2	7.38	1.33	1.25

The worst 5 of 129 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	70	ASP	N-CA-CB	-13.51	86.29	110.60
1	B	70	ASP	CB-CA-C	13.23	136.85	110.40
1	D	157	CYS	C-N-CD	-12.20	93.76	120.60
1	B	46	ASP	CB-CG-OD2	-8.62	110.54	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	204	ARG	NE-CZ-NH1	8.53	124.57	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	D	229	HIS	CA

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2960	0	2947	286	0
1	B	2942	0	2930	328	0
1	C	2944	0	2929	302	0
1	D	2952	0	2939	311	0
2	A	12	0	12	1	0
2	B	12	0	12	0	0
2	C	12	0	12	0	0
2	D	12	0	12	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	31	0	13	6	0
4	B	31	0	13	7	0
4	C	31	0	13	8	0
4	D	31	0	13	3	0
5	A	94	0	0	6	0
5	B	89	0	0	7	0
5	C	105	0	0	9	0
5	D	96	0	0	14	0
All	All	12358	0	11845	1220	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including

hydrogens) of the entry. The overall clashscore for this entry is 51.

The worst 5 of 1220 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:201:ILE:HG23	1:B:208:THR:HG22	1.24	1.18
1:B:250:LEU:HD21	1:B:266:ALA:HB2	1.20	1.16
1:A:266:ALA:HB1	1:A:269:LEU:HB2	1.29	1.14
1:A:307:MSE:HE1	1:A:355:LEU:HB2	1.30	1.13
1:A:246:VAL:HG22	1:A:270:VAL:HG11	1.27	1.12

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	387/399 (97%)	326 (84%)	52 (13%)	9 (2%)	10	14
1	B	386/399 (97%)	320 (83%)	50 (13%)	16 (4%)	4	5
1	C	386/399 (97%)	331 (86%)	42 (11%)	13 (3%)	6	7
1	D	387/399 (97%)	319 (82%)	52 (13%)	16 (4%)	4	5
All	All	1546/1596 (97%)	1296 (84%)	196 (13%)	54 (4%)	6	7

5 of 54 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	99	LEU
1	A	271	SER
1	B	18	ARG
1	B	115	GLN
1	B	158	PRO

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	309/308 (100%)	261 (84%)	48 (16%)	4	7
1	B	307/308 (100%)	260 (85%)	47 (15%)	4	7
1	C	307/308 (100%)	276 (90%)	31 (10%)	11	20
1	D	309/308 (100%)	257 (83%)	52 (17%)	3	5
All	All	1232/1232 (100%)	1054 (86%)	178 (14%)	5	8

5 of 178 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	222	ILE
1	C	37	ARG
1	D	279	ARG
1	B	250	LEU
1	B	356	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	89	GLN
1	C	171	GLN
1	D	226	ASN
1	C	155	GLN
1	C	187	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 12 ligands modelled in this entry, 4 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
2	GLA	A	393	-	12,12,12	0.67	0	17,17,17	1.10	0
4	ANP	A	395	3	33,33,33	1.57	5 (15%)	51,52,52	1.82	11 (21%)
2	GLA	B	393	-	12,12,12	0.51	0	17,17,17	1.46	4 (23%)
4	ANP	B	395	3	33,33,33	2.10	6 (18%)	51,52,52	1.68	9 (17%)
2	GLA	C	393	-	12,12,12	0.55	0	17,17,17	1.10	1 (5%)
4	ANP	C	395	3	33,33,33	1.76	8 (24%)	51,52,52	1.68	10 (19%)
2	GLA	D	393	-	12,12,12	0.51	0	17,17,17	1.10	0
4	ANP	D	395	3	33,33,33	1.45	5 (15%)	51,52,52	1.61	8 (15%)

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
2	GLA	A	393	-	-	0/2/22/22	0/1/1/1
4	ANP	A	395	3	-	0/18/38/38	0/1/3/3
2	GLA	B	393	-	-	0/2/22/22	0/1/1/1
4	ANP	B	395	3	-	0/18/38/38	0/1/3/3
2	GLA	C	393	-	-	0/2/22/22	0/1/1/1
4	ANP	C	395	3	-	0/18/38/38	0/1/3/3
2	GLA	D	393	-	-	0/2/22/22	0/1/1/1
4	ANP	D	395	3	-	0/18/38/38	0/1/3/3

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	395	ANP	PG-N3B	-6.41	1.58	1.64
4	B	395	ANP	PB-N3B	-6.37	1.58	1.64
4	C	395	ANP	PB-N3B	-5.05	1.59	1.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	395	ANP	PB-N3B	-4.27	1.60	1.64
4	C	395	ANP	PG-N3B	-4.27	1.60	1.64

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	395	ANP	N3-C2-N1	-6.79	123.03	128.71
4	B	395	ANP	N3-C2-N1	-6.49	123.28	128.71
4	C	395	ANP	N3-C2-N1	-5.82	123.84	128.71
4	A	395	ANP	N3-C2-N1	-5.58	124.05	128.71
4	A	395	ANP	O4'-C1'-N9	-4.50	104.25	108.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	391/399 (97%)	-0.30	3 (0%) 83 84	22, 41, 69, 84	0
1	B	390/399 (97%)	-0.07	12 (3%) 47 48	19, 48, 76, 93	0
1	C	390/399 (97%)	-0.26	6 (1%) 70 72	15, 40, 73, 91	0
1	D	390/399 (97%)	-0.31	4 (1%) 79 81	21, 41, 68, 88	0
All	All	1561/1596 (97%)	-0.24	25 (1%) 68 71	15, 42, 73, 93	0

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	94	THR	4.0
1	B	97	ARG	3.8
1	C	26	ALA	3.4
1	D	1	HIS	3.3
1	C	121	PRO	3.2

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 carbohydrates 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. 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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	GLA	B	393	12/12	0.17	2.44	22,34,54,71	0
3	MG	A	394	1/1	0.14	0.54	38,38,38,38	0
4	ANP	B	395	31/31	0.15	0.06	0,44,81,94	0
2	GLA	D	393	12/12	0.12	-0.31	2,22,31,55	0
2	GLA	A	393	12/12	0.12	-0.50	22,33,49,66	0
2	GLA	C	393	12/12	0.11	-0.65	6,19,58,80	0
4	ANP	A	395	31/31	0.09	-1.01	19,34,50,66	0
4	ANP	C	395	31/31	0.10	-1.03	0,36,57,92	0
4	ANP	D	395	31/31	0.08	-1.71	12,26,51,80	0
3	MG	C	394	1/1	0.05	-3.46	26,26,26,26	0
3	MG	B	394	1/1	0.09	-4.17	41,41,41,41	0
3	MG	D	394	1/1	0.08	-10.09	27,27,27,27	0

6.5 Other polymers ⓘ

There are no such residues in this entry.