



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 06:09 PM GMT

PDB ID : 1A5U
Title : PYRUVATE KINASE COMPLEX WITH BIS MG-ATP-NA-OXALATE
Authors : Larsen, T.M.; Benning, M.M.; Rayment, I.; Reed, G.H.
Deposited on : 1998-02-18
Resolution : 2.35 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>

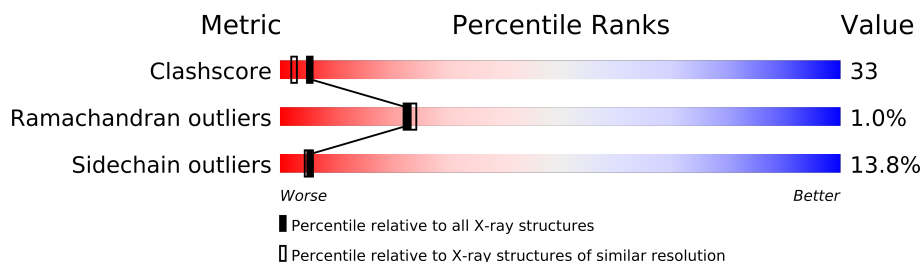
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	21963
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 2.35 Å.

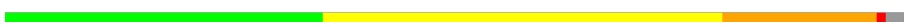

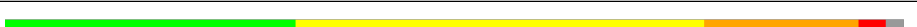

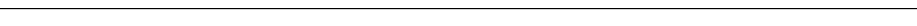



Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	1064 (2.38-2.34)
Ramachandran outliers	78287	1048 (2.38-2.34)
Sidechain outliers	78261	1049 (2.38-2.34)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	530	
1	B	530	
1	C	530	
1	D	530	
1	E	530	
1	F	530	
1	G	530	
1	H	530	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 33890 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 PYRUVATE KINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	519	Total	C	N	O	S	0	0	0
			3978	2498	708	744	28			
1	B	519	Total	C	N	O	S	0	0	0
			3978	2498	708	744	28			
1	C	519	Total	C	N	O	S	0	0	0
			3978	2498	708	744	28			
1	D	519	Total	C	N	O	S	0	0	0
			3978	2498	708	744	28			
1	E	519	Total	C	N	O	S	0	0	0
			3978	2498	708	744	28			
1	F	519	Total	C	N	O	S	0	0	0
			3978	2498	708	744	28			
1	G	519	Total	C	N	O	S	0	0	0
			3978	2498	708	744	28			
1	H	519	Total	C	N	O	S	0	0	0
			3978	2498	708	744	28			

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

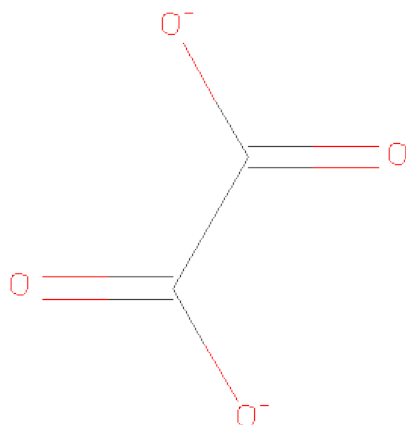
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	1	Total	Na	0	0
			1	1		
2	D	1	Total	Na	0	0
			1	1		
2	E	1	Total	Na	0	0
			1	1		
2	H	1	Total	Na	0	0
			1	1		
2	B	1	Total	Na	0	0
			1	1		
2	C	1	Total	Na	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Na	0	0
			1	1		
2	F	1	Total	Na	0	0
			1	1		

- Molecule 3 is OXALATE ION (three-letter code: OXL) (formula: C_2O_4).

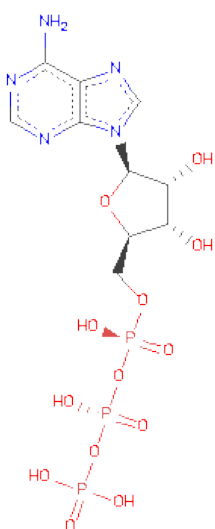


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	2	4		
3	B	1	Total	C	O	0	0
			6	2	4		
3	C	1	Total	C	O	0	0
			6	2	4		
3	D	1	Total	C	O	0	0
			6	2	4		
3	E	1	Total	C	O	0	0
			6	2	4		
3	F	1	Total	C	O	0	0
			6	2	4		
3	G	1	Total	C	O	0	0
			6	2	4		
3	H	1	Total	C	O	0	0
			6	2	4		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	G	2	Total Mg 2 2	0	0
4	D	2	Total Mg 2 2	0	0
4	E	2	Total Mg 2 2	0	0
4	H	1	Total Mg 1 1	0	0
4	B	1	Total Mg 1 1	0	0
4	C	2	Total Mg 2 2	0	0
4	A	2	Total Mg 2 2	0	0
4	F	2	Total Mg 2 2	0	0

- Molecule 5 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N O P 31 10 5 13 3	0	0
5	C	1	Total C N O P 31 10 5 13 3	0	0
5	D	1	Total C N O P 31 10 5 13 3	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	E	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
5	F	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
5	G	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	176	Total	O	0	0
			176	176		
6	B	260	Total	O	0	0
			260	260		
6	C	166	Total	O	0	0
			166	166		
6	D	250	Total	O	0	0
			250	250		
6	E	267	Total	O	0	0
			267	267		
6	F	185	Total	O	0	0
			185	185		
6	G	210	Total	O	0	0
			210	210		
6	H	296	Total	O	0	0
			296	296		

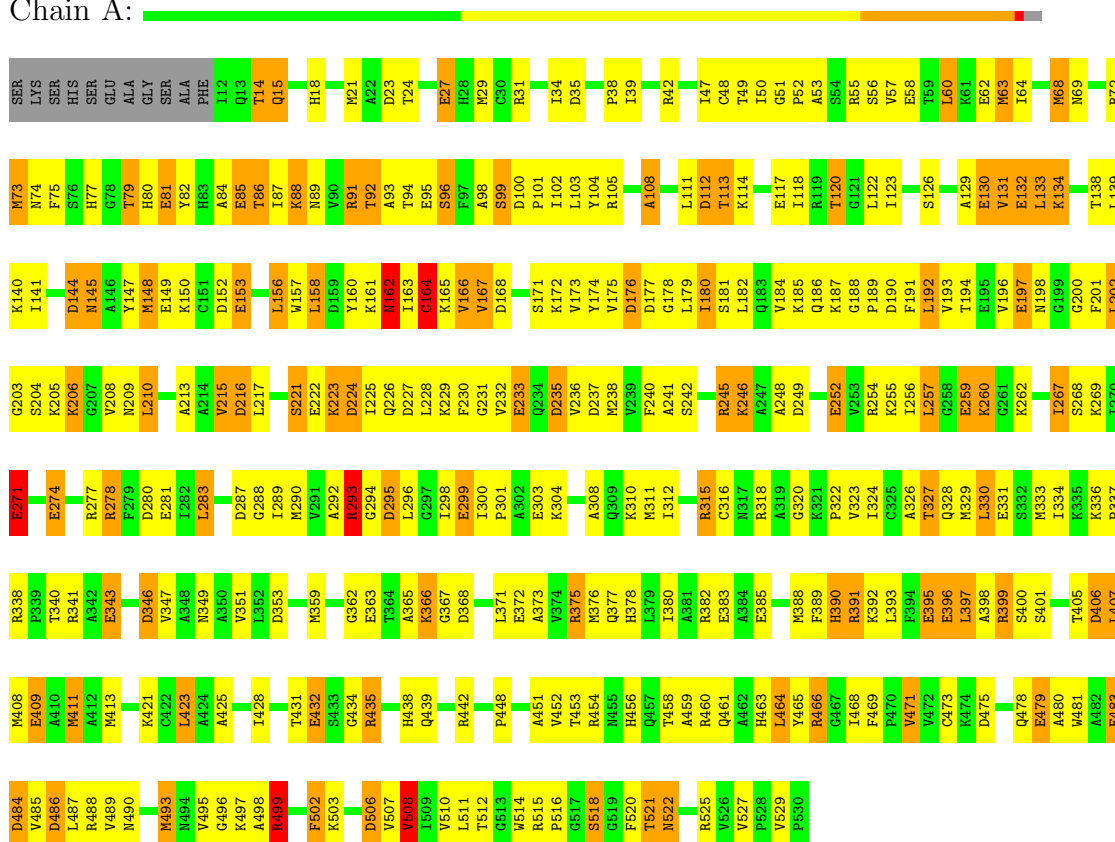
3 Residue-property plots

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.

Note EDS was not executed.

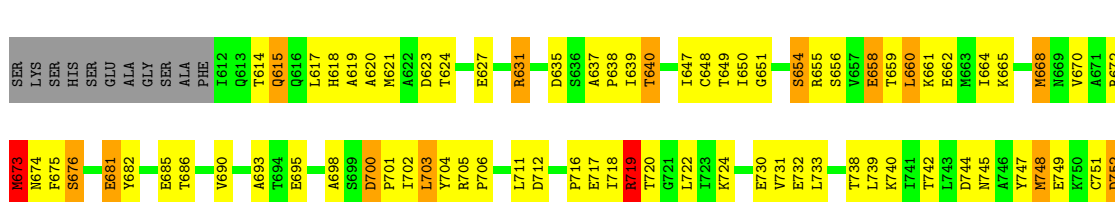
• Molecule 1: PYRUVATE KINASE

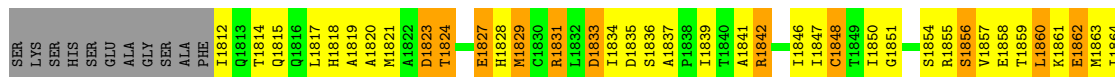
Chain A:

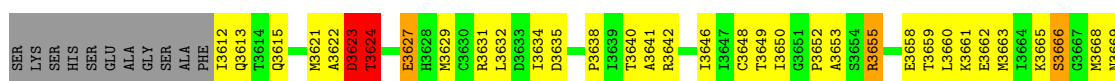


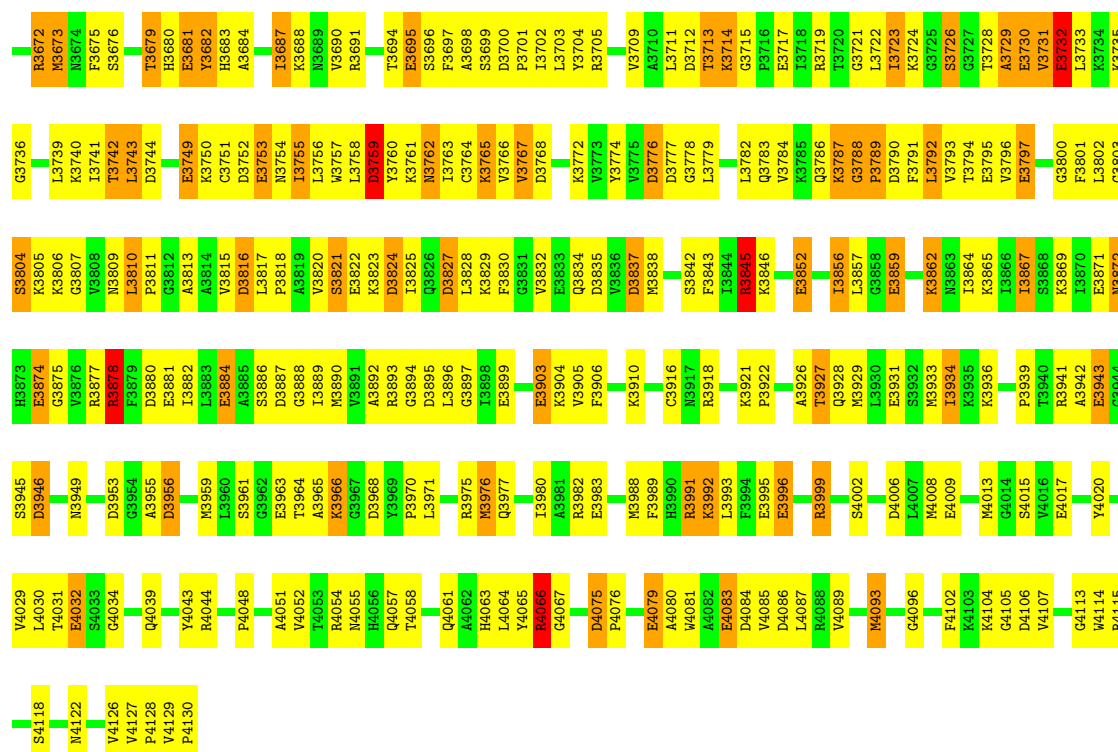
• Molecule 1: PYRUVATE KINASE

Chain B:



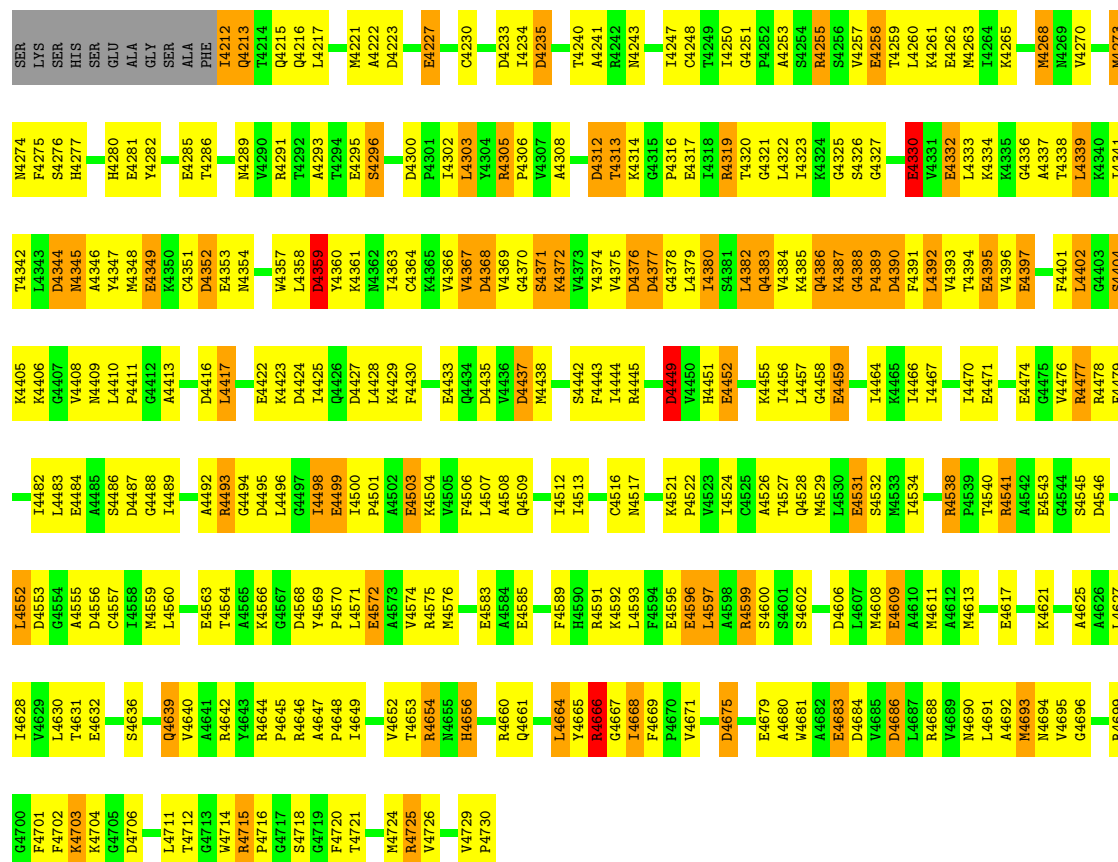






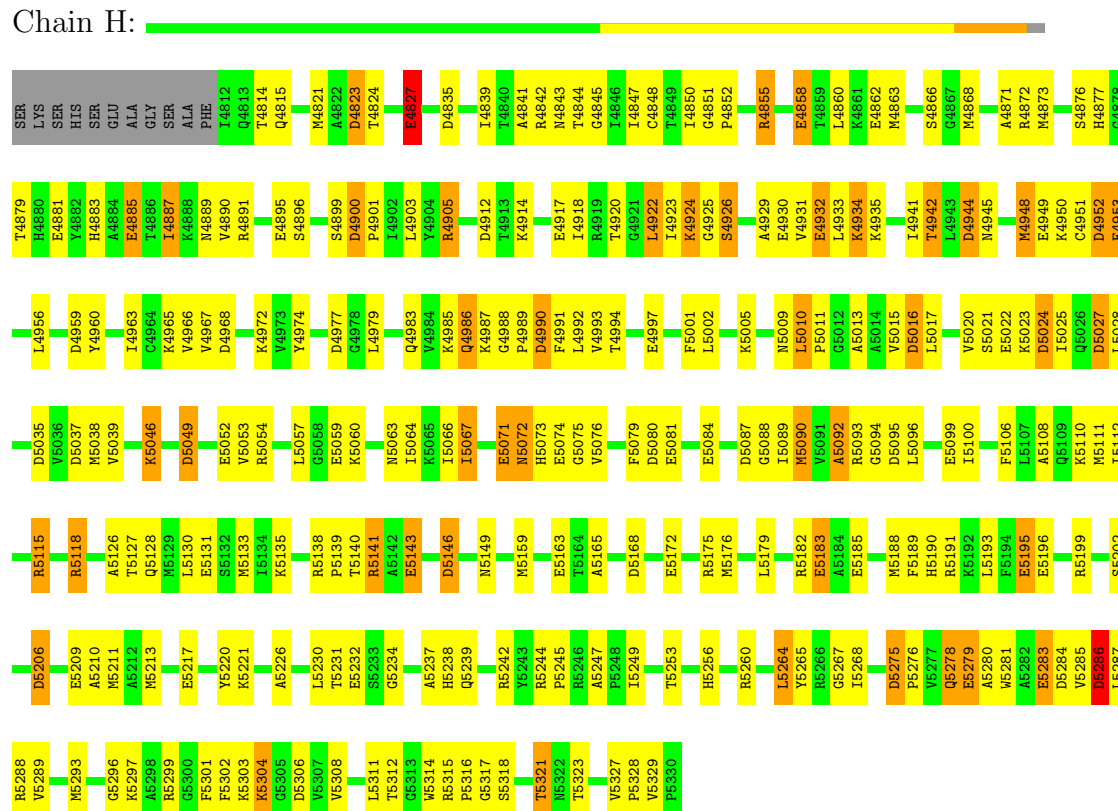
• Molecule 1: PYRUVATE KINASE

Chain G:



● Molecule 1: PYRUVATE KINASE

Chain H:



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	95.30Å 216.50Å 258.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.35	Depositor
% Data completeness (in resolution range)	85.0 (30.00-2.35)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT V. 5-D	Depositor
R, R_{free}	0.190 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	33890	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

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: OXL, NA, MG, ATP

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	1.06	31/4041 (0.8%)	1.39	57/5452 (1.0%)
1	B	1.02	25/4041 (0.6%)	1.39	59/5452 (1.1%)
1	C	0.98	26/4041 (0.6%)	1.39	66/5452 (1.2%)
1	D	1.01	29/4041 (0.7%)	1.39	56/5452 (1.0%)
1	E	1.01	29/4041 (0.7%)	1.43	63/5452 (1.2%)
1	F	0.97	24/4041 (0.6%)	1.40	62/5452 (1.1%)
1	G	0.99	30/4041 (0.7%)	1.39	60/5452 (1.1%)
1	H	1.01	29/4041 (0.7%)	1.37	62/5452 (1.1%)
All	All	1.00	223/32328 (0.7%)	1.39	485/43616 (1.1%)

The worst 5 of 223 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	162	ASN	N-CA	18.25	1.82	1.46
1	A	241	ALA	C-N	-8.32	1.15	1.34
1	D	1917	GLU	CD-OE2	8.30	1.34	1.25
1	B	681	GLU	CD-OE2	8.22	1.34	1.25
1	G	4595	GLU	CD-OE1	8.00	1.34	1.25

The worst 5 of 485 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	1919	ARG	NE-CZ-NH1	14.55	127.58	120.30
1	D	1919	ARG	NE-CZ-NH2	-12.64	113.98	120.30
1	F	4066	ARG	NE-CZ-NH1	11.98	126.29	120.30
1	B	1127	VAL	C-N-CD	-11.61	95.06	120.60
1	A	164	CYS	O-C-N	11.47	141.05	122.70

There are no chirality outliers.

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	3978	0	4054	349	2
1	B	3978	0	4056	228	0
1	C	3978	0	4056	364	5
1	D	3978	0	4055	269	5
1	E	3978	0	4056	251	12
1	F	3978	0	4056	264	2
1	G	3978	0	4056	293	2
1	H	3978	0	4056	208	18
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	6	0	0	2	0
3	B	6	0	0	0	0
3	C	6	0	0	1	0
3	D	6	0	0	1	0
3	E	6	0	0	1	0
3	F	6	0	0	2	0
3	G	6	0	0	2	0
3	H	6	0	0	1	0
4	A	2	0	0	0	0
4	B	1	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
4	E	2	0	0	0	0
4	F	2	0	0	0	0
4	G	2	0	0	0	0
4	H	1	0	0	0	0
5	A	31	0	12	4	0
5	C	31	0	12	4	0
5	D	31	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	31	0	12	2	0
5	F	31	0	12	0	0
5	G	31	0	12	0	0
6	A	176	0	0	10	0
6	B	260	0	0	13	0
6	C	166	0	0	12	0
6	D	250	0	0	18	0
6	E	267	0	0	17	0
6	F	185	0	0	11	0
6	G	210	0	0	6	0
6	H	296	0	0	15	2
All	All	33890	0	32517	2117	24

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 33.

The worst 5 of 2117 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:162:ASN:N	1:A:162:ASN:CA	1.82	1.40
1:C:1678:GLN:HB2	1:C:1684:ASP:HB2	1.31	1.13
1:A:122:LEU:HD23	1:A:204:SER:HB3	1.28	1.12
1:E:3142:THR:HG22	1:E:3144:ASP:H	1.06	1.07
1:E:3493:MET:HE2	1:E:3530:PRO:HD2	1.37	1.06

The worst 5 of 24 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:3149:GLU:OE1	1:H:4934:LYS:CE[3_655]	0.67	1.53
1:E:3149:GLU:CD	1:H:4934:LYS:NZ[3_655]	1.03	1.17
1:E:3149:GLU:CD	1:H:4934:LYS:CE[3_655]	1.23	0.97
1:D:1924:LYS:NZ	1:H:4858:GLU:OE1[1_455]	1.38	0.82
1:E:3149:GLU:OE1	1:H:4934:LYS:CD[3_655]	1.43	0.77

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	517/530 (98%)	476 (92%)	36 (7%)	5 (1%)	22	24
1	B	517/530 (98%)	485 (94%)	30 (6%)	2 (0%)	43	52
1	C	517/530 (98%)	464 (90%)	42 (8%)	11 (2%)	11	7
1	D	517/530 (98%)	487 (94%)	27 (5%)	3 (1%)	33	39
1	E	517/530 (98%)	484 (94%)	26 (5%)	7 (1%)	16	15
1	F	517/530 (98%)	486 (94%)	27 (5%)	4 (1%)	27	31
1	G	517/530 (98%)	487 (94%)	27 (5%)	3 (1%)	33	39
1	H	517/530 (98%)	485 (94%)	27 (5%)	5 (1%)	22	24
All	All	4136/4240 (98%)	3854 (93%)	242 (6%)	40 (1%)	22	24

5 of 40 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	1337	ALA
1	C	1533	MET
1	F	3729	ALA
1	F	3789	PRO
1	G	4389	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	426/434 (98%)	348 (82%)	78 (18%)	2	2
1	B	426/434 (98%)	377 (88%)	49 (12%)	8	7
1	C	426/434 (98%)	346 (81%)	80 (19%)	2	2
1	D	426/434 (98%)	379 (89%)	47 (11%)	9	9
1	E	426/434 (98%)	370 (87%)	56 (13%)	6	6
1	F	426/434 (98%)	365 (86%)	61 (14%)	5	5
1	G	426/434 (98%)	367 (86%)	59 (14%)	5	5
1	H	426/434 (98%)	384 (90%)	42 (10%)	11	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3408/3472 (98%)	2936 (86%)	472 (14%)	5 5

5 of 472 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	1887	ILE
1	E	3081	GLU
1	H	4887	ILE
1	D	1931	VAL
1	D	2145	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 113 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	2063	ASN
1	E	3162	ASN
1	H	4986	GLN
1	D	2128	GLN
1	D	2257	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 36 ligands modelled in this entry, 22 are monoatomic - leaving 14 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	OXL	A	533	4	0,5,5	0.00	-	0,6,6	0.00	-
5	ATP	A	535	2,4	33,33,33	2.31	11 (33%)	52,52,52	1.51	4 (7%)
3	OXL	B	1133	4	0,5,5	0.00	-	0,6,6	0.00	-
3	OXL	C	1733	4	0,5,5	0.00	-	0,6,6	0.00	-
5	ATP	C	1735	4	33,33,33	2.33	9 (27%)	52,52,52	1.37	7 (13%)
3	OXL	D	2333	4	0,5,5	0.00	-	0,6,6	0.00	-
5	ATP	D	2335	2,4	33,33,33	2.29	9 (27%)	52,52,52	1.93	7 (13%)
3	OXL	E	3533	4	0,5,5	0.00	-	0,6,6	0.00	-
5	ATP	E	3535	2,4	33,33,33	1.98	7 (21%)	52,52,52	1.12	4 (7%)
3	OXL	F	4133	4	0,5,5	0.00	-	0,6,6	0.00	-
5	ATP	F	4135	2,4	33,33,33	2.29	8 (24%)	52,52,52	1.36	5 (9%)
3	OXL	G	4733	4	0,5,5	0.00	-	0,6,6	0.00	-
5	ATP	G	4735	2,4	33,33,33	2.23	9 (27%)	52,52,52	1.14	4 (7%)
3	OXL	H	5333	4	0,5,5	0.00	-	0,6,6	0.00	-

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	OXL	A	533	4	-	0/0/4/4	0/0/0/0
5	ATP	A	535	2,4	-	0/22/38/38	0/1/3/3
3	OXL	B	1133	4	-	0/0/4/4	0/0/0/0
3	OXL	C	1733	4	-	0/0/4/4	0/0/0/0
5	ATP	C	1735	4	-	0/22/38/38	0/1/3/3
3	OXL	D	2333	4	-	0/0/4/4	0/0/0/0
5	ATP	D	2335	2,4	-	0/22/38/38	0/1/3/3
3	OXL	E	3533	4	-	0/0/4/4	0/0/0/0
5	ATP	E	3535	2,4	-	0/22/38/38	0/1/3/3
3	OXL	F	4133	4	-	0/0/4/4	0/0/0/0
5	ATP	F	4135	2,4	-	0/22/38/38	0/1/3/3
3	OXL	G	4733	4	-	0/0/4/4	0/0/0/0
5	ATP	G	4735	2,4	-	0/22/38/38	0/1/3/3
3	OXL	H	5333	4	-	0/0/4/4	0/0/0/0

The worst 5 of 53 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	535	ATP	PG-O3B	9.18	1.76	1.60
5	C	1735	ATP	PG-O3B	8.55	1.75	1.60
5	D	2335	ATP	PG-O3B	7.95	1.74	1.60
5	G	4735	ATP	PB-O3B	-7.92	1.45	1.59
5	F	4135	ATP	PB-O3B	-6.88	1.47	1.59

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	2335	ATP	O3A-PB-O3B	9.86	121.71	101.66
5	F	4135	ATP	O3A-PB-O3B	5.88	113.61	101.66
5	A	535	ATP	O3A-PB-O3B	-5.77	89.94	101.66
5	D	2335	ATP	O2G-PG-O1G	5.33	127.86	110.44
5	A	535	ATP	O2B-PB-O3B	4.69	127.39	105.14

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 ⓘ

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.