



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 24, 2017 – 05:00 PM EDT

PDB ID : 5L13
Title : Structure of ALDH2 in complex with 2P3
Authors : Buchman, C.D.; Hurley, T.D.
Deposited on : unknown
Resolution : 2.40 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 : rb-20030345
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) : rb-20030345

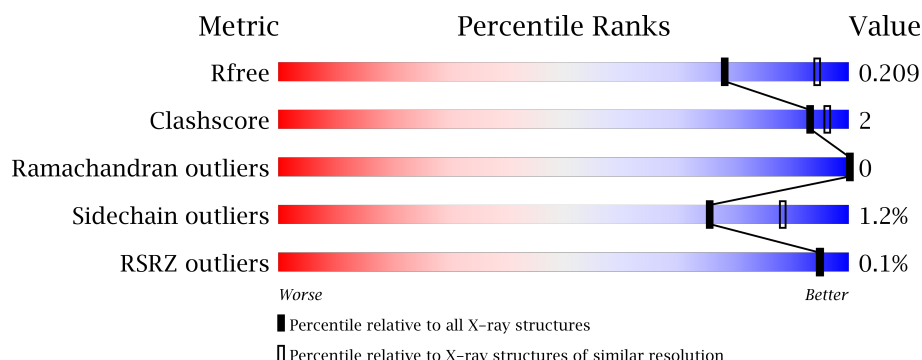
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	3166 (2.40-2.40)
Clashscore	112137	3674 (2.40-2.40)
Ramachandran outliers	110173	3616 (2.40-2.40)
Sidechain outliers	110143	3617 (2.40-2.40)
RSRZ outliers	101464	3195 (2.40-2.40)

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	517	
1	B	517	
1	C	517	
1	D	517	
1	E	517	

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Mol	Chain	Length	Quality of chain
1	F	517	 91% . .
1	G	517	 90% 6% . .
1	H	517	 91% . .

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	EDO	A	602	-	-	-	X
3	EDO	B	603	-	-	-	X
3	EDO	E	602	-	-	-	X
3	EDO	F	602	-	-	-	X
3	EDO	G	602	-	-	-	X
3	EDO	G	603	-	-	-	X
3	EDO	G	604	-	-	-	X
4	GAI	A	605	-	-	-	X
4	GAI	C	602	-	-	-	X
4	GAI	D	605	-	-	-	X
4	GAI	E	605	-	-	-	X
4	GAI	E	606	-	-	-	X
4	GAI	F	604	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 32476 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 Aldehyde dehydrogenase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	494	Total	C	N	O	S	0	1	0
			3804	2419	649	718	18			
1	B	494	Total	C	N	O	S	0	1	0
			3803	2419	648	717	19			
1	C	494	Total	C	N	O	S	0	2	0
			3810	2423	649	719	19			
1	D	494	Total	C	N	O	S	0	3	0
			3816	2427	649	722	18			
1	E	495	Total	C	N	O	S	0	1	0
			3813	2424	651	720	18			
1	F	494	Total	C	N	O	S	0	1	0
			3804	2419	649	718	18			
1	G	494	Total	C	N	O	S	0	3	0
			3818	2428	652	720	18			
1	H	494	Total	C	N	O	S	0	2	0
			3817	2430	652	717	18			

- 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 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



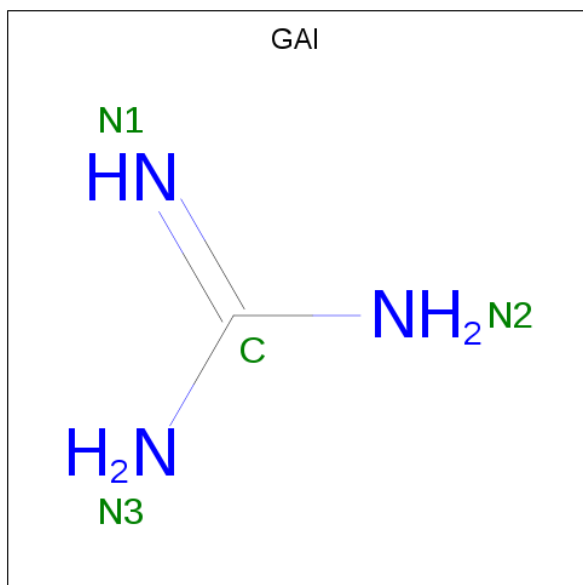
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		
3	E	1	Total	C	O	0	0
			4	2	2		
3	E	1	Total	C	O	0	0
			4	2	2		
3	F	1	Total	C	O	0	0
			4	2	2		
3	F	1	Total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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	G	1	Total	C	O	0	0
			4	2	2		
3	G	1	Total	C	O	0	0
			4	2	2		
3	G	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is GUANIDINE (three-letter code: GAI) (formula: CH_5N_3).



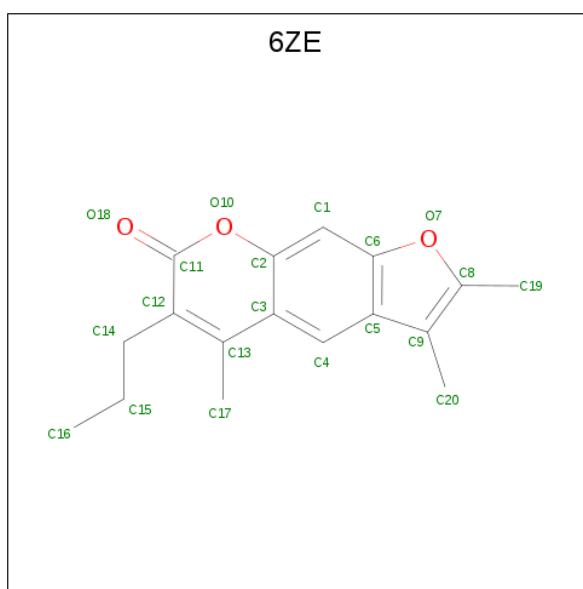
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	N	0	0
			4	1	3		
4	A	1	Total	C	N	0	0
			4	1	3		
4	B	1	Total	C	N	0	0
			4	1	3		
4	C	1	Total	C	N	0	0
			4	1	3		
4	D	1	Total	C	N	0	0
			4	1	3		
4	D	1	Total	C	N	0	0
			4	1	3		
4	D	1	Total	C	N	0	0
			4	1	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	E	1	Total	C	N	0	0
			4	1	3		
4	E	1	Total	C	N	0	0
			4	1	3		
4	E	1	Total	C	N	0	0
			4	1	3		
4	F	1	Total	C	N	0	0
			4	1	3		
4	G	1	Total	C	N	0	0
			4	1	3		
4	G	1	Total	C	N	0	0
			4	1	3		
4	G	1	Total	C	N	0	0
			4	1	3		
4	H	1	Total	C	N	0	0
			4	1	3		

- Molecule 5 is 2,3,5-trimethyl-6-propyl-7H-furo[3,2-g][1]benzopyran-7-one (three-letter code: 6ZE) (formula: C₁₇H₁₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			20	17	3		
5	B	1	Total	C	O	0	0
			20	17	3		
5	C	1	Total	C	O	0	0
			20	17	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	C	O	0	0
			20	17	3		
5	E	1	Total	C	O	0	0
			20	17	3		
5	F	1	Total	C	O	0	0
			20	17	3		
5	G	1	Total	C	O	0	0
			20	17	3		
5	H	1	Total	C	O	0	0
			20	17	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	273	Total	O	0	0
			273	273		
6	B	244	Total	O	0	0
			244	244		
6	C	261	Total	O	0	0
			261	261		
6	D	279	Total	O	0	0
			279	279		
6	E	202	Total	O	0	0
			202	202		
6	F	148	Total	O	0	0
			148	148		
6	G	138	Total	O	0	0
			138	138		
6	H	166	Total	O	0	0
			166	166		

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.

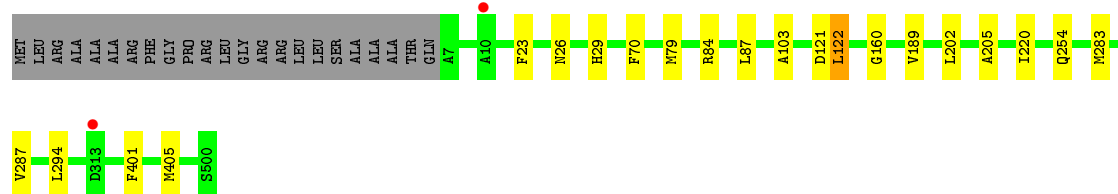
- Molecule 1: Aldehyde dehydrogenase, mitochondrial

Chain A: 



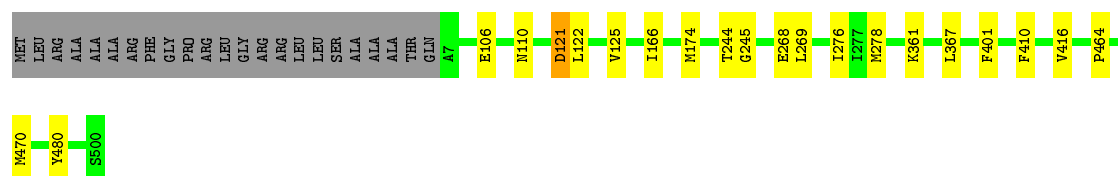
- Molecule 1: Aldehyde dehydrogenase, mitochondrial

Chain B: 



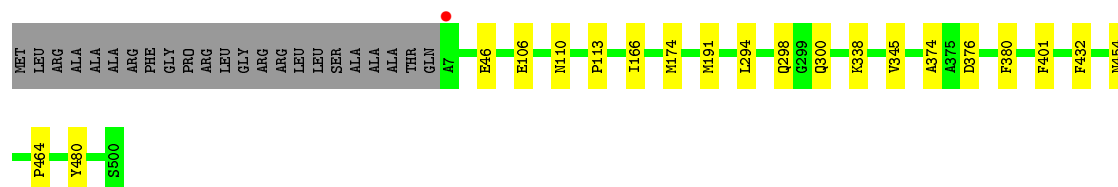
- Molecule 1: Aldehyde dehydrogenase, mitochondrial

Chain C: 




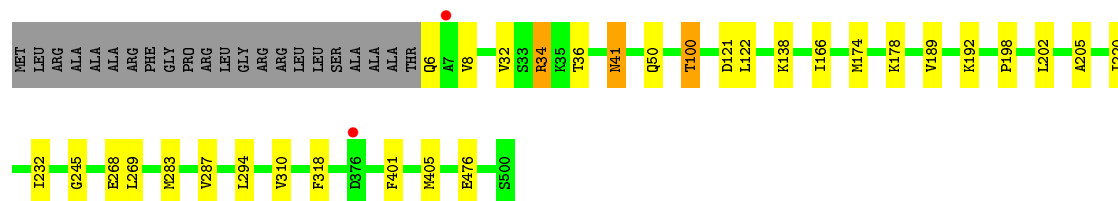
- Molecule 1: Aldehyde dehydrogenase, mitochondrial

Chain D: 



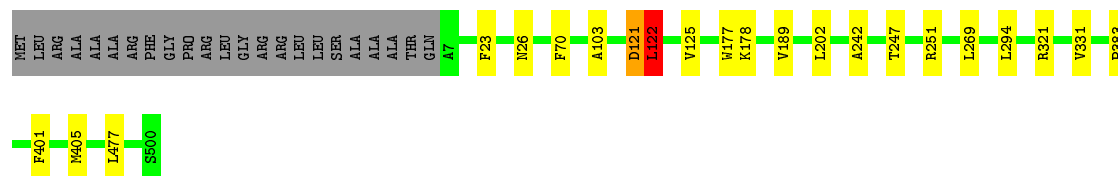
- Molecule 1: Aldehyde dehydrogenase, mitochondrial

Chain E:  90% 6% . .



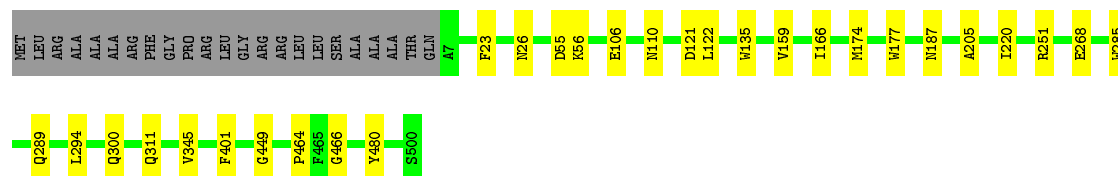
- Molecule 1: Aldehyde dehydrogenase, mitochondrial

Chain F:  91% . .



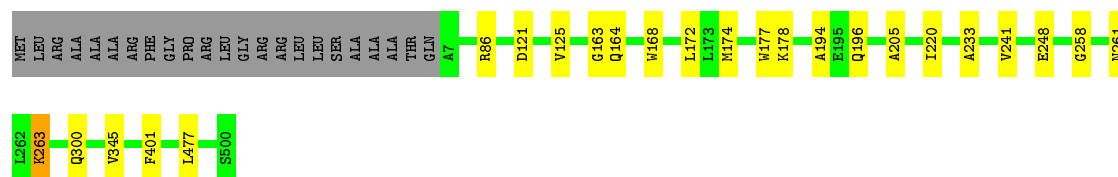
- Molecule 1: Aldehyde dehydrogenase, mitochondrial

Chain G:  90% 6% .



- Molecule 1: Aldehyde dehydrogenase, mitochondrial

Chain H:  91% . .



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	99.41Å 127.05Å 294.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.40 48.12 – 2.40	Depositor EDS
% Data completeness (in resolution range)	94.5 (50.00-2.40) 94.5 (48.12-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.61 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.155 , 0.206 0.162 , 0.209	Depositor DCC
R_{free} test set	6961 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	26.2	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 35.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	32476	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.00% 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: NA, EDO, 6ZE, GAI

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	0.49	0/3891	0.64	1/5279 (0.0%)
1	B	0.49	0/3890	0.64	1/5277 (0.0%)
1	C	0.49	0/3897	0.65	0/5287
1	D	0.53	0/3909	0.65	0/5303
1	E	0.51	0/3900	0.64	0/5291
1	F	0.50	0/3891	0.65	1/5279 (0.0%)
1	G	0.52	0/3911	0.65	0/5305
1	H	0.52	0/3909	0.65	0/5304
All	All	0.51	0/31198	0.65	3/42325 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	84	ARG	NE-CZ-NH2	-5.79	117.41	120.30
1	F	122	LEU	CA-CB-CG	-5.18	103.39	115.30
1	A	122	LEU	CA-CB-CG	-5.13	103.50	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	A	3804	0	3753	8	0
1	B	3803	0	3754	8	0
1	C	3810	0	3760	16	0
1	D	3816	0	3765	11	0
1	E	3813	0	3760	19	0
1	F	3804	0	3753	10	0
1	G	3818	0	3772	16	0
1	H	3817	0	3768	17	0
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	8	0	12	0	0
3	B	8	0	12	0	0
3	D	4	0	6	0	0
3	E	8	0	12	0	0
3	F	8	0	12	0	0
3	G	12	0	18	0	0
4	A	8	0	8	0	0
4	B	4	0	4	0	0
4	C	4	0	4	0	0
4	D	16	0	16	0	0
4	E	12	0	12	0	0
4	F	4	0	4	0	0
4	G	12	0	12	0	0
4	H	4	0	4	0	0
5	A	20	0	0	0	0
5	B	20	0	0	0	0
5	C	20	0	0	0	0
5	D	20	0	0	0	0
5	E	20	0	0	0	0
5	F	20	0	0	0	0
5	G	20	0	0	0	0
5	H	20	0	0	0	0
6	A	273	0	0	2	1
6	B	244	0	0	1	0
6	C	261	0	0	1	0
6	D	279	0	0	2	0
6	E	202	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	F	148	0	0	1	1
6	G	138	0	0	2	0
6	H	166	0	0	0	0
All	All	32476	0	30221	103	1

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 2.

The worst 5 of 103 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:H:86[B]:ARG:HH21	1:H:86[B]:ARG:CG	1.68	1.07
1:H:86[B]:ARG:NH2	1:H:86[B]:ARG:HG3	1.52	0.94
1:H:86[B]:ARG:HH21	1:H:86[B]:ARG:HG3	0.76	0.85
1:C:276:ILE:HG22	1:C:278:MET:CE	2.12	0.79
1:A:311[B]:GLN:OE1	6:A:701:HOH:O	2.02	0.76

All (1) 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	Interatomic distance (Å)	Clash overlap (Å)
6:A:927:HOH:O	6:F:814:HOH:O[1_565]	2.11	0.09

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	493/517 (95%)	478 (97%)	15 (3%)	0	100	100
1	B	493/517 (95%)	474 (96%)	19 (4%)	0	100	100
1	C	494/517 (96%)	480 (97%)	14 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	495/517 (96%)	480 (97%)	15 (3%)	0	100	100
1	E	493/517 (95%)	479 (97%)	14 (3%)	0	100	100
1	F	493/517 (95%)	478 (97%)	15 (3%)	0	100	100
1	G	495/517 (96%)	477 (96%)	18 (4%)	0	100	100
1	H	494/517 (96%)	475 (96%)	19 (4%)	0	100	100
All	All	3950/4136 (96%)	3821 (97%)	129 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	400/414 (97%)	396 (99%)	4 (1%)	80	91
1	B	400/414 (97%)	394 (98%)	6 (2%)	70	85
1	C	401/414 (97%)	398 (99%)	3 (1%)	87	94
1	D	402/414 (97%)	399 (99%)	3 (1%)	87	94
1	E	401/414 (97%)	394 (98%)	7 (2%)	66	82
1	F	400/414 (97%)	394 (98%)	6 (2%)	70	85
1	G	402/414 (97%)	397 (99%)	5 (1%)	75	88
1	H	401/414 (97%)	397 (99%)	4 (1%)	80	91
All	All	3207/3312 (97%)	3169 (99%)	38 (1%)	75	88

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	41	ASN
1	E	189	VAL
1	H	248	GLU
1	E	121	ASP
1	E	401	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	13	GLN
1	E	382	GLN
1	H	164	GLN
1	E	26	ASN
1	E	41	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 44 ligands modelled in this entry, 8 are monoatomic - leaving 36 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	EDO	A	602	-	3,3,3	0.49	0	2,2,2	0.20	0
3	EDO	A	603	-	3,3,3	0.35	0	2,2,2	0.50	0
4	GAI	A	604	-	3,3,3	3.19	1 (33%)	3,3,3	1.12	0
4	GAI	A	605	-	3,3,3	3.15	1 (33%)	3,3,3	1.15	0
5	6ZE	A	606	-	17,22,22	2.96	4 (23%)	19,33,33	2.59	9 (47%)
3	EDO	B	602	-	3,3,3	0.41	0	2,2,2	0.57	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	B	603	-	3,3,3	0.47	0	2,2,2	0.43	0
4	GAI	B	604	-	3,3,3	2.99	1 (33%)	3,3,3	1.23	0
5	6ZE	B	605	-	17,22,22	2.97	4 (23%)	19,33,33	2.40	6 (31%)
4	GAI	C	602	-	3,3,3	3.04	1 (33%)	3,3,3	1.49	1 (33%)
5	6ZE	C	603	-	17,22,22	2.87	5 (29%)	19,33,33	2.48	10 (52%)
3	EDO	D	602	-	3,3,3	0.40	0	2,2,2	0.78	0
4	GAI	D	603	-	3,3,3	2.99	2 (66%)	3,3,3	1.08	0
4	GAI	D	604	-	3,3,3	3.37	1 (33%)	3,3,3	1.32	0
4	GAI	D	605	-	3,3,3	1.38	0	3,3,3	1.29	0
4	GAI	D	606	-	3,3,3	3.01	1 (33%)	3,3,3	1.00	0
5	6ZE	D	607	-	17,22,22	2.94	4 (23%)	19,33,33	2.42	7 (36%)
3	EDO	E	602	-	3,3,3	0.39	0	2,2,2	0.51	0
3	EDO	E	603	-	3,3,3	0.39	0	2,2,2	0.58	0
4	GAI	E	604	-	3,3,3	3.22	1 (33%)	3,3,3	1.00	0
4	GAI	E	605	-	3,3,3	3.14	1 (33%)	3,3,3	1.11	0
4	GAI	E	606	-	3,3,3	2.97	1 (33%)	3,3,3	1.32	0
5	6ZE	E	607	-	17,22,22	3.02	5 (29%)	19,33,33	2.15	6 (31%)
3	EDO	F	602	-	3,3,3	0.49	0	2,2,2	0.30	0
3	EDO	F	603	-	3,3,3	0.40	0	2,2,2	0.55	0
4	GAI	F	604	-	3,3,3	3.07	1 (33%)	3,3,3	1.14	0
5	6ZE	F	605	-	17,22,22	3.13	5 (29%)	19,33,33	2.29	7 (36%)
3	EDO	G	602	-	3,3,3	0.42	0	2,2,2	0.61	0
3	EDO	G	603	-	3,3,3	0.47	0	2,2,2	0.38	0
3	EDO	G	604	-	3,3,3	0.51	0	2,2,2	0.32	0
4	GAI	G	605	-	3,3,3	3.20	1 (33%)	3,3,3	1.46	1 (33%)
4	GAI	G	606	-	3,3,3	3.09	1 (33%)	3,3,3	0.82	0
4	GAI	G	607	-	3,3,3	2.06	2 (66%)	3,3,3	1.07	0
5	6ZE	G	608	-	17,22,22	3.02	5 (29%)	19,33,33	2.44	7 (36%)
4	GAI	H	602	-	3,3,3	1.72	0	3,3,3	1.07	0
5	6ZE	H	603	-	17,22,22	2.92	6 (35%)	19,33,33	2.53	7 (36%)

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	EDO	A	602	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	A	603	-	-	0/1/1/1	0/0/0/0
4	GAI	A	604	-	-	0/0/0/0	0/0/0/0
4	GAI	A	605	-	-	0/0/0/0	0/0/0/0
5	6ZE	A	606	-	-	0/3/3/3	0/2/3/3
3	EDO	B	602	-	-	0/1/1/1	0/0/0/0
3	EDO	B	603	-	-	0/1/1/1	0/0/0/0
4	GAI	B	604	-	-	0/0/0/0	0/0/0/0
5	6ZE	B	605	-	-	0/3/3/3	0/2/3/3
4	GAI	C	602	-	-	0/0/0/0	0/0/0/0
5	6ZE	C	603	-	-	0/3/3/3	0/2/3/3
3	EDO	D	602	-	-	0/1/1/1	0/0/0/0
4	GAI	D	603	-	-	0/0/0/0	0/0/0/0
4	GAI	D	604	-	-	0/0/0/0	0/0/0/0
4	GAI	D	605	-	-	0/0/0/0	0/0/0/0
4	GAI	D	606	-	-	0/0/0/0	0/0/0/0
5	6ZE	D	607	-	-	0/3/3/3	0/2/3/3
3	EDO	E	602	-	-	0/1/1/1	0/0/0/0
3	EDO	E	603	-	-	0/1/1/1	0/0/0/0
4	GAI	E	604	-	-	0/0/0/0	0/0/0/0
4	GAI	E	605	-	-	0/0/0/0	0/0/0/0
4	GAI	E	606	-	-	0/0/0/0	0/0/0/0
5	6ZE	E	607	-	-	0/3/3/3	0/2/3/3
3	EDO	F	602	-	-	0/1/1/1	0/0/0/0
3	EDO	F	603	-	-	0/1/1/1	0/0/0/0
4	GAI	F	604	-	-	0/0/0/0	0/0/0/0
5	6ZE	F	605	-	-	0/3/3/3	0/2/3/3
3	EDO	G	602	-	-	0/1/1/1	0/0/0/0
3	EDO	G	603	-	-	0/1/1/1	0/0/0/0
3	EDO	G	604	-	-	0/1/1/1	0/0/0/0
4	GAI	G	605	-	-	0/0/0/0	0/0/0/0
4	GAI	G	606	-	-	0/0/0/0	0/0/0/0
4	GAI	G	607	-	-	0/0/0/0	0/0/0/0
5	6ZE	G	608	-	-	0/3/3/3	0/2/3/3
4	GAI	H	602	-	-	0/0/0/0	0/0/0/0
5	6ZE	H	603	-	-	0/3/3/3	0/2/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	604	GAI	C-N3	-5.62	1.26	1.36
4	E	604	GAI	C-N2	-5.26	1.26	1.36
4	A	604	GAI	C-N2	-5.22	1.26	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	605	GAI	C-N3	-5.20	1.26	1.36
4	F	604	GAI	C-N2	-5.04	1.27	1.36

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	605	6ZE	C4-C3-C13	-3.30	120.22	122.13
5	G	608	6ZE	C15-C14-C12	-3.28	107.11	112.87
5	A	606	6ZE	C4-C3-C13	-3.23	120.26	122.13
5	C	603	6ZE	O10-C2-C3	-3.17	118.14	121.20
5	C	603	6ZE	C15-C14-C12	-3.16	107.33	112.87

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	A	494/517 (95%)	-0.62	0 100 100	16, 25, 39, 55	0
1	B	494/517 (95%)	-0.44	2 (0%) 92 91	15, 28, 43, 63	1 (0%)
1	C	494/517 (95%)	-0.65	0 100 100	15, 26, 42, 62	0
1	D	494/517 (95%)	-0.67	1 (0%) 94 94	13, 23, 37, 63	1 (0%)
1	E	495/517 (95%)	-0.64	2 (0%) 92 91	15, 27, 44, 69	0
1	F	494/517 (95%)	-0.59	0 100 100	15, 28, 43, 69	0
1	G	494/517 (95%)	-0.61	0 100 100	13, 26, 41, 56	0
1	H	494/517 (95%)	-0.61	0 100 100	15, 24, 38, 65	0
All	All	3953/4136 (95%)	-0.60	5 (0%) 95 95	13, 26, 41, 69	2 (0%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	313	ASP	2.9
1	E	7	ALA	2.5
1	B	10	ALA	2.4
1	D	7	ALA	2.2
1	E	376	ASP	2.1

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 ⓘ

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
4	GAI	D	605	4/4	0.90	0.17	15.93	43,43,43,45	0
3	EDO	F	602	4/4	0.82	0.32	10.06	55,58,61,62	0
3	EDO	E	602	4/4	0.90	0.27	7.17	50,55,57,59	0
3	EDO	G	603	4/4	0.94	0.21	6.02	42,45,47,51	0
4	GAI	E	606	4/4	0.84	0.19	5.21	38,38,38,39	0
4	GAI	F	604	4/4	0.91	0.20	4.89	37,39,40,40	0
4	GAI	E	605	4/4	0.96	0.15	4.46	40,41,42,43	0
3	EDO	B	603	4/4	0.92	0.20	3.85	49,51,54,55	0
3	EDO	G	602	4/4	0.94	0.16	3.83	43,48,51,53	0
3	EDO	A	602	4/4	0.89	0.20	3.20	49,53,54,54	0
4	GAI	A	605	4/4	0.94	0.14	3.07	37,37,37,38	0
4	GAI	C	602	4/4	0.94	0.14	3.04	44,45,46,47	0
3	EDO	G	604	4/4	0.89	0.27	2.23	36,38,38,39	0
2	NA	E	601	1/1	0.97	0.13	1.88	21,21,21,21	0
3	EDO	B	602	4/4	0.95	0.14	1.71	41,43,44,44	0
4	GAI	H	602	4/4	0.97	0.14	1.52	36,38,38,38	0
4	GAI	G	605	4/4	0.96	0.13	1.40	43,43,45,47	0
4	GAI	D	606	4/4	0.94	0.14	1.38	38,38,39,41	0
5	6ZE	A	606	20/20	0.95	0.14	1.01	23,25,31,33	0
5	6ZE	C	603	20/20	0.96	0.13	0.97	26,28,32,35	0
4	GAI	A	604	4/4	0.94	0.16	0.95	37,39,39,39	0
5	6ZE	G	608	20/20	0.96	0.14	0.92	30,33,40,41	0
4	GAI	B	604	4/4	0.95	0.12	0.76	30,31,33,33	0
4	GAI	D	604	4/4	0.96	0.12	0.64	29,31,31,32	0
5	6ZE	E	607	20/20	0.97	0.12	0.63	25,26,31,33	0
4	GAI	G	606	4/4	0.95	0.12	0.48	38,39,39,42	0
5	6ZE	F	605	20/20	0.95	0.13	0.45	35,38,42,42	0
4	GAI	D	603	4/4	0.95	0.12	0.39	36,36,36,37	0
5	6ZE	D	607	20/20	0.95	0.12	0.18	24,24,33,33	0
4	GAI	E	604	4/4	0.96	0.10	-0.09	28,29,29,31	0
5	6ZE	B	605	20/20	0.95	0.12	-0.10	30,32,36,40	0
2	NA	G	601	1/1	0.85	0.11	-0.36	33,33,33,33	0
5	6ZE	H	603	20/20	0.97	0.10	-0.39	26,27,30,32	0
2	NA	B	601	1/1	0.99	0.10	-0.73	32,32,32,32	0
2	NA	C	601	1/1	0.87	0.07	-2.45	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	NA	D	601	1/1	0.93	0.05	-2.64	26,26,26,26	0
2	NA	F	601	1/1	0.94	0.05	-3.16	31,31,31,31	0
2	NA	H	601	1/1	0.96	0.07	-3.17	28,28,28,28	0
2	NA	A	601	1/1	0.94	0.05	-4.17	32,32,32,32	0
3	EDO	D	602	4/4	0.83	0.24	-	52,54,56,60	0
3	EDO	A	603	4/4	0.88	0.19	-	47,47,49,49	0
3	EDO	E	603	4/4	0.83	0.28	-	48,49,49,52	0
4	GAI	G	607	4/4	0.95	0.19	-	43,43,44,45	0
3	EDO	F	603	4/4	0.87	0.22	-	52,54,54,56	0

6.5 Other polymers [i](#)

There are no such residues in this entry.