



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:49 PM GMT

PDB ID : 3U33
Title : Crystal Structure of the E. coli adaptive response protein AidB in the space group P3(2)
Authors : Wong, C.; Jost, M.; Drennan, C.L.
Deposited on : 2011-10-04
Resolution : 2.80 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 (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

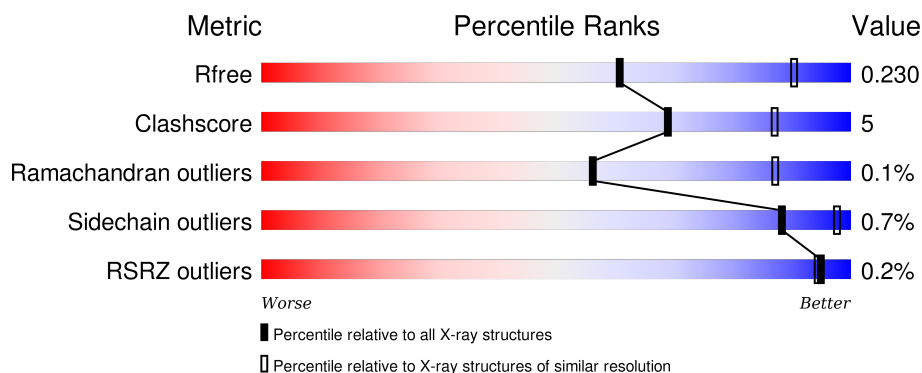
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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	541	<div> <div>89%</div> <div>11%</div> </div>
1	B	541	<div> <div>88%</div> <div>11%</div> </div>
1	C	541	<div> <div>88%</div> <div>12%</div> </div>
1	D	541	<div> <div>87%</div> <div>12%</div> </div>
1	E	541	<div> <div>88%</div> <div>12%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	541	<div><div></div><div>88%</div><div>12%</div></div>
1	G	541	<div><div></div><div>89%</div><div>10%</div></div>
1	H	541	<div><div></div><div>88%</div><div>12%</div></div>
1	I	541	<div><div></div><div>89%</div><div>10%</div></div>
1	J	541	<div><div>%</div><div><div></div><div>87%</div><div>13%</div></div></div>
1	K	541	<div><div></div><div>89%</div><div>11%</div></div>
1	L	541	<div><div>%</div><div><div></div><div>87%</div><div>12%</div></div><div>.</div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 50594 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 Putative acyl-CoA dehydrogenase AidB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	540	Total	C	N	O	S	0	0	0
			4160	2640	743	745	32			
1	B	539	Total	C	N	O	S	0	0	0
			4141	2627	742	740	32			
1	C	539	Total	C	N	O	S	0	0	0
			4117	2609	735	741	32			
1	D	539	Total	C	N	O	S	0	0	0
			4140	2623	747	739	31			
1	E	539	Total	C	N	O	S	0	0	0
			4133	2619	743	739	32			
1	F	539	Total	C	N	O	S	0	0	0
			4134	2622	740	740	32			
1	G	539	Total	C	N	O	S	0	0	0
			4146	2627	740	747	32			
1	H	539	Total	C	N	O	S	0	0	0
			4163	2639	746	746	32			
1	I	539	Total	C	N	O	S	0	0	0
			4151	2631	745	744	31			
1	J	540	Total	C	N	O	S	0	0	0
			4137	2619	742	744	32			
1	K	540	Total	C	N	O	S	0	0	0
			4112	2608	730	742	32			
1	L	539	Total	C	N	O	S	0	0	0
			4115	2612	732	739	32			

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	E	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	F	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	G	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	H	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	I	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	J	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	K	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	L	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	G	1	Total Cl 1 1	0	0
3	J	1	Total Cl 1 1	0	0
3	D	1	Total Cl 1 1	0	0
3	K	1	Total Cl 1 1	0	0
3	E	1	Total Cl 1 1	0	0
3	H	1	Total Cl 1 1	0	0
3	B	1	Total Cl 1 1	0	0
3	I	1	Total Cl 1 1	0	0
3	C	1	Total Cl 1 1	0	0
3	A	1	Total Cl 1 1	0	0
3	L	1	Total Cl 1 1	0	0
3	F	1	Total Cl 1 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	40	Total O 40 40	0	0
4	B	33	Total O 33 33	0	0
4	C	25	Total O 25 25	0	0
4	D	24	Total O 24 24	0	0
4	E	21	Total O 21 21	0	0
4	F	21	Total O 21 21	0	0
4	G	30	Total O 30 30	0	0
4	H	10	Total O 10 10	0	0

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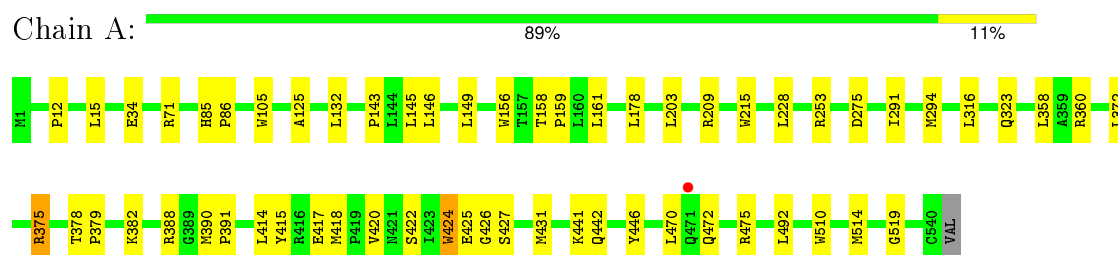
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	I	23	Total 23	O 23	0	0
4	J	20	Total 20	O 20	0	0
4	K	24	Total 24	O 24	0	0
4	L	26	Total 26	O 26	0	0

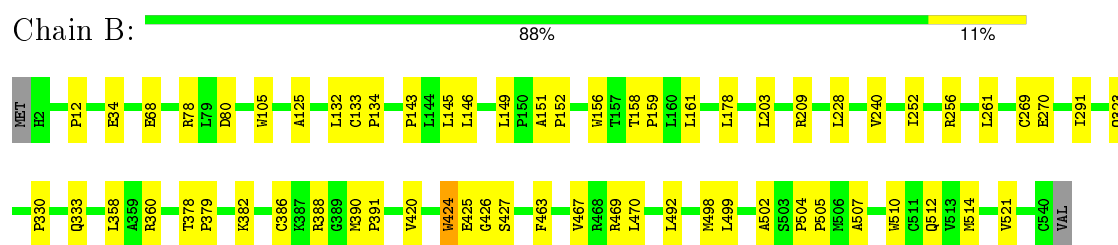
3 Residue-property plots

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.

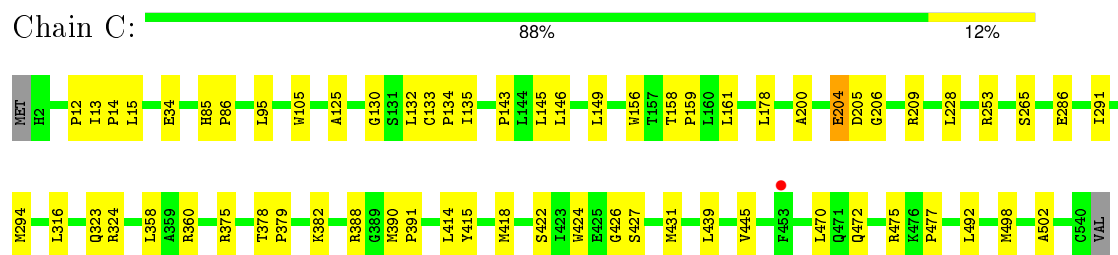
• Molecule 1: Putative acyl-CoA dehydrogenase AidB



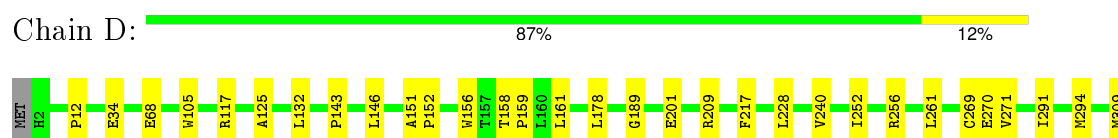
• Molecule 1: Putative acyl-CoA dehydrogenase AidB

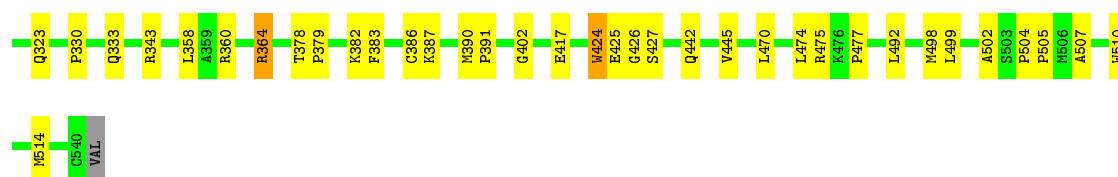


• Molecule 1: Putative acyl-CoA dehydrogenase AidB



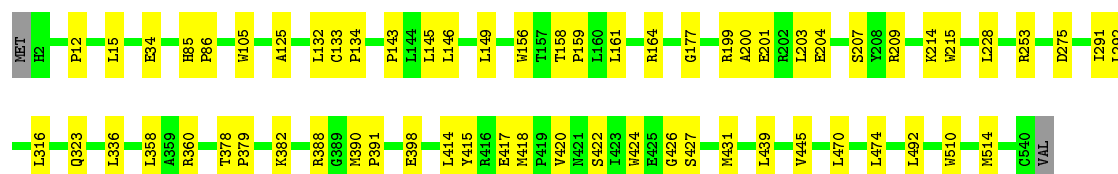
• Molecule 1: Putative acyl-CoA dehydrogenase AidB





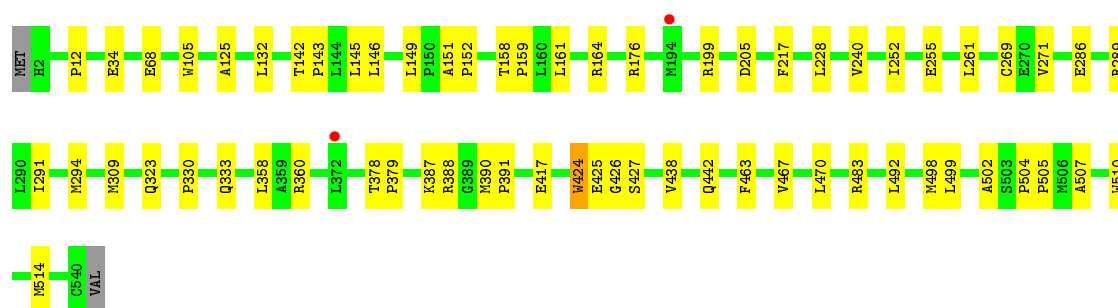
- Molecule 1: Putative acyl-CoA dehydrogenase AidB

Chain E: 88% 12%



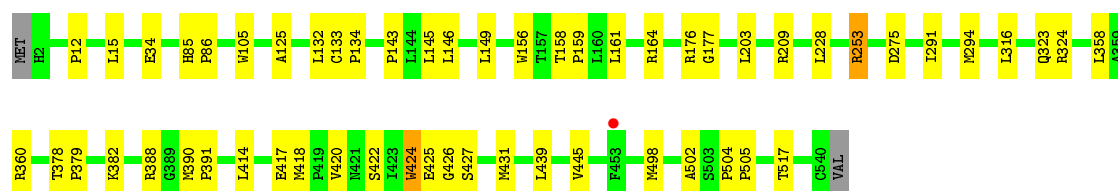
- Molecule 1: Putative acyl-CoA dehydrogenase AidB

Chain F: 88% 12%



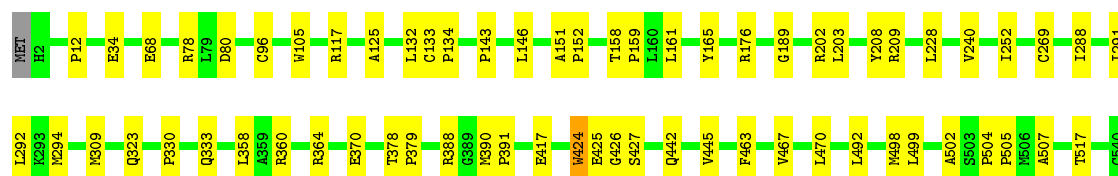
- Molecule 1: Putative acyl-CoA dehydrogenase AidB

Chain G: 89% 10%



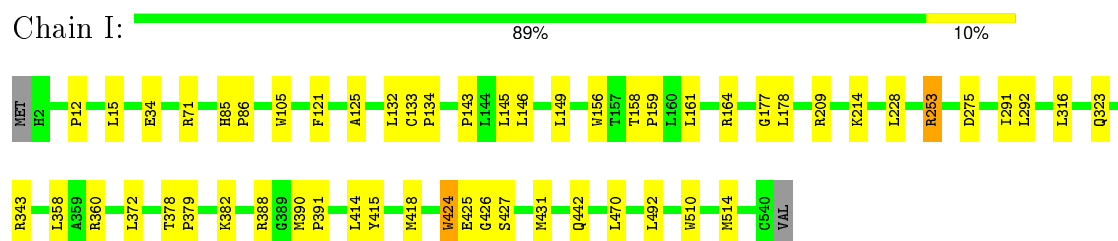
- Molecule 1: Putative acyl-CoA dehydrogenase AidB

Chain H: 88% 12%

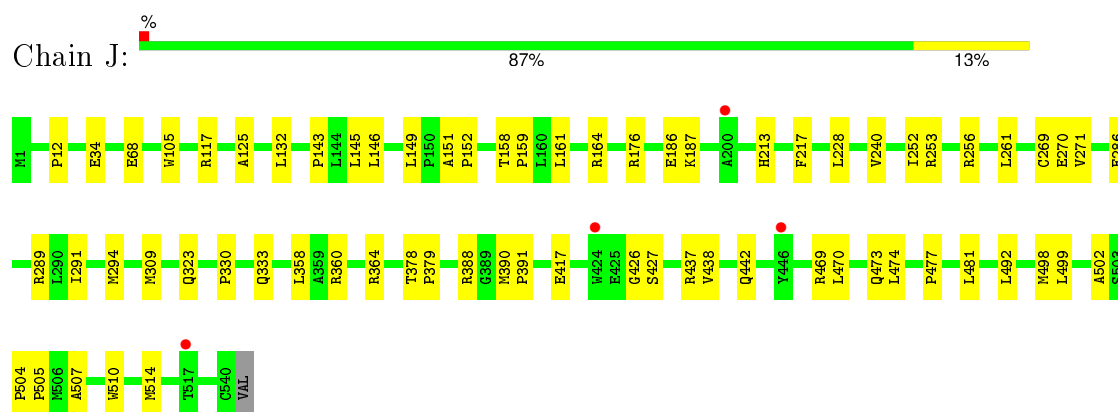


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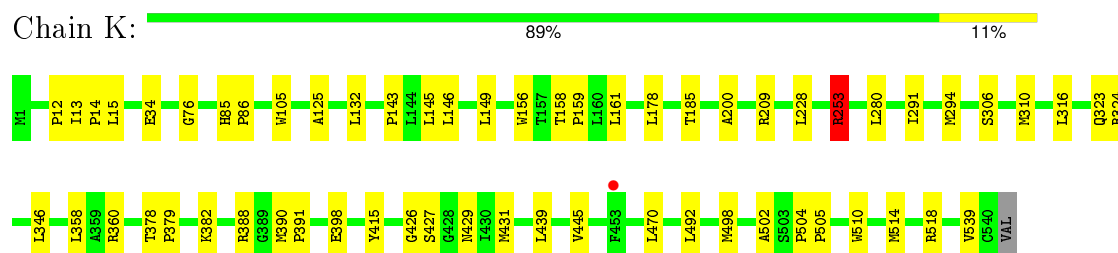
- Molecule 1: Putative acyl-CoA dehydrogenase AidB



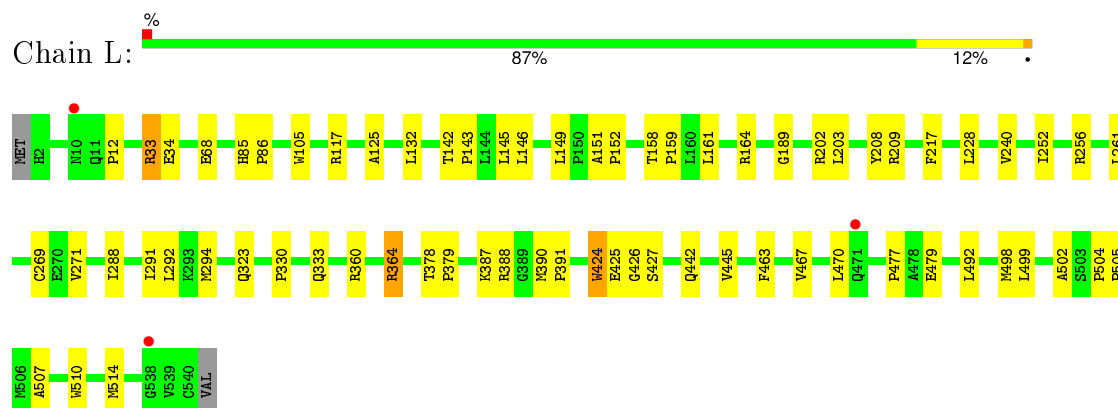
- Molecule 1: Putative acyl-CoA dehydrogenase AidB



- Molecule 1: Putative acyl-CoA dehydrogenase AidB



- Molecule 1: Putative acyl-CoA dehydrogenase AidB



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	179.72Å 179.72Å 204.24Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.25 – 2.80 46.25 – 2.80	Depositor EDS
% Data completeness (in resolution range)	95.0 (46.25-2.80) 95.1 (46.25-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.94 (at 2.81Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.204 , 0.229 0.205 , 0.230	Depositor DCC
R_{free} test set	8764 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	45.1	Xtriage
Anisotropy	0.021	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 36.8	EDS
Estimated twinning fraction	0.000 for -h,-k,l 0.026 for h,-h-k,-l 0.000 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 174695 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	50594	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 37.02 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to $4.5721e-04$. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: FAD, CL

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	0.29	0/4252	0.48	4/5760 (0.1%)
1	B	0.28	0/4233	0.48	2/5737 (0.0%)
1	C	0.28	0/4209	0.47	4/5708 (0.1%)
1	D	0.28	0/4232	0.53	5/5736 (0.1%)
1	E	0.29	0/4225	0.45	2/5728 (0.0%)
1	F	0.28	0/4226	0.44	0/5728
1	G	0.28	0/4238	0.45	2/5745 (0.0%)
1	H	0.28	0/4255	0.44	1/5764 (0.0%)
1	I	0.29	0/4243	0.50	5/5750 (0.1%)
1	J	0.28	0/4227	0.44	2/5730 (0.0%)
1	K	0.29	0/4202	0.45	2/5700 (0.0%)
1	L	0.29	0/4207	0.56	8/5707 (0.1%)
All	All	0.29	0/50749	0.48	37/68793 (0.1%)

There are no bond length outliers.

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	343	ARG	NE-CZ-NH2	-13.57	113.52	120.30
1	I	343	ARG	NE-CZ-NH2	-13.36	113.62	120.30
1	L	33	ARG	NE-CZ-NH2	-12.05	114.27	120.30
1	L	33	ARG	NE-CZ-NH1	11.94	126.27	120.30
1	I	343	ARG	NE-CZ-NH1	11.69	126.14	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	4160	0	4073	40	0
1	B	4141	0	4050	36	0
1	C	4117	0	3990	39	0
1	D	4140	0	4041	40	0
1	E	4133	0	4029	44	0
1	F	4134	0	4027	41	0
1	G	4146	0	4046	37	0
1	H	4163	0	4074	39	0
1	I	4151	0	4057	40	0
1	J	4137	0	4032	39	0
1	K	4112	0	3995	42	0
1	L	4115	0	3997	42	0
2	A	53	0	31	0	0
2	B	53	0	31	1	0
2	C	53	0	31	1	0
2	D	53	0	31	0	0
2	E	53	0	31	0	0
2	F	53	0	31	0	0
2	G	53	0	31	0	0
2	H	53	0	31	0	0
2	I	53	0	31	0	0
2	J	53	0	31	0	0
2	K	53	0	31	2	0
2	L	53	0	31	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
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
3	I	1	0	0	0	0
3	J	1	0	0	0	0
3	K	1	0	0	0	0
3	L	1	0	0	0	0
4	A	40	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	33	0	0	0	0
4	C	25	0	0	1	0
4	D	24	0	0	0	0
4	E	21	0	0	1	0
4	F	21	0	0	2	0
4	G	30	0	0	0	0
4	H	10	0	0	0	0
4	I	23	0	0	1	0
4	J	20	0	0	0	0
4	K	24	0	0	1	0
4	L	26	0	0	0	0
All	All	50594	0	48783	458	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 5.

The worst 5 of 458 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:I:424:TRP:HE3	1:I:425:GLU:HG2	1.36	0.89
1:A:424:TRP:HE3	1:A:425:GLU:HG2	1.38	0.88
1:G:424:TRP:HE3	1:G:425:GLU:HG2	1.38	0.87
1:H:203:LEU:HD21	1:H:209:ARG:HG3	1.59	0.85
1:H:424:TRP:HE3	1:H:425:GLU:HG2	1.43	0.83

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	538/541 (99%)	530 (98%)	7 (1%)	1 (0%)	52 84

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	537/541 (99%)	523 (97%)	14 (3%)	0	100	100
1	C	537/541 (99%)	527 (98%)	8 (2%)	2 (0%)	39	74
1	D	537/541 (99%)	521 (97%)	16 (3%)	0	100	100
1	E	537/541 (99%)	524 (98%)	13 (2%)	0	100	100
1	F	537/541 (99%)	524 (98%)	13 (2%)	0	100	100
1	G	537/541 (99%)	529 (98%)	8 (2%)	0	100	100
1	H	537/541 (99%)	523 (97%)	14 (3%)	0	100	100
1	I	537/541 (99%)	529 (98%)	8 (2%)	0	100	100
1	J	538/541 (99%)	525 (98%)	13 (2%)	0	100	100
1	K	538/541 (99%)	526 (98%)	11 (2%)	1 (0%)	52	84
1	L	537/541 (99%)	521 (97%)	16 (3%)	0	100	100
All	All	6447/6492 (99%)	6302 (98%)	141 (2%)	4 (0%)	56	87

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	204	GLU
1	C	205	ASP
1	A	519	GLY
1	K	518	ARG

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	419/442 (95%)	416 (99%)	3 (1%)	88	97
1	B	417/442 (94%)	414 (99%)	3 (1%)	88	97
1	C	411/442 (93%)	410 (100%)	1 (0%)	95	99
1	D	416/442 (94%)	412 (99%)	4 (1%)	82	96
1	E	415/442 (94%)	413 (100%)	2 (0%)	92	98

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	414/442 (94%)	411 (99%)	3 (1%)	88	97
1	G	420/442 (95%)	418 (100%)	2 (0%)	92	98
1	H	420/442 (95%)	416 (99%)	4 (1%)	82	96
1	I	419/442 (95%)	417 (100%)	2 (0%)	92	98
1	J	416/442 (94%)	413 (99%)	3 (1%)	88	97
1	K	412/442 (93%)	411 (100%)	1 (0%)	95	99
1	L	412/442 (93%)	407 (99%)	5 (1%)	78	95
All	All	4991/5304 (94%)	4958 (99%)	33 (1%)	88	97

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	269	CYS
1	H	68	GLU
1	L	269	CYS
1	F	424	TRP
1	G	253	ARG

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

Mol	Chain	Res	Type
1	F	65	ASN
1	H	65	ASN
1	L	65	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 24 ligands modelled in this entry, 12 are monoatomic - leaving 12 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	FAD	A	1000	-	48,58,58	1.32	6 (12%)	54,89,89	2.21	11 (20%)
2	FAD	B	1000	-	48,58,58	1.41	5 (10%)	54,89,89	2.11	10 (18%)
2	FAD	C	1000	-	48,58,58	1.41	6 (12%)	54,89,89	2.22	12 (22%)
2	FAD	D	1000	-	48,58,58	1.35	5 (10%)	54,89,89	2.13	13 (24%)
2	FAD	E	1000	-	48,58,58	1.39	6 (12%)	54,89,89	2.25	11 (20%)
2	FAD	F	1000	-	48,58,58	1.34	5 (10%)	54,89,89	2.20	10 (18%)
2	FAD	G	1000	-	48,58,58	1.40	6 (12%)	54,89,89	2.26	9 (16%)
2	FAD	H	1000	-	48,58,58	1.32	6 (12%)	54,89,89	2.28	11 (20%)
2	FAD	I	1000	-	48,58,58	1.32	7 (14%)	54,89,89	2.05	10 (18%)
2	FAD	J	1000	-	48,58,58	1.37	6 (12%)	54,89,89	2.16	11 (20%)
2	FAD	K	1000	-	48,58,58	1.42	7 (14%)	54,89,89	2.11	10 (18%)
2	FAD	L	1000	-	48,58,58	1.34	5 (10%)	54,89,89	2.27	14 (25%)

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	FAD	A	1000	-	-	0/30/50/50	0/6/6/6
2	FAD	B	1000	-	-	0/30/50/50	0/6/6/6
2	FAD	C	1000	-	-	0/30/50/50	0/6/6/6
2	FAD	D	1000	-	-	0/30/50/50	0/6/6/6
2	FAD	E	1000	-	-	0/30/50/50	0/6/6/6
2	FAD	F	1000	-	-	0/30/50/50	0/6/6/6
2	FAD	G	1000	-	-	0/30/50/50	0/6/6/6
2	FAD	H	1000	-	-	0/30/50/50	0/6/6/6
2	FAD	I	1000	-	-	0/30/50/50	0/6/6/6
2	FAD	J	1000	-	-	0/30/50/50	0/6/6/6

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FAD	K	1000	-	-	0/30/50/50	0/6/6/6
2	FAD	L	1000	-	-	0/30/50/50	0/6/6/6

The worst 5 of 70 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	1000	FAD	C1'-N10	-2.34	1.46	1.48
2	H	1000	FAD	C1'-N10	-2.21	1.46	1.48
2	A	1000	FAD	C1'-N10	-2.05	1.46	1.48
2	I	1000	FAD	C1'-N10	-2.03	1.46	1.48
2	I	1000	FAD	C6-C5X	-2.03	1.38	1.41

The worst 5 of 132 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1000	FAD	N3A-C2A-N1A	-7.56	123.10	128.89
2	A	1000	FAD	N3A-C2A-N1A	-7.09	123.47	128.89
2	G	1000	FAD	N3A-C2A-N1A	-6.82	123.67	128.89
2	F	1000	FAD	N3A-C2A-N1A	-6.75	123.73	128.89
2	I	1000	FAD	N3A-C2A-N1A	-6.69	123.77	128.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1000	FAD	1	0
2	C	1000	FAD	1	0
2	K	1000	FAD	2	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	A	540/541 (99%)	-0.45	1 (0%) 95 94	22, 43, 76, 113	2 (0%)
1	B	539/541 (99%)	-0.47	0 100 100	24, 46, 81, 113	2 (0%)
1	C	539/541 (99%)	-0.51	1 (0%) 95 94	23, 44, 79, 124	3 (0%)
1	D	539/541 (99%)	-0.49	0 100 100	24, 46, 83, 114	2 (0%)
1	E	539/541 (99%)	-0.52	0 100 100	24, 44, 76, 113	2 (0%)
1	F	539/541 (99%)	-0.47	2 (0%) 93 90	25, 46, 84, 114	1 (0%)
1	G	539/541 (99%)	-0.55	1 (0%) 95 94	23, 43, 78, 113	0
1	H	539/541 (99%)	-0.51	0 100 100	25, 46, 82, 114	0
1	I	539/541 (99%)	-0.49	0 100 100	23, 43, 76, 113	1 (0%)
1	J	540/541 (99%)	-0.42	4 (0%) 89 84	24, 46, 84, 118	2 (0%)
1	K	540/541 (99%)	-0.47	1 (0%) 95 94	24, 43, 81, 126	0
1	L	539/541 (99%)	-0.47	3 (0%) 90 86	24, 46, 82, 113	0
All	All	6471/6492 (99%)	-0.49	13 (0%) 95 94	22, 45, 80, 126	15 (0%)

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	453	PHE	2.9
1	C	453	PHE	2.7
1	J	517	THR	2.6
1	J	424	TRP	2.5
1	K	453	PHE	2.4

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
2	FAD	H	1000	53/53	0.96	0.14	0.05	23,42,51,56	0
2	FAD	C	1000	53/53	0.95	0.15	-0.06	40,55,73,141	0
2	FAD	E	1000	53/53	0.97	0.13	-0.14	20,37,46,50	0
2	FAD	F	1000	53/53	0.96	0.15	-0.23	30,51,69,171	0
2	FAD	J	1000	53/53	0.95	0.16	-0.24	39,60,79,99	0
2	FAD	K	1000	53/53	0.94	0.14	-0.31	42,59,74,207	0
2	FAD	G	1000	53/53	0.96	0.13	-0.55	33,48,58,69	0
2	FAD	L	1000	53/53	0.97	0.12	-0.69	13,40,49,53	0
2	FAD	B	1000	53/53	0.96	0.12	-0.94	32,51,60,61	0
2	FAD	D	1000	53/53	0.98	0.11	-1.08	15,32,40,42	0
2	FAD	I	1000	53/53	0.97	0.12	-1.16	19,30,38,41	0
2	FAD	A	1000	53/53	0.98	0.11	-1.47	5,25,34,37	0
3	CL	J	542	1/1	0.98	0.10	-	61,61,61,61	0
3	CL	K	542	1/1	0.97	0.06	-	56,56,56,56	0
3	CL	G	542	1/1	0.97	0.12	-	62,62,62,62	0
3	CL	B	542	1/1	0.97	0.06	-	44,44,44,44	0
3	CL	L	542	1/1	0.99	0.08	-	39,39,39,39	0
3	CL	C	542	1/1	0.99	0.07	-	44,44,44,44	0
3	CL	E	542	1/1	0.98	0.07	-	54,54,54,54	0
3	CL	D	542	1/1	0.98	0.07	-	39,39,39,39	0
3	CL	F	542	1/1	0.97	0.13	-	65,65,65,65	0
3	CL	A	542	1/1	0.99	0.15	-	42,42,42,42	0
3	CL	I	542	1/1	0.98	0.07	-	46,46,46,46	0
3	CL	H	542	1/1	0.97	0.07	-	53,53,53,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.