



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 10:04 AM GMT

PDB ID : 3KP0
Title : Crystal Structure of ORNITHINE 4,5 AMINOMUTASE in complex with 2,4-diaminobutyrate (DAB) (Aerobic)
Authors : Wolthers, K.R.; Levy, C.W.; Scrutton, N.S.; Leys, D.
Deposited on : 2009-11-14
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

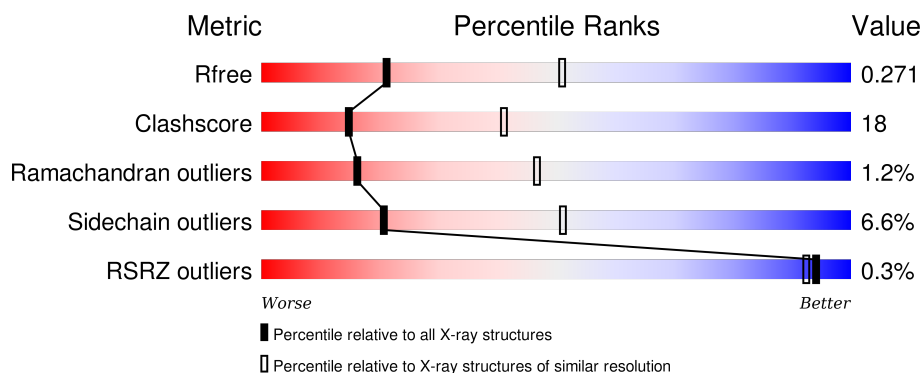
1 Overall quality at a glance

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	763	 50% 24% • 24%
1	B	763	 59% 33% • 5%
1	C	763	 60% 32% • 5%
1	D	763	 50% 23% •• 24%
2	E	121	 60% 26% • 10%

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Mol	Chain	Length	Quality of chain
2	F	121	 70% 18% • 10%
2	G	121	 63% 27% 10%
2	H	121	 69% 19% • 10%

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	B12	B	1801	X	-	X	-
3	B12	C	1801	X	-	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 24133 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 D-ornithine aminomutase E component.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	578	Total	C	N	O	S	0	0	0
			4537	2861	782	864	30			
1	B	728	Total	C	N	O	S	0	0	0
			5669	3576	984	1075	34			
1	C	728	Total	C	N	O	S	0	0	0
			5654	3570	981	1069	34			
1	D	578	Total	C	N	O	S	0	0	0
			4540	2864	782	864	30			

There are 104 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ILE	SEE REMARK 999	UNP Q8VPJ5
A	?	-	ASP	SEE REMARK 999	UNP Q8VPJ5
A	?	-	GLY	SEE REMARK 999	UNP Q8VPJ5
A	744	SER	-	EXPRESSION TAG	UNP Q8VPJ5
A	745	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
A	746	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
A	747	PRO	-	EXPRESSION TAG	UNP Q8VPJ5
A	748	ASN	-	EXPRESSION TAG	UNP Q8VPJ5
A	749	SER	-	EXPRESSION TAG	UNP Q8VPJ5
A	750	SER	-	EXPRESSION TAG	UNP Q8VPJ5
A	751	SER	-	EXPRESSION TAG	UNP Q8VPJ5
A	752	VAL	-	EXPRESSION TAG	UNP Q8VPJ5
A	753	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
A	754	LYS	-	EXPRESSION TAG	UNP Q8VPJ5
A	755	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
A	756	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
A	757	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
A	758	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
A	759	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
A	760	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
A	761	HIS	-	EXPRESSION TAG	UNP Q8VPJ5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	762	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
A	763	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
A	764	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
A	765	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
A	766	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
B	?	-	ILE	SEE REMARK 999	UNP Q8VPJ5
B	?	-	ASP	SEE REMARK 999	UNP Q8VPJ5
B	?	-	GLY	SEE REMARK 999	UNP Q8VPJ5
B	744	SER	-	EXPRESSION TAG	UNP Q8VPJ5
B	745	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
B	746	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
B	747	PRO	-	EXPRESSION TAG	UNP Q8VPJ5
B	748	ASN	-	EXPRESSION TAG	UNP Q8VPJ5
B	749	SER	-	EXPRESSION TAG	UNP Q8VPJ5
B	750	SER	-	EXPRESSION TAG	UNP Q8VPJ5
B	751	SER	-	EXPRESSION TAG	UNP Q8VPJ5
B	752	VAL	-	EXPRESSION TAG	UNP Q8VPJ5
B	753	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
B	754	LYS	-	EXPRESSION TAG	UNP Q8VPJ5
B	755	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
B	756	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
B	757	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
B	758	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
B	759	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
B	760	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
B	761	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
B	762	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
B	763	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
B	764	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
B	765	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
B	766	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
C	?	-	ILE	SEE REMARK 999	UNP Q8VPJ5
C	?	-	ASP	SEE REMARK 999	UNP Q8VPJ5
C	?	-	GLY	SEE REMARK 999	UNP Q8VPJ5
C	744	SER	-	EXPRESSION TAG	UNP Q8VPJ5
C	745	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
C	746	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
C	747	PRO	-	EXPRESSION TAG	UNP Q8VPJ5
C	748	ASN	-	EXPRESSION TAG	UNP Q8VPJ5
C	749	SER	-	EXPRESSION TAG	UNP Q8VPJ5
C	750	SER	-	EXPRESSION TAG	UNP Q8VPJ5
C	751	SER	-	EXPRESSION TAG	UNP Q8VPJ5

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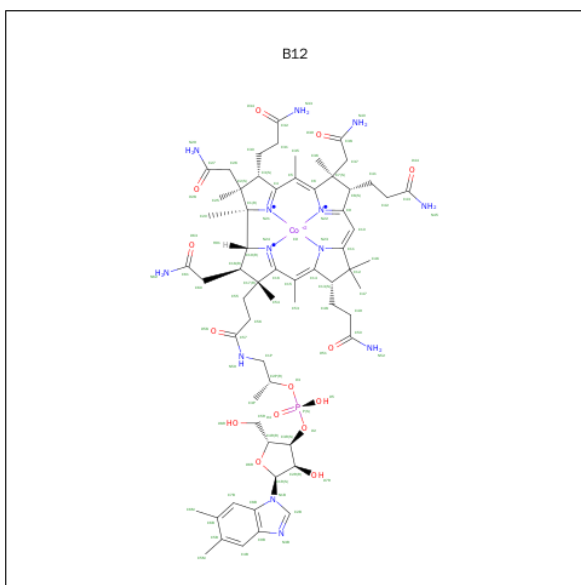
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Chain	Residue	Modelled	Actual	Comment	Reference
C	752	VAL	-	EXPRESSION TAG	UNP Q8VPJ5
C	753	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
C	754	LYS	-	EXPRESSION TAG	UNP Q8VPJ5
C	755	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
C	756	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
C	757	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
C	758	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
C	759	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
C	760	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
C	761	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
C	762	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
C	763	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
C	764	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
C	765	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
C	766	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
D	?	-	ILE	SEE REMARK 999	UNP Q8VPJ5
D	?	-	ASP	SEE REMARK 999	UNP Q8VPJ5
D	?	-	GLY	SEE REMARK 999	UNP Q8VPJ5
D	744	SER	-	EXPRESSION TAG	UNP Q8VPJ5
D	745	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
D	746	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
D	747	PRO	-	EXPRESSION TAG	UNP Q8VPJ5
D	748	ASN	-	EXPRESSION TAG	UNP Q8VPJ5
D	749	SER	-	EXPRESSION TAG	UNP Q8VPJ5
D	750	SER	-	EXPRESSION TAG	UNP Q8VPJ5
D	751	SER	-	EXPRESSION TAG	UNP Q8VPJ5
D	752	VAL	-	EXPRESSION TAG	UNP Q8VPJ5
D	753	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
D	754	LYS	-	EXPRESSION TAG	UNP Q8VPJ5
D	755	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
D	756	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
D	757	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
D	758	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
D	759	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
D	760	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
D	761	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
D	762	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
D	763	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
D	764	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
D	765	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
D	766	HIS	-	EXPRESSION TAG	UNP Q8VPJ5

- Molecule 2 is a protein called D-ornithine aminomutase S component.

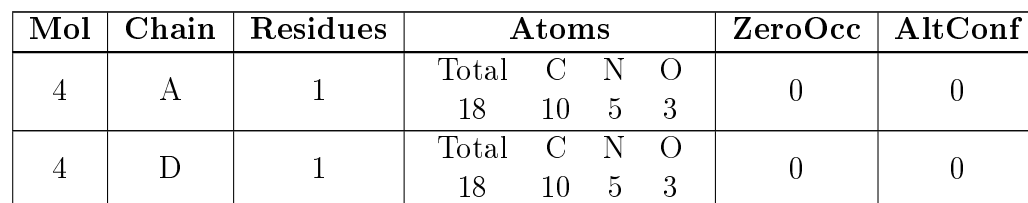
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	109	Total	C	N	O	S	0	0	0
			855	538	152	161	4			
2	F	109	Total	C	N	O	S	0	0	0
			858	539	152	163	4			
2	G	109	Total	C	N	O	S	0	0	0
			855	538	152	161	4			
2	H	109	Total	C	N	O	S	0	0	0
			855	538	152	161	4			

- Molecule 3 is COBALAMIN (three-letter code: B12) (formula: $C_{62}H_{89}CoN_{13}O_{14}P$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	C	1	Total	C	Co	N	O	P	0	0
			91	62	1	13	14	1		
3	B	1	Total	C	Co	N	O	P	0	0
			91	62	1	13	14	1		

- Molecule 4 is 5'-DEOXYADENOSINE (three-letter code: 5AD) (formula: $C_{10}H_{13}N_5O_3$).



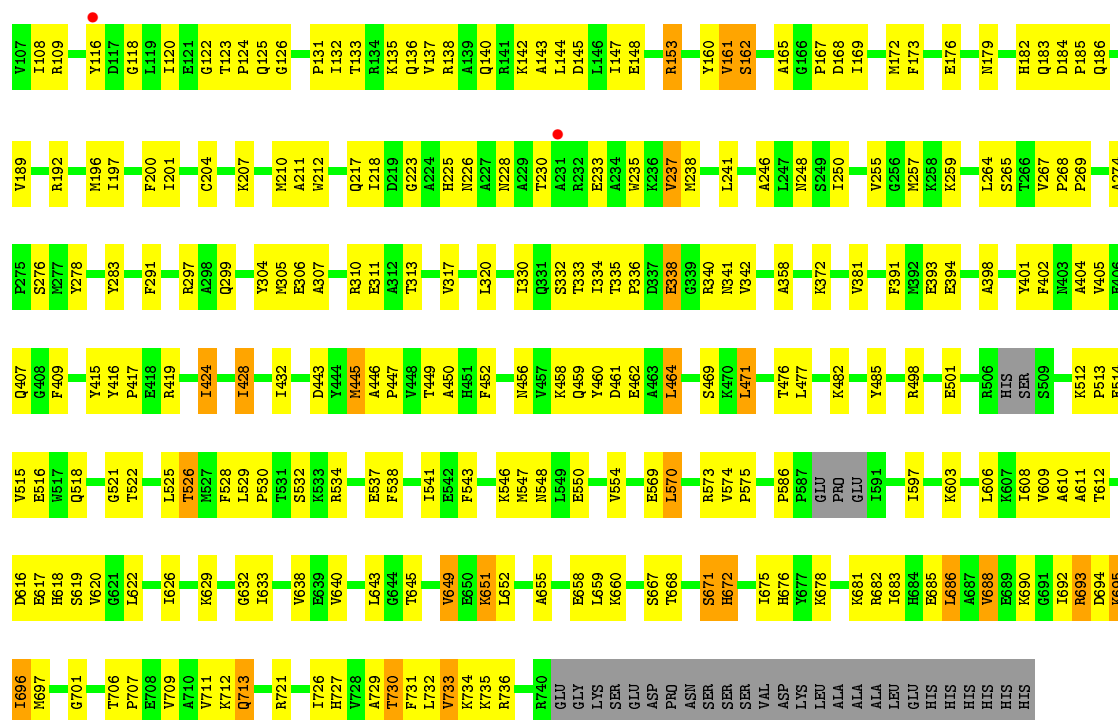
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- Chemical structure of Z98, a pyridine derivative. The structure features a pyridine ring with atoms labeled N1, C2, C3, C4, C5, and C6. A phosphate group is attached to the ring at C5 via an oxygen atom (OP4), with other phosphate oxygens labeled OP1, OP2, and OP3. A side chain is attached to the ring at C3, consisting of a methylene group (CG), a methylene group (CB), and a 2-amino-2-oxoethyl group (C, OXT, OH, NH2, N). The amino group (NH2) is shown with a wedge bond, indicating stereochemistry. The side chain also includes an oxygen atom (O3) and a carbonyl group (C=O).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	P	0	0
			23	12	3	7	1		

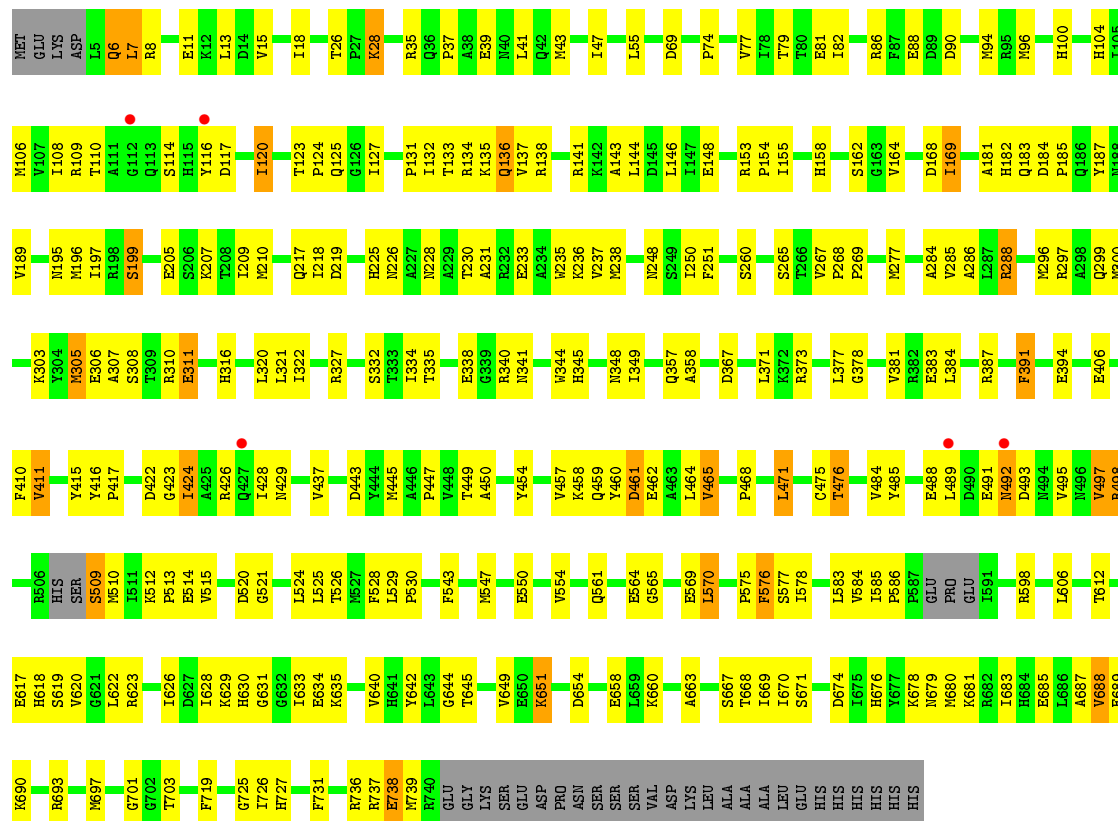


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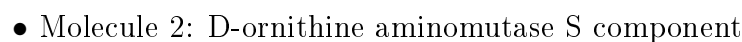
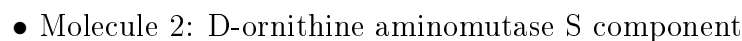
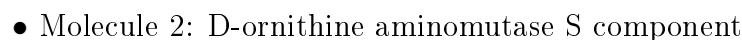
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	D	1	Total	C	N	O	P	0	0
			23	12	3	7	1		
5	A	1	Total	C	N	O	P	0	0
			23	12	3	7	1		
5	C	1	Total	C	N	O	P	0	0
			23	12	3	7	1		

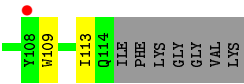


• Molecule 1: D-ornithine aminomutase E component

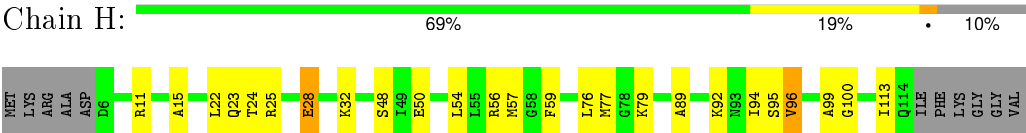


• Molecule 1: D-ornithine aminomutase E component





● Molecule 2: D-ornithine aminomutase S component



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	66.09Å 231.95Å 124.32Å 90.00° 103.24° 90.00°	Depositor
Resolution (Å)	63.11 – 2.80 64.33 – 2.80	Depositor EDS
% Data completeness (in resolution range)	92.3 (63.11-2.80) 92.4 (64.33-2.80)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.56 (at 2.81Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.191 , 0.270 0.192 , 0.271	Depositor DCC
R_{free} test set	4130 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	40.9	Xtriage
Anisotropy	0.594	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 34.8	EDS
Estimated twinning fraction	0.030 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 82521 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	24133	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.36% of the height of the origin peak. No significant pseudotranslation is detected.*

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: B12, 5AD, Z98

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	0.45	0/4628	0.63	0/6272
1	B	0.45	0/5774	0.61	0/7814
1	C	0.42	0/5759	0.59	0/7796
1	D	0.47	0/4631	0.63	0/6276
2	E	0.45	0/867	0.55	0/1163
2	F	0.43	0/870	0.59	0/1167
2	G	0.40	0/867	0.56	0/1163
2	H	0.45	0/867	0.58	0/1163
All	All	0.45	0/24263	0.61	0/32814

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
2	H	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	113	ILE	Peptide

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	4537	0	4469	154	0
1	B	5669	0	5635	238	0
1	C	5654	0	5621	229	0
1	D	4540	0	4478	160	0
2	E	855	0	863	34	0
2	F	858	0	865	23	0
2	G	855	0	863	24	0
2	H	855	0	863	29	0
3	B	91	0	87	24	0
3	C	91	0	87	17	0
4	A	18	0	11	3	0
4	D	18	0	10	1	0
5	A	23	0	15	4	0
5	B	23	0	15	4	0
5	C	23	0	15	4	0
5	D	23	0	15	3	0
All	All	24133	0	23912	849	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 18.

The worst 5 of 849 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:C:158:HIS:HE1	1:C:218:ILE:HD12	1.16	1.11
1:B:398:ALA:HB1	1:B:407:GLN:HE22	1.25	0.98
1:A:225:HIS:O	1:A:228:ASN:HB2	1.64	0.97
1:B:172:MET:HE2	1:B:173:PHE:HD1	1.30	0.95
1:B:526:THR:HG23	1:B:569:GLU:HG2	1.47	0.95

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	574/763 (75%)	525 (92%)	41 (7%)	8 (1%)	14	42
1	B	722/763 (95%)	662 (92%)	54 (8%)	6 (1%)	24	58
1	C	722/763 (95%)	666 (92%)	47 (6%)	9 (1%)	16	47
1	D	574/763 (75%)	534 (93%)	31 (5%)	9 (2%)	12	38
2	E	107/121 (88%)	104 (97%)	2 (2%)	1 (1%)	21	55
2	F	107/121 (88%)	98 (92%)	8 (8%)	1 (1%)	21	55
2	G	107/121 (88%)	99 (92%)	8 (8%)	0	100	100
2	H	107/121 (88%)	102 (95%)	4 (4%)	1 (1%)	21	55
All	All	3020/3536 (85%)	2790 (92%)	195 (6%)	35 (1%)	16	47

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	40	ASN
1	A	230	THR
1	A	234	ALA
1	A	504	GLU
1	B	6	GLN

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	484/644 (75%)	456 (94%)	28 (6%)	25	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	603/644 (94%)	560 (93%)	43 (7%)	18	46
1	C	600/644 (93%)	551 (92%)	49 (8%)	14	38
1	D	485/644 (75%)	455 (94%)	30 (6%)	23	54
2	E	89/100 (89%)	82 (92%)	7 (8%)	15	40
2	F	90/100 (90%)	85 (94%)	5 (6%)	26	59
2	G	89/100 (89%)	85 (96%)	4 (4%)	34	68
2	H	89/100 (89%)	87 (98%)	2 (2%)	60	89
All	All	2529/2976 (85%)	2361 (93%)	168 (7%)	21	51

5 of 168 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	730	THR
1	C	125	GLN
1	D	445	MET
2	F	61	SER
1	C	13	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	228	ASN
1	C	319	ASN
1	D	518	GLN
1	C	316	HIS
1	C	331	GLN

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 ⓘ

8 ligands are modelled in this entry.

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$
4	5AD	A	1500	3	15,20,20	2.82	5 (33%)	14,30,30	5.91	8 (57%)
5	Z98	A	767	-	20,23,23	4.30	8 (40%)	24,32,32	2.36	11 (45%)
3	B12	B	1801	1,4	74,101,101	1.13	6 (8%)	111,166,166	2.27	23 (20%)
5	Z98	B	767	-	20,23,23	4.42	8 (40%)	24,32,32	2.06	4 (16%)
3	B12	C	1801	1,4	74,101,101	1.11	5 (6%)	111,166,166	2.38	27 (24%)
5	Z98	C	767	-	20,23,23	4.38	8 (40%)	24,32,32	1.82	9 (37%)
4	5AD	D	1500	3	15,20,20	3.01	7 (46%)	14,30,30	5.81	7 (50%)
5	Z98	D	767	-	20,23,23	4.09	7 (35%)	24,32,32	1.87	6 (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
4	5AD	A	1500	3	-	0/0/20/20	0/3/3/3
5	Z98	A	767	-	-	1/13/17/17	0/1/1/1
3	B12	B	1801	1,4	1/1/36/38	0/51/223/223	0/3/11/11
5	Z98	B	767	-	-	1/13/17/17	0/1/1/1
3	B12	C	1801	1,4	1/1/36/38	1/51/223/223	0/3/11/11
5	Z98	C	767	-	-	0/13/17/17	0/1/1/1
4	5AD	D	1500	3	-	0/0/20/20	0/3/3/3
5	Z98	D	767	-	-	0/13/17/17	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1801	B12	C11-C10	-4.21	1.33	1.41
3	B	1801	B12	C11-C10	-4.16	1.33	1.41
3	C	1801	B12	C8B-N1B	-3.35	1.34	1.38
3	B	1801	B12	C8B-N1B	-3.17	1.34	1.38
3	C	1801	B12	C2-C3	-2.92	1.53	1.58

The worst 5 of 95 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1500	5AD	N3-C2-N1	-13.14	118.83	128.89
4	D	1500	5AD	N3-C2-N1	-12.96	118.97	128.89
3	C	1801	B12	C20-C1-C19	-9.60	99.96	109.38
3	B	1801	B12	C46-C12-C13	-6.82	84.03	112.81
3	C	1801	B12	C46-C12-C13	-6.78	84.20	112.81

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	B	1801	B12	C19
3	C	1801	B12	C19

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	767	Z98	C4-C4A-ND-CG
3	C	1801	B12	C16-C17-C55-C56
5	A	767	Z98	C4-C4A-ND-CG

There are no ring outliers.

8 monomers are involved in 57 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1500	5AD	3	0
5	A	767	Z98	4	0
3	B	1801	B12	24	0
5	B	767	Z98	4	0
3	C	1801	B12	17	0
5	C	767	Z98	4	0
4	D	1500	5AD	1	0
5	D	767	Z98	3	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 ⓘ

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	578/763 (75%)	-0.61	2 (0%) 94 92	17, 31, 57, 84	0
1	B	728/763 (95%)	-0.51	2 (0%) 94 92	18, 34, 61, 80	0
1	C	728/763 (95%)	-0.47	5 (0%) 89 84	19, 38, 62, 85	0
1	D	578/763 (75%)	-0.68	0 100 100	15, 27, 51, 74	0
2	E	109/121 (90%)	-0.39	0 100 100	22, 40, 60, 67	0
2	F	109/121 (90%)	-0.33	0 100 100	23, 35, 52, 58	0
2	G	109/121 (90%)	-0.28	1 (0%) 85 79	32, 45, 61, 75	0
2	H	109/121 (90%)	-0.47	0 100 100	21, 34, 56, 74	0
All	All	3048/3536 (86%)	-0.53	10 (0%) 94 92	15, 34, 60, 85	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	492	ASN	2.4
1	A	230	THR	2.4
1	C	112	GLY	2.4
1	C	489	LEU	2.3
1	A	587	PRO	2.3

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 [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(\AA^2)	Q<0.9
4	5AD	A	1500	18/18	0.93	0.20	1.65	34,48,54,57	0
5	Z98	C	767	23/23	0.93	0.20	1.18	28,40,48,56	0
5	Z98	B	767	23/23	0.97	0.18	1.09	21,34,38,43	0
5	Z98	A	767	23/23	0.95	0.17	0.94	21,30,37,40	0
5	Z98	D	767	23/23	0.96	0.17	0.89	22,31,42,44	0
4	5AD	D	1500	18/18	0.94	0.15	0.72	33,41,46,50	0
3	B12	C	1801	91/91	0.97	0.16	0.56	22,38,46,51	0
3	B12	B	1801	91/91	0.97	0.17	0.32	15,37,45,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.