



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 4, 2026 – 08:27 PM UTC

PDB ID : 2FG6 / pdb_00002fg6
Title : N-succinyl-L-ornithine transcarbamylase from *B. fragilis* complexed with sulfate and N-succinyl-L-norvaline
Authors : Shi, D.; Yu, X.; Malamy, M.H.; Allewell, N.M.; Mendel, T.
Deposited on : 2005-12-21
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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

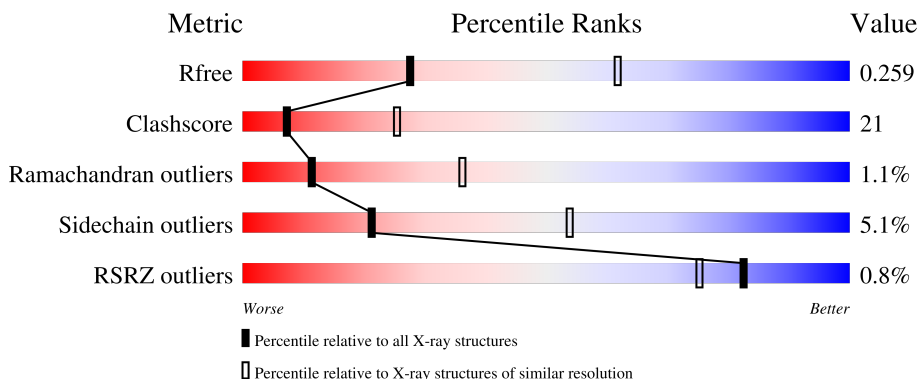
1 Overall quality at a glance

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}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	C	338	 54% 37% 5%
1	D	338	 50% 41% 5%
1	E	338	 53% 37% 5% 5%
1	X	338	 57% 34% 5%
1	Y	338	 60% 31% 5%

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Mol	Chain	Length	Quality of chain
1	Z	338	 55% 36% 5%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 15978 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 ornithine carbamoyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	X	322	2593	1651	448	478	16	0	0	0
1	Y	322	2593	1651	448	478	16	0	0	0
1	Z	320	2578	1643	443	476	16	0	0	0
1	C	321	2582	1645	444	477	16	0	0	0
1	D	322	2593	1651	448	478	16	0	0	0
1	E	322	2593	1651	448	478	16	0	0	0

There are 126 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	-19	MET	-	expression tag	UNP Q5LI27
X	-18	GLY	-	expression tag	UNP Q5LI27
X	-17	SER	-	expression tag	UNP Q5LI27
X	-16	SER	-	expression tag	UNP Q5LI27
X	-15	HIS	-	expression tag	UNP Q5LI27
X	-14	HIS	-	expression tag	UNP Q5LI27
X	-13	HIS	-	expression tag	UNP Q5LI27
X	-12	HIS	-	expression tag	UNP Q5LI27
X	-11	HIS	-	expression tag	UNP Q5LI27
X	-10	HIS	-	expression tag	UNP Q5LI27
X	-9	SER	-	expression tag	UNP Q5LI27
X	-8	SER	-	expression tag	UNP Q5LI27
X	-7	GLY	-	expression tag	UNP Q5LI27
X	-6	LEU	-	expression tag	UNP Q5LI27
X	-5	VAL	-	expression tag	UNP Q5LI27
X	-4	PRO	-	expression tag	UNP Q5LI27
X	-3	ARG	-	expression tag	UNP Q5LI27

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Chain	Residue	Modelled	Actual	Comment	Reference
X	-2	GLY	-	expression tag	UNP Q5LI27
X	-1	SER	-	expression tag	UNP Q5LI27
X	0	HIS	-	expression tag	UNP Q5LI27
X	242	LEU	THR	engineered mutation	UNP Q5LI27
Y	-19	MET	-	expression tag	UNP Q5LI27
Y	-18	GLY	-	expression tag	UNP Q5LI27
Y	-17	SER	-	expression tag	UNP Q5LI27
Y	-16	SER	-	expression tag	UNP Q5LI27
Y	-15	HIS	-	expression tag	UNP Q5LI27
Y	-14	HIS	-	expression tag	UNP Q5LI27
Y	-13	HIS	-	expression tag	UNP Q5LI27
Y	-12	HIS	-	expression tag	UNP Q5LI27
Y	-11	HIS	-	expression tag	UNP Q5LI27
Y	-10	HIS	-	expression tag	UNP Q5LI27
Y	-9	SER	-	expression tag	UNP Q5LI27
Y	-8	SER	-	expression tag	UNP Q5LI27
Y	-7	GLY	-	expression tag	UNP Q5LI27
Y	-6	LEU	-	expression tag	UNP Q5LI27
Y	-5	VAL	-	expression tag	UNP Q5LI27
Y	-4	PRO	-	expression tag	UNP Q5LI27
Y	-3	ARG	-	expression tag	UNP Q5LI27
Y	-2	GLY	-	expression tag	UNP Q5LI27
Y	-1	SER	-	expression tag	UNP Q5LI27
Y	0	HIS	-	expression tag	UNP Q5LI27
Y	242	LEU	THR	engineered mutation	UNP Q5LI27
Z	-19	MET	-	expression tag	UNP Q5LI27
Z	-18	GLY	-	expression tag	UNP Q5LI27
Z	-17	SER	-	expression tag	UNP Q5LI27
Z	-16	SER	-	expression tag	UNP Q5LI27
Z	-15	HIS	-	expression tag	UNP Q5LI27
Z	-14	HIS	-	expression tag	UNP Q5LI27
Z	-13	HIS	-	expression tag	UNP Q5LI27
Z	-12	HIS	-	expression tag	UNP Q5LI27
Z	-11	HIS	-	expression tag	UNP Q5LI27
Z	-10	HIS	-	expression tag	UNP Q5LI27
Z	-9	SER	-	expression tag	UNP Q5LI27
Z	-8	SER	-	expression tag	UNP Q5LI27
Z	-7	GLY	-	expression tag	UNP Q5LI27
Z	-6	LEU	-	expression tag	UNP Q5LI27
Z	-5	VAL	-	expression tag	UNP Q5LI27
Z	-4	PRO	-	expression tag	UNP Q5LI27
Z	-3	ARG	-	expression tag	UNP Q5LI27

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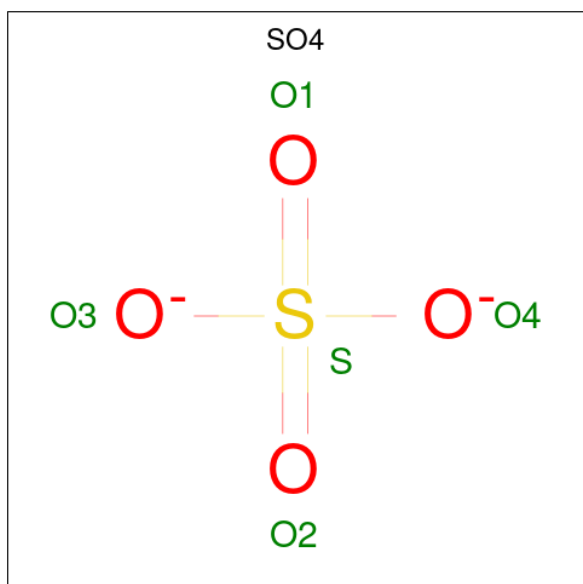
Chain	Residue	Modelled	Actual	Comment	Reference
Z	-2	GLY	-	expression tag	UNP Q5LI27
Z	-1	SER	-	expression tag	UNP Q5LI27
Z	0	HIS	-	expression tag	UNP Q5LI27
Z	242	LEU	THR	engineered mutation	UNP Q5LI27
C	-19	MET	-	expression tag	UNP Q5LI27
C	-18	GLY	-	expression tag	UNP Q5LI27
C	-17	SER	-	expression tag	UNP Q5LI27
C	-16	SER	-	expression tag	UNP Q5LI27
C	-15	HIS	-	expression tag	UNP Q5LI27
C	-14	HIS	-	expression tag	UNP Q5LI27
C	-13	HIS	-	expression tag	UNP Q5LI27
C	-12	HIS	-	expression tag	UNP Q5LI27
C	-11	HIS	-	expression tag	UNP Q5LI27
C	-10	HIS	-	expression tag	UNP Q5LI27
C	-9	SER	-	expression tag	UNP Q5LI27
C	-8	SER	-	expression tag	UNP Q5LI27
C	-7	GLY	-	expression tag	UNP Q5LI27
C	-6	LEU	-	expression tag	UNP Q5LI27
C	-5	VAL	-	expression tag	UNP Q5LI27
C	-4	PRO	-	expression tag	UNP Q5LI27
C	-3	ARG	-	expression tag	UNP Q5LI27
C	-2	GLY	-	expression tag	UNP Q5LI27
C	-1	SER	-	expression tag	UNP Q5LI27
C	0	HIS	-	expression tag	UNP Q5LI27
C	242	LEU	THR	engineered mutation	UNP Q5LI27
D	-19	MET	-	expression tag	UNP Q5LI27
D	-18	GLY	-	expression tag	UNP Q5LI27
D	-17	SER	-	expression tag	UNP Q5LI27
D	-16	SER	-	expression tag	UNP Q5LI27
D	-15	HIS	-	expression tag	UNP Q5LI27
D	-14	HIS	-	expression tag	UNP Q5LI27
D	-13	HIS	-	expression tag	UNP Q5LI27
D	-12	HIS	-	expression tag	UNP Q5LI27
D	-11	HIS	-	expression tag	UNP Q5LI27
D	-10	HIS	-	expression tag	UNP Q5LI27
D	-9	SER	-	expression tag	UNP Q5LI27
D	-8	SER	-	expression tag	UNP Q5LI27
D	-7	GLY	-	expression tag	UNP Q5LI27
D	-6	LEU	-	expression tag	UNP Q5LI27
D	-5	VAL	-	expression tag	UNP Q5LI27
D	-4	PRO	-	expression tag	UNP Q5LI27
D	-3	ARG	-	expression tag	UNP Q5LI27

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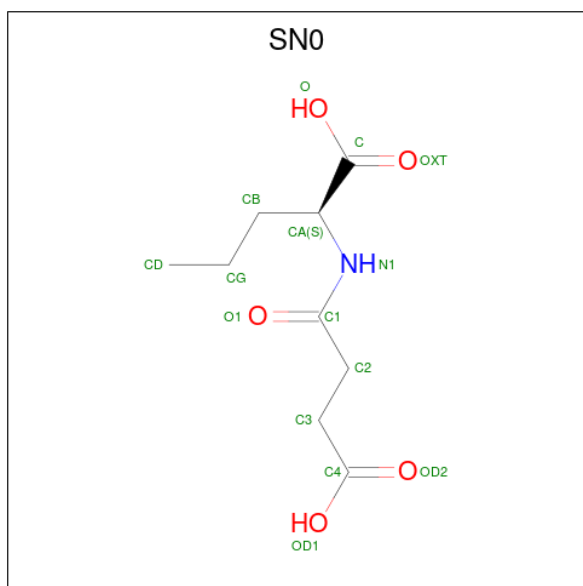
Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	GLY	-	expression tag	UNP Q5LI27
D	-1	SER	-	expression tag	UNP Q5LI27
D	0	HIS	-	expression tag	UNP Q5LI27
D	242	LEU	THR	engineered mutation	UNP Q5LI27
E	-19	MET	-	expression tag	UNP Q5LI27
E	-18	GLY	-	expression tag	UNP Q5LI27
E	-17	SER	-	expression tag	UNP Q5LI27
E	-16	SER	-	expression tag	UNP Q5LI27
E	-15	HIS	-	expression tag	UNP Q5LI27
E	-14	HIS	-	expression tag	UNP Q5LI27
E	-13	HIS	-	expression tag	UNP Q5LI27
E	-12	HIS	-	expression tag	UNP Q5LI27
E	-11	HIS	-	expression tag	UNP Q5LI27
E	-10	HIS	-	expression tag	UNP Q5LI27
E	-9	SER	-	expression tag	UNP Q5LI27
E	-8	SER	-	expression tag	UNP Q5LI27
E	-7	GLY	-	expression tag	UNP Q5LI27
E	-6	LEU	-	expression tag	UNP Q5LI27
E	-5	VAL	-	expression tag	UNP Q5LI27
E	-4	PRO	-	expression tag	UNP Q5LI27
E	-3	ARG	-	expression tag	UNP Q5LI27
E	-2	GLY	-	expression tag	UNP Q5LI27
E	-1	SER	-	expression tag	UNP Q5LI27
E	0	HIS	-	expression tag	UNP Q5LI27
E	242	LEU	THR	engineered mutation	UNP Q5LI27

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	X	1	Total O S 5 4 1	0	0
2	X	1	Total O S 5 4 1	0	0
2	Y	1	Total O S 5 4 1	0	0
2	Z	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	E	1	Total O S 5 4 1	0	0

- Molecule 3 is N-(3-CARBOXYPROPANOYL)-L-NORVALINE (CCD ID: SN0) (formula: C₉H₁₅NO₅).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	X	1	Total C N O 15 9 1 5	0	0
3	Y	1	Total C N O 15 9 1 5	0	0
3	Z	1	Total C N O 15 9 1 5	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	C	1	Total	C	N	O	0	0
			15	9	1	5		
3	D	1	Total	C	N	O	0	0
			15	9	1	5		
3	E	1	Total	C	N	O	0	0
			15	9	1	5		

- Molecule 4 is water.

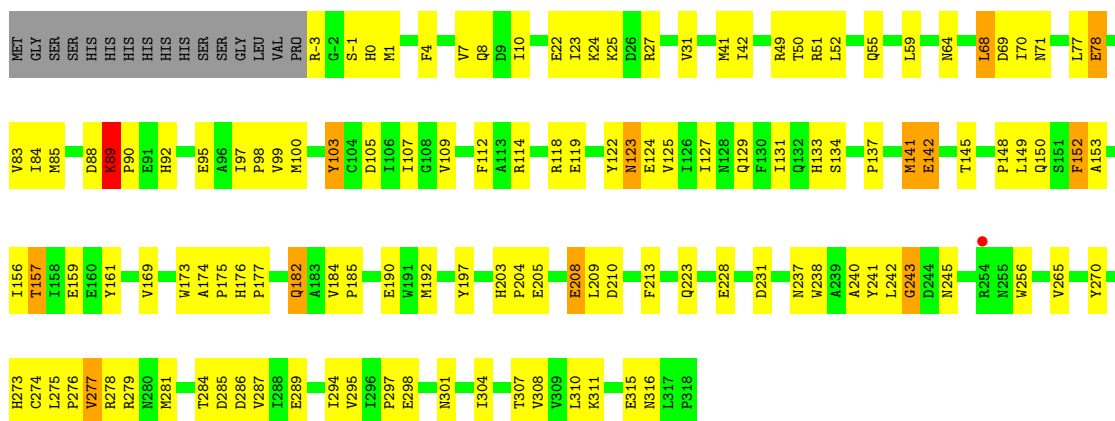
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	X	62	Total	O	0	0
			62	62		
4	Y	109	Total	O	0	0
			109	109		
4	Z	55	Total	O	0	0
			55	55		
4	C	27	Total	O	0	0
			27	27		
4	D	25	Total	O	0	0
			25	25		
4	E	38	Total	O	0	0
			38	38		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

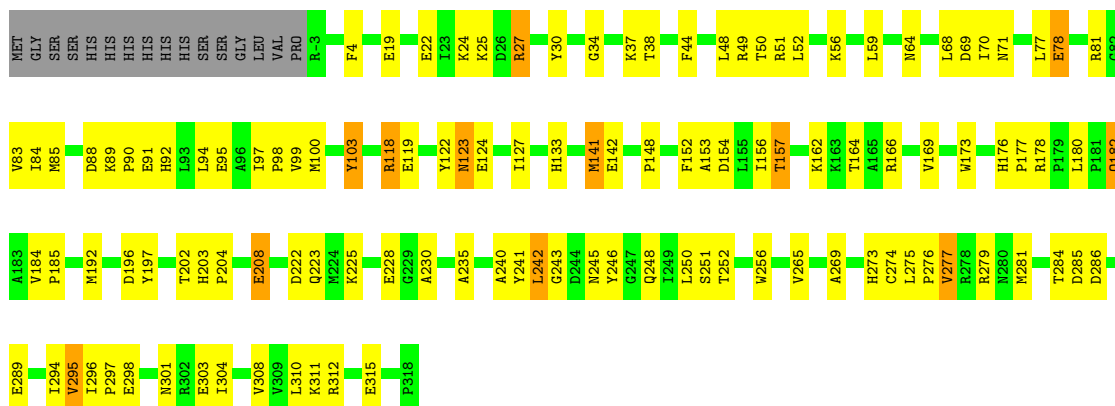
- Molecule 1: putative ornithine carbamoyltransferase

Chain X: 



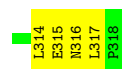
- Molecule 1: putative ornithine carbamoyltransferase

Chain Y: 

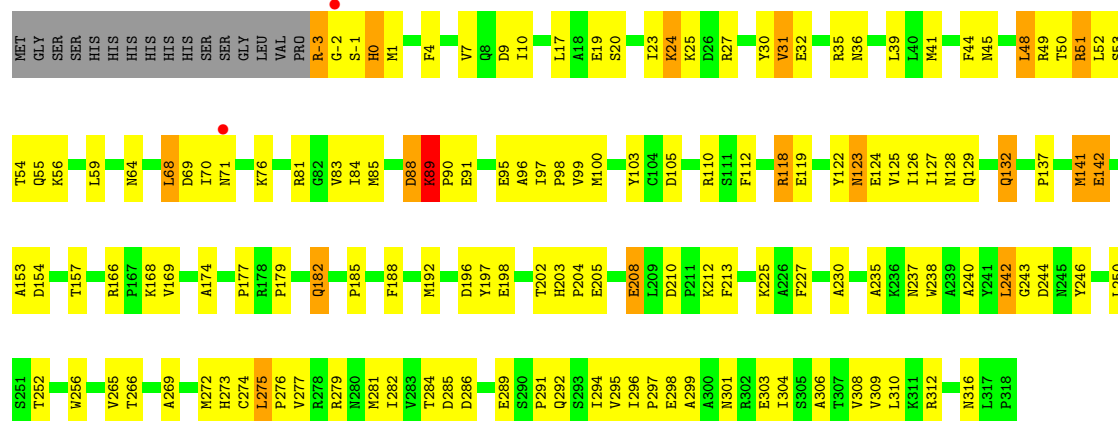


- Molecule 1: putative ornithine carbamoyltransferase

Chain Z: 



- Molecule 1: putative ornithine carbamoyltransferase



4 Data and refinement statistics i

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	155.70Å 155.70Å 120.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.99 – 2.80 19.99 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.5 (19.99-2.80) 99.3 (19.99-2.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 2.79Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.216 , 0.260 0.216 , 0.259	Depositor DCC
R_{free} test set	3585 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	51.6	Xtrriage
Anisotropy	0.314	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 56.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	0.012 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	15978	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.23% 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: SN0, SO4

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	C	0.39	0/2642	0.98	14/3579 (0.4%)
1	D	0.41	0/2653	0.95	10/3593 (0.3%)
1	E	0.44	0/2653	0.99	13/3593 (0.4%)
1	X	0.49	1/2653 (0.0%)	1.00	8/3593 (0.2%)
1	Y	0.52	0/2653	1.02	11/3593 (0.3%)
1	Z	0.49	0/2638	0.99	9/3574 (0.3%)
All	All	0.46	1/15892 (0.0%)	0.99	65/21525 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	X	141	MET	SD-CE	-5.43	1.66	1.79

The worst 5 of 65 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Z	44	PHE	N-CA-C	-7.69	103.92	113.38
1	Y	88	ASP	N-CA-C	7.31	120.11	111.71
1	X	133	HIS	N-CA-C	6.95	121.93	113.38
1	Y	141	MET	N-CA-C	-6.87	104.21	112.59
1	Y	27	ARG	N-CA-C	6.75	119.50	111.33

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	C	2582	0	2551	125	0
1	D	2593	0	2564	129	0
1	E	2593	0	2564	120	0
1	X	2593	0	2564	106	0
1	Y	2593	0	2564	98	0
1	Z	2578	0	2548	97	0
2	C	10	0	0	1	0
2	D	5	0	0	0	0
2	E	5	0	0	0	0
2	X	10	0	0	0	0
2	Y	5	0	0	0	0
2	Z	5	0	0	0	0
3	C	15	0	13	2	0
3	D	15	0	13	1	0
3	E	15	0	13	2	0
3	X	15	0	13	0	0
3	Y	15	0	13	1	0
3	Z	15	0	13	0	0
4	C	27	0	0	4	0
4	D	25	0	0	8	0
4	E	38	0	0	4	0
4	X	62	0	0	5	0
4	Y	109	0	0	1	0
4	Z	55	0	0	4	0
All	All	15978	0	15433	640	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 21.

The worst 5 of 640 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:X:41:MET:HE3	1:X:141:MET:HE1	1.42	1.00
1:Z:169:VAL:HG11	1:Z:192:MET:HE2	1.45	0.97
1:Y:153:ALA:O	1:Y:157:THR:HG22	1.67	0.94
1:X:70:ILE:HD11	1:X:100:MET:HE1	1.50	0.93
1:Y:177:PRO:HD3	1:Y:281:MET:HE2	1.52	0.91

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	C	319/338 (94%)	290 (91%)	26 (8%)	3 (1%)	14	41
1	D	320/338 (95%)	289 (90%)	25 (8%)	6 (2%)	6	22
1	E	320/338 (95%)	292 (91%)	24 (8%)	4 (1%)	9	31
1	X	320/338 (95%)	290 (91%)	27 (8%)	3 (1%)	14	41
1	Y	320/338 (95%)	298 (93%)	20 (6%)	2 (1%)	21	51
1	Z	318/338 (94%)	287 (90%)	28 (9%)	3 (1%)	14	41
All	All	1917/2028 (94%)	1746 (91%)	150 (8%)	21 (1%)	11	36

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	X	142	GLU
1	Y	142	GLU
1	Z	142	GLU
1	C	142	GLU
1	D	142	GLU

5.3.2 Protein sidechains [i](#)

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	C	279/294 (95%)	264 (95%)	15 (5%)	20	51
1	D	280/294 (95%)	265 (95%)	15 (5%)	20	51
1	E	280/294 (95%)	267 (95%)	13 (5%)	24	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	X	280/294 (95%)	265 (95%)	15 (5%)	20	51
1	Y	280/294 (95%)	266 (95%)	14 (5%)	22	54
1	Z	279/294 (95%)	266 (95%)	13 (5%)	23	57
All	All	1678/1764 (95%)	1593 (95%)	85 (5%)	21	54

5 of 85 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	-3	ARG
1	D	310	LEU
1	D	48	LEU
1	D	178	ARG
1	E	51	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 57 such sidechains are listed below:

Mol	Chain	Res	Type
1	Z	301	ASN
1	E	301	ASN
1	C	267	ASN
1	E	292	GLN
1	E	72	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry

14 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
3	SN0	X	345	-	14,14,14	0.76	0	17,17,17	1.27	2 (11%)
3	SN0	C	351	-	14,14,14	0.80	0	17,17,17	1.21	2 (11%)
3	SN0	Y	347	-	14,14,14	0.79	0	17,17,17	1.25	3 (17%)
3	SN0	Z	349	-	14,14,14	0.95	0	17,17,17	1.41	1 (5%)
3	SN0	D	353	-	14,14,14	0.89	0	17,17,17	1.21	2 (11%)
2	SO4	X	357	-	4,4,4	0.30	0	6,6,6	0.11	0
2	SO4	C	352	-	4,4,4	0.31	0	6,6,6	0.10	0
2	SO4	X	346	-	4,4,4	0.35	0	6,6,6	0.18	0
2	SO4	Z	350	-	4,4,4	0.41	0	6,6,6	0.14	0
2	SO4	C	358	-	4,4,4	0.41	0	6,6,6	0.14	0
2	SO4	E	356	-	4,4,4	0.36	0	6,6,6	0.21	0
2	SO4	D	354	-	4,4,4	0.38	0	6,6,6	0.26	0
3	SN0	E	355	-	14,14,14	0.78	0	17,17,17	0.95	0
2	SO4	Y	348	-	4,4,4	0.38	0	6,6,6	0.19	0

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	SN0	X	345	-	-	3/16/16/16	-
3	SN0	C	351	-	-	1/16/16/16	-
3	SN0	Z	349	-	-	0/16/16/16	-
3	SN0	D	353	-	-	1/16/16/16	-
3	SN0	Y	347	-	-	0/16/16/16	-
3	SN0	E	355	-	-	3/16/16/16	-

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Z	349	SN0	C-CA-N1	4.42	120.82	110.57
3	D	353	SN0	CB-CA-N1	3.05	116.95	110.91
3	Y	347	SN0	OD2-C4-C3	-2.76	114.35	123.09
3	Y	347	SN0	OD1-C4-C3	2.64	122.34	114.00
3	C	351	SN0	CB-CA-N1	2.50	115.86	110.91

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	355	SN0	C1-C2-C3-C4
3	E	355	SN0	C2-C3-C4-OD2
3	E	355	SN0	C2-C3-C4-OD1
3	X	345	SN0	C1-C2-C3-C4
3	X	345	SN0	C2-C3-C4-OD2

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	351	SN0	2	0
3	Y	347	SN0	1	0
3	D	353	SN0	1	0
2	C	352	SO4	1	0
3	E	355	SN0	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	C	321/338 (94%)	0.34	5 (1%) 70 61	54, 72, 92, 108	0
1	D	322/338 (95%)	0.55	7 (2%) 62 52	46, 71, 96, 117	0
1	E	322/338 (95%)	0.04	2 (0%) 85 80	38, 58, 78, 101	0
1	X	322/338 (95%)	-0.27	1 (0%) 90 86	28, 48, 71, 84	0
1	Y	322/338 (95%)	-0.61	0 100 100	22, 35, 51, 78	0
1	Z	320/338 (94%)	-0.34	1 (0%) 90 86	27, 44, 62, 82	0
All	All	1929/2028 (95%)	-0.05	16 (0%) 82 75	22, 55, 86, 117	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	-2	GLY	3.3
1	C	254	ARG	3.1
1	D	227	PHE	2.7
1	D	254	ARG	2.6
1	D	232	PHE	2.5

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 oligosaccharides 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. 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	B-factors(Å ²)	Q<0.9
2	SO4	D	354	5/5	0.85	0.12	57,60,62,63	0
2	SO4	C	358	5/5	0.86	0.12	83,83,85,85	0
3	SN0	D	353	15/15	0.89	0.12	41,52,57,57	0
3	SN0	C	351	15/15	0.92	0.11	68,69,71,71	0
3	SN0	X	345	15/15	0.94	0.09	46,51,54,56	0
2	SO4	E	356	5/5	0.95	0.09	49,50,53,55	0
3	SN0	E	355	15/15	0.95	0.09	46,51,54,56	0
2	SO4	X	357	5/5	0.96	0.06	53,55,56,58	0
3	SN0	Y	347	15/15	0.96	0.07	30,35,41,41	0
3	SN0	Z	349	15/15	0.96	0.08	37,39,41,41	0
2	SO4	X	346	5/5	0.98	0.04	42,44,44,44	0
2	SO4	Z	350	5/5	0.98	0.05	32,36,38,38	0
2	SO4	C	352	5/5	0.98	0.05	59,60,60,62	0
2	SO4	Y	348	5/5	0.99	0.06	32,35,35,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.