



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 12:50 AM UTC

PDB ID : 3DBY / pdb_00003dby
Title : Crystal structure of uncharacterized protein from *Bacillus cereus* G9241 (CSAP Target)
Authors : Ramagopal, U.A.; Bonanno, J.B.; Ozyurt, S.; Freeman, J.; Wasserman, S.; Hu, S.; Groshong, C.; Rodgers, L.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2008-06-02
Resolution : 2.10 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)
Xtrriage (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

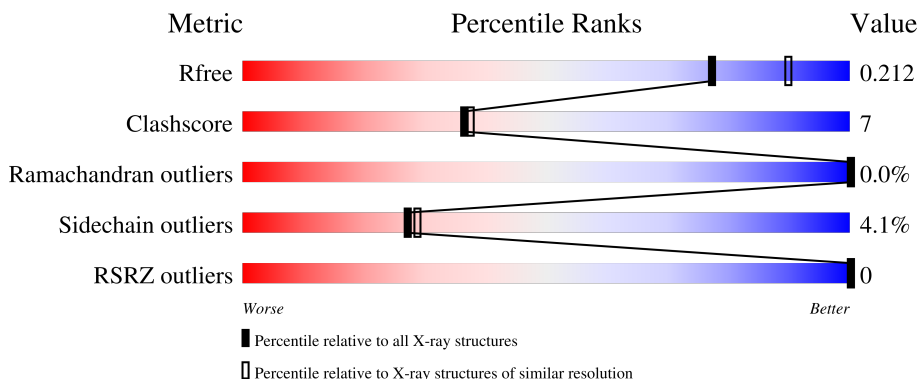
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	A	269	 82% 12% . .
1	B	269	 86% 12% . . .
1	C	269	 84% 14% . .
1	D	269	 84% 14% . .

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Mol	Chain	Length	Quality of chain	
1	E	269	83%	10% ..
1	F	269	84%	13% ..
1	G	269	75%	17% ..
1	H	269	84%	13% ..
1	I	269	70%	24% ..
1	J	269	80%	17% ..
1	K	269	79%	14% ..
1	L	269	81%	15% ..
1	M	269	79%	16% ..
1	N	269	80%	14% ..
1	O	269	72%	20% ..
1	P	269	81%	15% ..
1	Q	269	86%	12% ..
1	R	269	85%	13% ..
1	S	269	79%	16% ..
1	T	269	88%	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	EDO	R	308	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 45580 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 uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	257	Total 2130	C 1382	N 347	O 393	S 8	0	3	0
1	B	266	Total 2217	C 1435	N 374	O 399	S 9	0	4	0
1	C	267	Total 2215	C 1433	N 373	O 401	S 8	0	2	0
1	D	266	Total 2226	C 1441	N 376	O 400	S 9	0	5	0
1	E	257	Total 2139	C 1387	N 348	O 396	S 8	0	4	0
1	F	267	Total 2228	C 1443	N 377	O 399	S 9	0	4	0
1	G	257	Total 2113	C 1372	N 349	O 384	S 8	0	1	0
1	H	265	Total 2219	C 1434	N 376	O 400	S 9	0	4	0
1	I	257	Total 2114	C 1373	N 346	O 386	S 9	0	1	0
1	J	266	Total 2230	C 1441	N 376	O 405	S 8	0	5	0
1	K	257	Total 2121	C 1377	N 346	O 390	S 8	0	2	0
1	L	260	Total 2146	C 1392	N 356	O 389	S 9	0	2	0
1	M	259	Total 2127	C 1380	N 351	O 388	S 8	0	1	0
1	N	259	Total 2124	C 1377	N 351	O 388	S 8	0	0	0
1	O	257	Total 2123	C 1378	N 347	O 389	S 9	0	2	0
1	P	266	Total 2207	C 1427	N 372	O 400	S 8	0	2	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	266	Total	C	N	O	S	0	6	0
			2227	1441	372	405	9			
1	R	265	Total	C	N	O	S	0	4	0
			2216	1434	373	400	9			
1	S	257	Total	C	N	O	S	0	3	0
			2130	1382	347	392	9			
1	T	267	Total	C	N	O	S	0	1	0
			2207	1428	371	399	9			

There are 200 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	expression tag	UNP Q4MWP8
A	2	LEU	-	expression tag	UNP Q4MWP8
A	261	GLU	-	expression tag	UNP Q4MWP8
A	262	GLY	-	expression tag	UNP Q4MWP8
A	263	HIS	-	expression tag	UNP Q4MWP8
A	264	HIS	-	expression tag	UNP Q4MWP8
A	265	HIS	-	expression tag	UNP Q4MWP8
A	266	HIS	-	expression tag	UNP Q4MWP8
A	267	HIS	-	expression tag	UNP Q4MWP8
A	268	HIS	-	expression tag	UNP Q4MWP8
B	1	SER	-	expression tag	UNP Q4MWP8
B	2	LEU	-	expression tag	UNP Q4MWP8
B	261	GLU	-	expression tag	UNP Q4MWP8
B	262	GLY	-	expression tag	UNP Q4MWP8
B	263	HIS	-	expression tag	UNP Q4MWP8
B	264	HIS	-	expression tag	UNP Q4MWP8
B	265	HIS	-	expression tag	UNP Q4MWP8
B	266	HIS	-	expression tag	UNP Q4MWP8
B	267	HIS	-	expression tag	UNP Q4MWP8
B	268	HIS	-	expression tag	UNP Q4MWP8
C	1	SER	-	expression tag	UNP Q4MWP8
C	2	LEU	-	expression tag	UNP Q4MWP8
C	261	GLU	-	expression tag	UNP Q4MWP8
C	262	GLY	-	expression tag	UNP Q4MWP8
C	263	HIS	-	expression tag	UNP Q4MWP8
C	264	HIS	-	expression tag	UNP Q4MWP8
C	265	HIS	-	expression tag	UNP Q4MWP8
C	266	HIS	-	expression tag	UNP Q4MWP8
C	267	HIS	-	expression tag	UNP Q4MWP8
C	268	HIS	-	expression tag	UNP Q4MWP8
D	1	SER	-	expression tag	UNP Q4MWP8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	2	LEU	-	expression tag	UNP Q4MWP8
D	261	GLU	-	expression tag	UNP Q4MWP8
D	262	GLY	-	expression tag	UNP Q4MWP8
D	263	HIS	-	expression tag	UNP Q4MWP8
D	264	HIS	-	expression tag	UNP Q4MWP8
D	265	HIS	-	expression tag	UNP Q4MWP8
D	266	HIS	-	expression tag	UNP Q4MWP8
D	267	HIS	-	expression tag	UNP Q4MWP8
D	268	HIS	-	expression tag	UNP Q4MWP8
E	1	SER	-	expression tag	UNP Q4MWP8
E	2	LEU	-	expression tag	UNP Q4MWP8
E	261	GLU	-	expression tag	UNP Q4MWP8
E	262	GLY	-	expression tag	UNP Q4MWP8
E	263	HIS	-	expression tag	UNP Q4MWP8
E	264	HIS	-	expression tag	UNP Q4MWP8
E	265	HIS	-	expression tag	UNP Q4MWP8
E	266	HIS	-	expression tag	UNP Q4MWP8
E	267	HIS	-	expression tag	UNP Q4MWP8
E	268	HIS	-	expression tag	UNP Q4MWP8
F	1	SER	-	expression tag	UNP Q4MWP8
F	2	LEU	-	expression tag	UNP Q4MWP8
F	261	GLU	-	expression tag	UNP Q4MWP8
F	262	GLY	-	expression tag	UNP Q4MWP8
F	263	HIS	-	expression tag	UNP Q4MWP8
F	264	HIS	-	expression tag	UNP Q4MWP8
F	265	HIS	-	expression tag	UNP Q4MWP8
F	266	HIS	-	expression tag	UNP Q4MWP8
F	267	HIS	-	expression tag	UNP Q4MWP8
F	268	HIS	-	expression tag	UNP Q4MWP8
G	1	SER	-	expression tag	UNP Q4MWP8
G	2	LEU	-	expression tag	UNP Q4MWP8
G	261	GLU	-	expression tag	UNP Q4MWP8
G	262	GLY	-	expression tag	UNP Q4MWP8
G	263	HIS	-	expression tag	UNP Q4MWP8
G	264	HIS	-	expression tag	UNP Q4MWP8
G	265	HIS	-	expression tag	UNP Q4MWP8
G	266	HIS	-	expression tag	UNP Q4MWP8
G	267	HIS	-	expression tag	UNP Q4MWP8
G	268	HIS	-	expression tag	UNP Q4MWP8
H	1	SER	-	expression tag	UNP Q4MWP8
H	2	LEU	-	expression tag	UNP Q4MWP8
H	261	GLU	-	expression tag	UNP Q4MWP8

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Chain	Residue	Modelled	Actual	Comment	Reference
H	262	GLY	-	expression tag	UNP Q4MWP8
H	263	HIS	-	expression tag	UNP Q4MWP8
H	264	HIS	-	expression tag	UNP Q4MWP8
H	265	HIS	-	expression tag	UNP Q4MWP8
H	266	HIS	-	expression tag	UNP Q4MWP8
H	267	HIS	-	expression tag	UNP Q4MWP8
H	268	HIS	-	expression tag	UNP Q4MWP8
I	1	SER	-	expression tag	UNP Q4MWP8
I	2	LEU	-	expression tag	UNP Q4MWP8
I	261	GLU	-	expression tag	UNP Q4MWP8
I	262	GLY	-	expression tag	UNP Q4MWP8
I	263	HIS	-	expression tag	UNP Q4MWP8
I	264	HIS	-	expression tag	UNP Q4MWP8
I	265	HIS	-	expression tag	UNP Q4MWP8
I	266	HIS	-	expression tag	UNP Q4MWP8
I	267	HIS	-	expression tag	UNP Q4MWP8
I	268	HIS	-	expression tag	UNP Q4MWP8
J	1	SER	-	expression tag	UNP Q4MWP8
J	2	LEU	-	expression tag	UNP Q4MWP8
J	261	GLU	-	expression tag	UNP Q4MWP8
J	262	GLY	-	expression tag	UNP Q4MWP8
J	263	HIS	-	expression tag	UNP Q4MWP8
J	264	HIS	-	expression tag	UNP Q4MWP8
J	265	HIS	-	expression tag	UNP Q4MWP8
J	266	HIS	-	expression tag	UNP Q4MWP8
J	267	HIS	-	expression tag	UNP Q4MWP8
J	268	HIS	-	expression tag	UNP Q4MWP8
K	1	SER	-	expression tag	UNP Q4MWP8
K	2	LEU	-	expression tag	UNP Q4MWP8
K	261	GLU	-	expression tag	UNP Q4MWP8
K	262	GLY	-	expression tag	UNP Q4MWP8
K	263	HIS	-	expression tag	UNP Q4MWP8
K	264	HIS	-	expression tag	UNP Q4MWP8
K	265	HIS	-	expression tag	UNP Q4MWP8
K	266	HIS	-	expression tag	UNP Q4MWP8
K	267	HIS	-	expression tag	UNP Q4MWP8
K	268	HIS	-	expression tag	UNP Q4MWP8
L	1	SER	-	expression tag	UNP Q4MWP8
L	2	LEU	-	expression tag	UNP Q4MWP8
L	261	GLU	-	expression tag	UNP Q4MWP8
L	262	GLY	-	expression tag	UNP Q4MWP8
L	263	HIS	-	expression tag	UNP Q4MWP8

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Chain	Residue	Modelled	Actual	Comment	Reference
L	264	HIS	-	expression tag	UNP Q4MWP8
L	265	HIS	-	expression tag	UNP Q4MWP8
L	266	HIS	-	expression tag	UNP Q4MWP8
L	267	HIS	-	expression tag	UNP Q4MWP8
L	268	HIS	-	expression tag	UNP Q4MWP8
M	1	SER	-	expression tag	UNP Q4MWP8
M	2	LEU	-	expression tag	UNP Q4MWP8
M	261	GLU	-	expression tag	UNP Q4MWP8
M	262	GLY	-	expression tag	UNP Q4MWP8
M	263	HIS	-	expression tag	UNP Q4MWP8
M	264	HIS	-	expression tag	UNP Q4MWP8
M	265	HIS	-	expression tag	UNP Q4MWP8
M	266	HIS	-	expression tag	UNP Q4MWP8
M	267	HIS	-	expression tag	UNP Q4MWP8
M	268	HIS	-	expression tag	UNP Q4MWP8
N	1	SER	-	expression tag	UNP Q4MWP8
N	2	LEU	-	expression tag	UNP Q4MWP8
N	261	GLU	-	expression tag	UNP Q4MWP8
N	262	GLY	-	expression tag	UNP Q4MWP8
N	263	HIS	-	expression tag	UNP Q4MWP8
N	264	HIS	-	expression tag	UNP Q4MWP8
N	265	HIS	-	expression tag	UNP Q4MWP8
N	266	HIS	-	expression tag	UNP Q4MWP8
N	267	HIS	-	expression tag	UNP Q4MWP8
N	268	HIS	-	expression tag	UNP Q4MWP8
O	1	SER	-	expression tag	UNP Q4MWP8
O	2	LEU	-	expression tag	UNP Q4MWP8
O	261	GLU	-	expression tag	UNP Q4MWP8
O	262	GLY	-	expression tag	UNP Q4MWP8
O	263	HIS	-	expression tag	UNP Q4MWP8
O	264	HIS	-	expression tag	UNP Q4MWP8
O	265	HIS	-	expression tag	UNP Q4MWP8
O	266	HIS	-	expression tag	UNP Q4MWP8
O	267	HIS	-	expression tag	UNP Q4MWP8
O	268	HIS	-	expression tag	UNP Q4MWP8
P	1	SER	-	expression tag	UNP Q4MWP8
P	2	LEU	-	expression tag	UNP Q4MWP8
P	261	GLU	-	expression tag	UNP Q4MWP8
P	262	GLY	-	expression tag	UNP Q4MWP8
P	263	HIS	-	expression tag	UNP Q4MWP8
P	264	HIS	-	expression tag	UNP Q4MWP8
P	265	HIS	-	expression tag	UNP Q4MWP8

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Chain	Residue	Modelled	Actual	Comment	Reference
P	266	HIS	-	expression tag	UNP Q4MWP8
P	267	HIS	-	expression tag	UNP Q4MWP8
P	268	HIS	-	expression tag	UNP Q4MWP8
Q	1	SER	-	expression tag	UNP Q4MWP8
Q	2	LEU	-	expression tag	UNP Q4MWP8
Q	261	GLU	-	expression tag	UNP Q4MWP8
Q	262	GLY	-	expression tag	UNP Q4MWP8
Q	263	HIS	-	expression tag	UNP Q4MWP8
Q	264	HIS	-	expression tag	UNP Q4MWP8
Q	265	HIS	-	expression tag	UNP Q4MWP8
Q	266	HIS	-	expression tag	UNP Q4MWP8
Q	267	HIS	-	expression tag	UNP Q4MWP8
Q	268	HIS	-	expression tag	UNP Q4MWP8
R	1	SER	-	expression tag	UNP Q4MWP8
R	2	LEU	-	expression tag	UNP Q4MWP8
R	261	GLU	-	expression tag	UNP Q4MWP8
R	262	GLY	-	expression tag	UNP Q4MWP8
R	263	HIS	-	expression tag	UNP Q4MWP8
R	264	HIS	-	expression tag	UNP Q4MWP8
R	265	HIS	-	expression tag	UNP Q4MWP8
R	266	HIS	-	expression tag	UNP Q4MWP8
R	267	HIS	-	expression tag	UNP Q4MWP8
R	268	HIS	-	expression tag	UNP Q4MWP8
S	1	SER	-	expression tag	UNP Q4MWP8
S	2	LEU	-	expression tag	UNP Q4MWP8
S	261	GLU	-	expression tag	UNP Q4MWP8
S	262	GLY	-	expression tag	UNP Q4MWP8
S	263	HIS	-	expression tag	UNP Q4MWP8
S	264	HIS	-	expression tag	UNP Q4MWP8
S	265	HIS	-	expression tag	UNP Q4MWP8
S	266	HIS	-	expression tag	UNP Q4MWP8
S	267	HIS	-	expression tag	UNP Q4MWP8
S	268	HIS	-	expression tag	UNP Q4MWP8
T	1	SER	-	expression tag	UNP Q4MWP8
T	2	LEU	-	expression tag	UNP Q4MWP8
T	261	GLU	-	expression tag	UNP Q4MWP8
T	262	GLY	-	expression tag	UNP Q4MWP8
T	263	HIS	-	expression tag	UNP Q4MWP8
T	264	HIS	-	expression tag	UNP Q4MWP8
T	265	HIS	-	expression tag	UNP Q4MWP8
T	266	HIS	-	expression tag	UNP Q4MWP8
T	267	HIS	-	expression tag	UNP Q4MWP8

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Chain	Residue	Modelled	Actual	Comment	Reference
T	268	HIS	-	expression tag	UNP Q4MWP8

- Molecule 2 is FE (III) ION (CCD ID: FE) (formula: Fe).

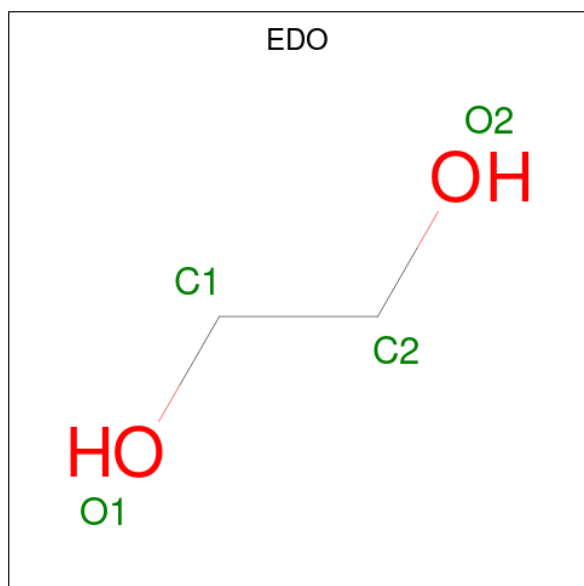
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Fe 2 2	0	0
2	B	2	Total Fe 2 2	0	0
2	C	2	Total Fe 2 2	0	0
2	D	2	Total Fe 2 2	0	0
2	E	2	Total Fe 2 2	0	0
2	F	2	Total Fe 2 2	0	0
2	G	2	Total Fe 2 2	0	0
2	H	2	Total Fe 2 2	0	0
2	I	2	Total Fe 2 2	0	0
2	J	2	Total Fe 2 2	0	0
2	K	2	Total Fe 2 2	0	0
2	L	2	Total Fe 2 2	0	0
2	M	2	Total Fe 2 2	0	0
2	N	2	Total Fe 2 2	0	0
2	O	2	Total Fe 2 2	0	0
2	P	2	Total Fe 2 2	0	0
2	Q	2	Total Fe 2 2	0	0
2	R	2	Total Fe 2 2	0	0
2	S	2	Total Fe 2 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	T	2	Total	Fe	0	0
			2	2		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	110	Total	O	0	0
			110	110		
4	B	152	Total	O	0	0
			152	152		
4	C	139	Total	O	0	0
			139	139		
4	D	132	Total	O	0	0
			132	132		
4	E	117	Total	O	0	0
			117	117		
4	F	147	Total	O	0	0
			147	147		

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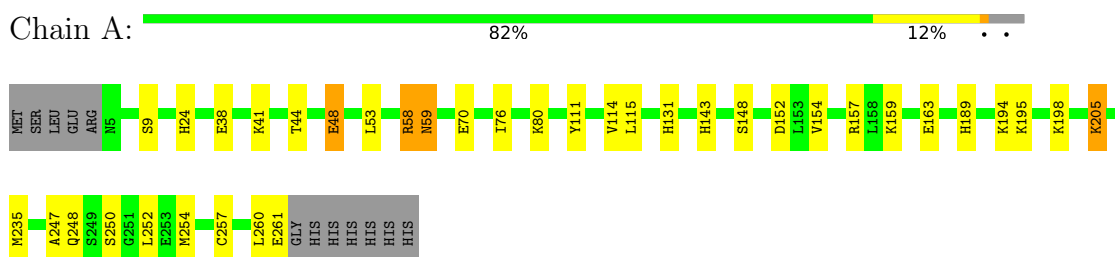
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	G	82	Total O 82 82	0	0
4	H	117	Total O 117 117	0	0
4	I	41	Total O 41 41	0	0
4	J	93	Total O 93 93	0	0
4	K	73	Total O 73 73	0	0
4	L	109	Total O 109 109	0	0
4	M	59	Total O 59 59	0	0
4	N	110	Total O 110 110	0	0
4	O	41	Total O 41 41	0	0
4	P	84	Total O 84 84	0	0
4	Q	123	Total O 123 123	0	0
4	R	128	Total O 128 128	0	0
4	S	84	Total O 84 84	0	0
4	T	132	Total O 132 132	0	0

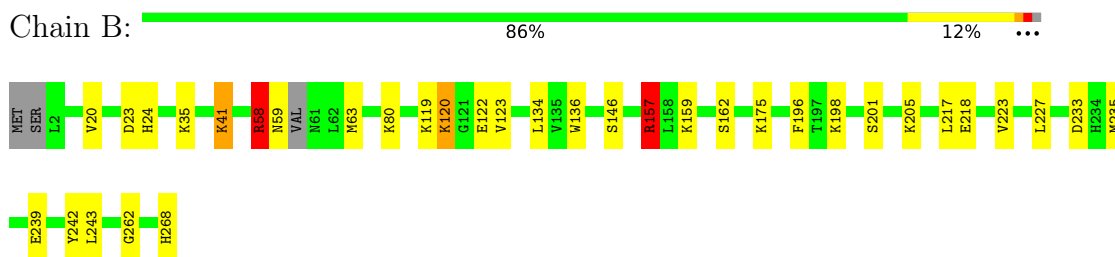
3 Residue-property plots [i](#)

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.

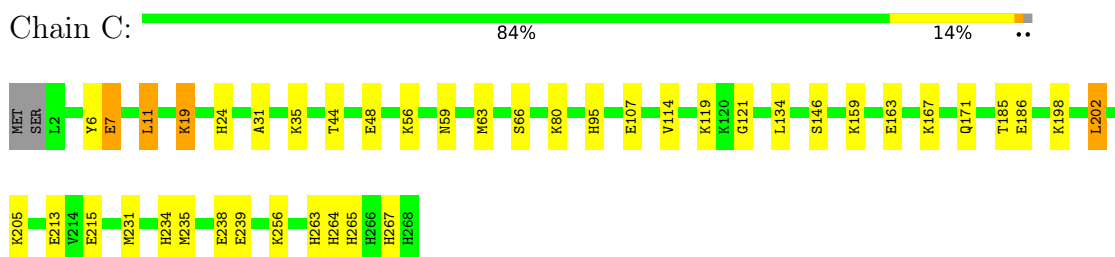
- Molecule 1: uncharacterized protein



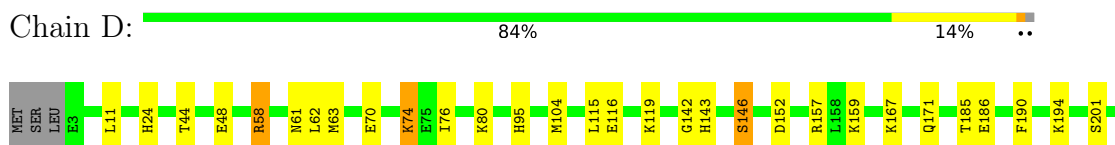
- Molecule 1: uncharacterized protein



- Molecule 1: uncharacterized protein

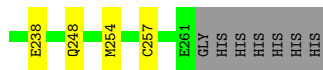
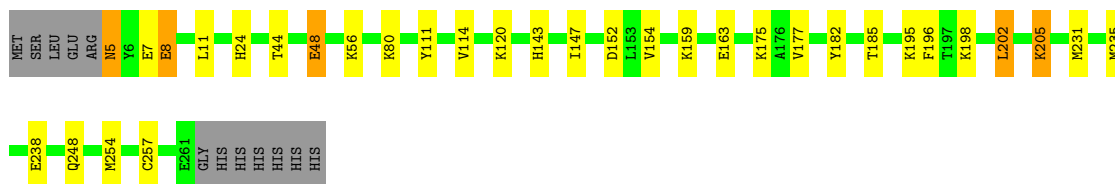
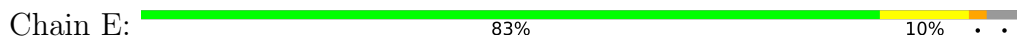


- Molecule 1: uncharacterized protein

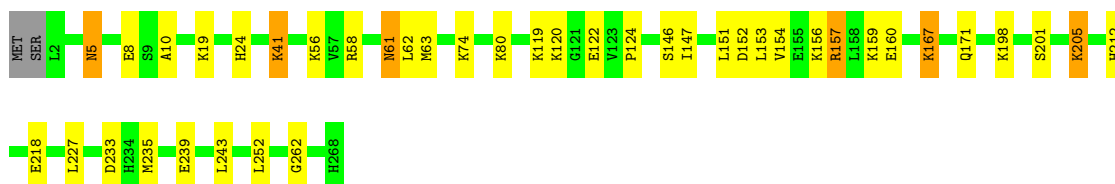
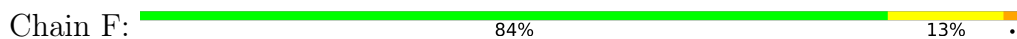




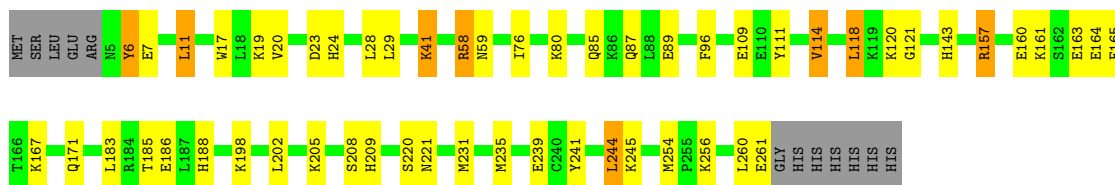
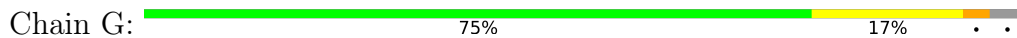
• Molecule 1: uncharacterized protein



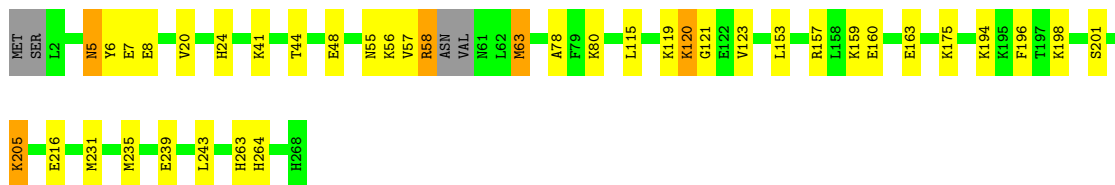
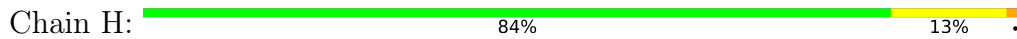
• Molecule 1: uncharacterized protein



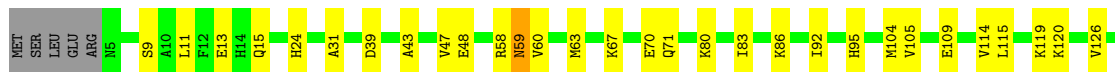
• Molecule 1: uncharacterized protein

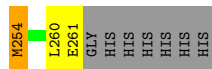


• Molecule 1: uncharacterized protein

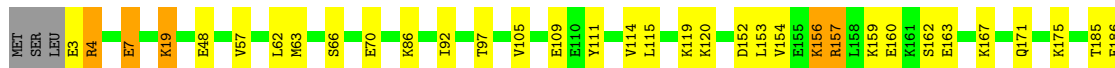
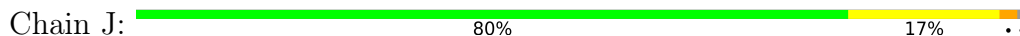


• Molecule 1: uncharacterized protein

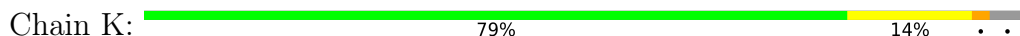




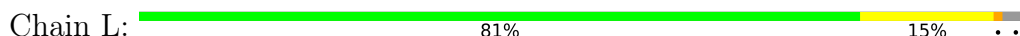
• Molecule 1: uncharacterized protein



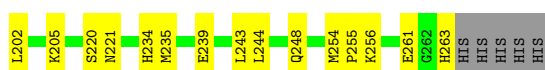
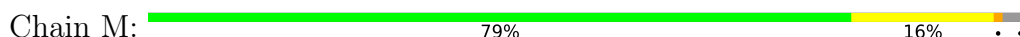
• Molecule 1: uncharacterized protein



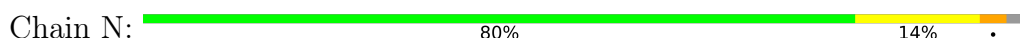
• Molecule 1: uncharacterized protein

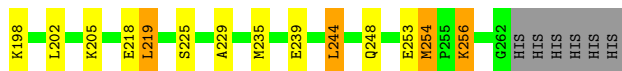


• Molecule 1: uncharacterized protein

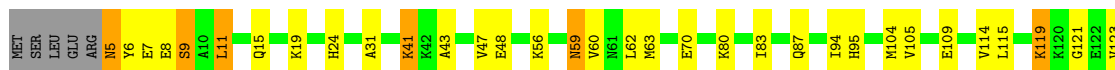


• Molecule 1: uncharacterized protein

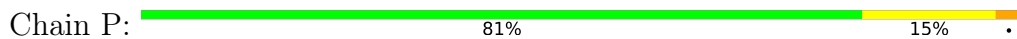




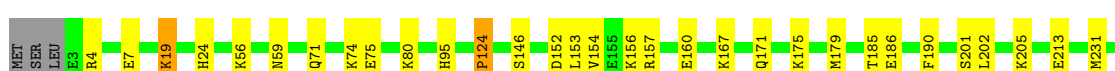
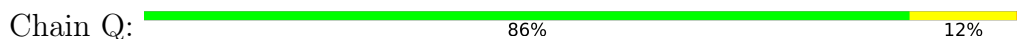
• Molecule 1: uncharacterized protein



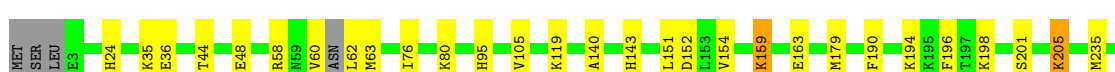
• Molecule 1: uncharacterized protein




• Molecule 1: uncharacterized protein

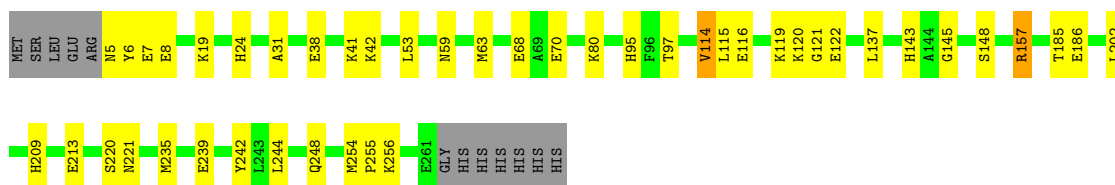


• Molecule 1: uncharacterized protein




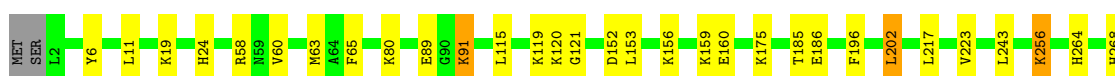
- Molecule 1: uncharacterized protein

Chain S:  79% 16% ..



- Molecule 1: uncharacterized protein

Chain T:  88% 10% ..



4 Data and refinement statistics i

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	167.81Å 167.81Å 582.66Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.10 50.00 – 2.10	Depositor EDS
% Data completeness (in resolution range)	96.6 (50.00-2.10) 96.7 (50.00-2.10)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.20 (at 2.10Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.198 , 0.258 (Not available) , 0.212	Depositor DCC
R_{free} test set	17434 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	22.1	Xtrriage
Anisotropy	0.026	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 18.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.36$	Xtrriage
Estimated twinning fraction	0.470 for -h-k,k,-l	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	45580	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 54.50 % 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 3.6188e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: FE, EDO

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	0.96	0/2186	1.00	1/2947 (0.0%)
1	B	1.03	0/2286	1.05	4/3078 (0.1%)
1	C	0.96	0/2278	1.01	1/3070 (0.0%)
1	D	1.01	0/2298	1.02	3/3094 (0.1%)
1	E	0.98	0/2195	1.01	3/2959 (0.1%)
1	F	1.04	1/2297 (0.0%)	1.04	2/3093 (0.1%)
1	G	0.86	0/2166	1.03	1/2920 (0.0%)
1	H	0.98	1/2278 (0.0%)	1.05	2/3066 (0.1%)
1	I	0.80	0/2167	0.97	3/2921 (0.1%)
1	J	0.87	0/2299	1.01	4/3097 (0.1%)
1	K	0.83	1/2177 (0.0%)	0.98	1/2935 (0.0%)
1	L	0.92	0/2204	1.01	2/2970 (0.1%)
1	M	0.84	1/2182 (0.0%)	0.97	1/2943 (0.0%)
1	N	0.90	0/2174	1.05	2/2930 (0.1%)
1	O	0.79	0/2176	1.01	2/2933 (0.1%)
1	P	0.87	0/2270	1.01	2/3059 (0.1%)
1	Q	0.97	0/2302	1.03	3/3101 (0.1%)
1	R	0.99	2/2278 (0.1%)	1.01	1/3066 (0.0%)
1	S	0.85	0/2183	0.99	3/2943 (0.1%)
1	T	0.97	0/2266	1.06	1/3053 (0.0%)
All	All	0.93	6/44662 (0.0%)	1.02	42/60178 (0.1%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	M	105	VAL	CA-CB	6.53	1.62	1.54
1	R	105	VAL	CA-CB	6.07	1.61	1.54
1	H	78	ALA	CA-CB	5.42	1.61	1.53
1	F	212	HIS	N-CA	5.32	1.52	1.46
1	K	105	VAL	CA-CB	5.26	1.60	1.54

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	123	VAL	N-CA-C	-7.84	101.89	108.63
1	F	124	PRO	CA-C-N	-7.76	112.35	120.03
1	F	124	PRO	C-N-CA	-7.76	112.35	120.03
1	J	190	PHE	CA-C-N	7.46	127.00	119.24
1	J	190	PHE	C-N-CA	7.46	127.00	119.24

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	2130	0	2118	32	0
1	B	2217	0	2194	24	0
1	C	2215	0	2189	25	0
1	D	2226	0	2213	27	0
1	E	2139	0	2123	28	0
1	F	2228	0	2218	33	0
1	G	2113	0	2110	49	0
1	H	2219	0	2191	41	0
1	I	2114	0	2110	44	0
1	J	2230	0	2202	38	0
1	K	2121	0	2113	30	0
1	L	2146	0	2140	36	0
1	M	2127	0	2109	24	0
1	N	2124	0	2117	39	0
1	O	2123	0	2115	37	0
1	P	2207	0	2178	35	0
1	Q	2227	0	2204	21	0
1	R	2216	0	2191	33	0
1	S	2130	0	2113	30	0
1	T	2207	0	2185	20	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
2	I	2	0	0	0	0
2	J	2	0	0	0	0
2	K	2	0	0	0	0
2	L	2	0	0	0	0
2	M	2	0	0	0	0
2	N	2	0	0	0	0
2	O	2	0	0	0	0
2	P	2	0	0	0	0
2	Q	2	0	0	0	0
2	R	2	0	0	0	0
2	S	2	0	0	0	0
2	T	2	0	0	0	0
3	B	4	0	6	2	0
3	R	4	0	6	4	0
4	A	110	0	0	1	0
4	B	152	0	0	3	0
4	C	139	0	0	3	0
4	D	132	0	0	2	0
4	E	117	0	0	2	0
4	F	147	0	0	3	0
4	G	82	0	0	5	0
4	H	117	0	0	5	0
4	I	41	0	0	1	0
4	J	93	0	0	2	0
4	K	73	0	0	0	0
4	L	109	0	0	6	0
4	M	59	0	0	0	0
4	N	110	0	0	1	0
4	O	41	0	0	1	0
4	P	84	0	0	1	0
4	Q	123	0	0	2	0
4	R	128	0	0	1	0
4	S	84	0	0	3	0
4	T	132	0	0	3	0
All	All	45580	0	43145	626	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 7.

The worst 5 of 626 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:J:159:LYS:HE2	1:J:163:GLU:OE1	1.33	1.24
1:D:58[B]:ARG:HH11	1:D:58[B]:ARG:HB2	1.00	1.12
1:K:58:ARG:HG3	1:K:58:ARG:HH21	1.01	1.12
1:F:157:ARG:HB3	1:F:157:ARG:NH2	1.65	1.11
1:G:41:LYS:HE3	1:G:41:LYS:HA	1.30	1.10

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	258/269 (96%)	256 (99%)	2 (1%)	0	100	100
1	B	266/269 (99%)	263 (99%)	2 (1%)	1 (0%)	30	28
1	C	267/269 (99%)	263 (98%)	4 (2%)	0	100	100
1	D	269/269 (100%)	266 (99%)	3 (1%)	0	100	100
1	E	259/269 (96%)	259 (100%)	0	0	100	100
1	F	269/269 (100%)	268 (100%)	1 (0%)	0	100	100
1	G	256/269 (95%)	250 (98%)	6 (2%)	0	100	100
1	H	265/269 (98%)	262 (99%)	3 (1%)	0	100	100
1	I	256/269 (95%)	253 (99%)	3 (1%)	0	100	100
1	J	269/269 (100%)	267 (99%)	2 (1%)	0	100	100
1	K	257/269 (96%)	254 (99%)	3 (1%)	0	100	100
1	L	260/269 (97%)	258 (99%)	2 (1%)	0	100	100
1	M	258/269 (96%)	256 (99%)	2 (1%)	0	100	100
1	N	257/269 (96%)	253 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	O	257/269 (96%)	254 (99%)	3 (1%)	0	100	100
1	P	266/269 (99%)	260 (98%)	6 (2%)	0	100	100
1	Q	270/269 (100%)	265 (98%)	5 (2%)	0	100	100
1	R	265/269 (98%)	263 (99%)	2 (1%)	0	100	100
1	S	258/269 (96%)	254 (98%)	4 (2%)	0	100	100
1	T	266/269 (99%)	264 (99%)	2 (1%)	0	100	100
All	All	5248/5380 (98%)	5188 (99%)	59 (1%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	58	ARG

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	A	232/240 (97%)	224 (97%)	8 (3%)	32	35
1	B	241/240 (100%)	234 (97%)	7 (3%)	37	42
1	C	240/240 (100%)	230 (96%)	10 (4%)	26	28
1	D	242/240 (101%)	233 (96%)	9 (4%)	30	33
1	E	233/240 (97%)	226 (97%)	7 (3%)	36	41
1	F	242/240 (101%)	233 (96%)	9 (4%)	30	33
1	G	229/240 (95%)	213 (93%)	16 (7%)	14	11
1	H	240/240 (100%)	230 (96%)	10 (4%)	26	28
1	I	230/240 (96%)	220 (96%)	10 (4%)	26	27
1	J	242/240 (101%)	227 (94%)	15 (6%)	16	14
1	K	231/240 (96%)	217 (94%)	14 (6%)	17	15
1	L	233/240 (97%)	226 (97%)	7 (3%)	36	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	230/240 (96%)	218 (95%)	12 (5%)	21	20
1	N	230/240 (96%)	215 (94%)	15 (6%)	15	13
1	O	231/240 (96%)	214 (93%)	17 (7%)	13	10
1	P	239/240 (100%)	232 (97%)	7 (3%)	37	42
1	Q	243/240 (101%)	237 (98%)	6 (2%)	42	48
1	R	240/240 (100%)	235 (98%)	5 (2%)	47	54
1	S	231/240 (96%)	224 (97%)	7 (3%)	36	41
1	T	239/240 (100%)	233 (98%)	6 (2%)	42	48
All	All	4718/4800 (98%)	4521 (96%)	197 (4%)	27	28

5 of 197 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	48	GLU
1	N	205	LYS
1	L	205	LYS
1	M	202	LEU
1	O	7	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 85 such sidechains are listed below:

Mol	Chain	Res	Type
1	N	95	HIS
1	R	102	ASN
1	O	102	ASN
1	P	264	HIS
1	S	5	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 42 ligands modelled in this entry, 40 are monoatomic - leaving 2 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	B	308	-	3,3,3	0.52	0	2,2,2	0.25	0
3	EDO	R	308	-	3,3,3	0.40	0	2,2,2	0.57	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	EDO	B	308	-	-	0/1/1/1	-
3	EDO	R	308	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	308	EDO	2	0
3	R	308	EDO	4	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	257/269 (95%)	-1.48	0 100 100	11, 19, 38, 50	3 (1%)
1	B	266/269 (98%)	-1.54	0 100 100	9, 16, 28, 45	4 (1%)
1	C	267/269 (99%)	-1.49	0 100 100	11, 18, 33, 46	2 (0%)
1	D	266/269 (98%)	-1.50	0 100 100	10, 18, 30, 40	5 (1%)
1	E	257/269 (95%)	-1.46	0 100 100	11, 19, 38, 49	4 (1%)
1	F	267/269 (99%)	-1.53	0 100 100	8, 16, 28, 38	4 (1%)
1	G	257/269 (95%)	-1.38	0 100 100	11, 24, 43, 52	1 (0%)
1	H	265/269 (98%)	-1.47	0 100 100	8, 19, 31, 39	4 (1%)
1	I	257/269 (95%)	-1.33	0 100 100	20, 30, 49, 56	1 (0%)
1	J	266/269 (98%)	-1.39	0 100 100	12, 25, 35, 47	5 (1%)
1	K	257/269 (95%)	-1.38	0 100 100	15, 25, 42, 53	2 (0%)
1	L	260/269 (96%)	-1.44	0 100 100	11, 22, 36, 51	2 (0%)
1	M	259/269 (96%)	-1.39	0 100 100	14, 25, 41, 55	1 (0%)
1	N	259/269 (96%)	-1.44	0 100 100	16, 22, 35, 46	0
1	O	257/269 (95%)	-1.32	0 100 100	16, 29, 50, 58	2 (0%)
1	P	266/269 (98%)	-1.38	0 100 100	13, 25, 35, 44	2 (0%)
1	Q	266/269 (98%)	-1.47	0 100 100	11, 18, 34, 45	6 (2%)
1	R	265/269 (98%)	-1.50	0 100 100	8, 18, 29, 45	4 (1%)
1	S	257/269 (95%)	-1.38	0 100 100	13, 24, 42, 52	3 (1%)
1	T	267/269 (99%)	-1.47	0 100 100	12, 20, 32, 43	1 (0%)
All	All	5238/5380 (97%)	-1.44	0 100 100	8, 22, 39, 58	56 (1%)

There are no RSRZ outliers to report.

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	FE	I	306	1/1	0.99	0.04	54,54,54,54	0
2	FE	K	306	1/1	0.99	0.06	48,48,48,48	0
2	FE	M	306	1/1	0.99	0.04	48,48,48,48	0
2	FE	N	307	1/1	0.99	0.04	48,48,48,48	0
3	EDO	B	308	4/4	0.99	0.03	30,34,35,36	0
3	EDO	R	308	4/4	0.99	0.03	27,28,29,30	0
2	FE	D	306	1/1	1.00	0.06	35,35,35,35	0
2	FE	D	307	1/1	1.00	0.03	37,37,37,37	0
2	FE	E	306	1/1	1.00	0.03	36,36,36,36	0
2	FE	E	307	1/1	1.00	0.05	42,42,42,42	0
2	FE	F	306	1/1	1.00	0.03	34,34,34,34	0
2	FE	F	307	1/1	1.00	0.04	29,29,29,29	0
2	FE	G	306	1/1	1.00	0.04	39,39,39,39	0
2	FE	G	307	1/1	1.00	0.04	42,42,42,42	0
2	FE	H	306	1/1	1.00	0.03	34,34,34,34	0
2	FE	H	307	1/1	1.00	0.04	35,35,35,35	0
2	FE	A	306	1/1	1.00	0.05	38,38,38,38	0
2	FE	I	307	1/1	1.00	0.03	54,54,54,54	0
2	FE	J	306	1/1	1.00	0.02	43,43,43,43	0
2	FE	J	307	1/1	1.00	0.04	44,44,44,44	0
2	FE	A	307	1/1	1.00	0.06	43,43,43,43	0
2	FE	K	307	1/1	1.00	0.04	49,49,49,49	0
2	FE	L	306	1/1	1.00	0.02	39,39,39,39	0
2	FE	L	307	1/1	1.00	0.03	49,49,49,49	0
2	FE	B	306	1/1	1.00	0.06	35,35,35,35	0
2	FE	M	307	1/1	1.00	0.04	46,46,46,46	0
2	FE	N	306	1/1	1.00	0.05	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	FE	B	307	1/1	1.00	0.03	32,32,32,32	0
2	FE	O	306	1/1	1.00	0.05	51,51,51,51	0
2	FE	O	307	1/1	1.00	0.04	53,53,53,53	0
2	FE	P	306	1/1	1.00	0.03	45,45,45,45	0
2	FE	P	307	1/1	1.00	0.05	45,45,45,45	0
2	FE	Q	306	1/1	1.00	0.03	40,40,40,40	0
2	FE	Q	307	1/1	1.00	0.03	32,32,32,32	0
2	FE	R	306	1/1	1.00	0.04	36,36,36,36	0
2	FE	R	307	1/1	1.00	0.02	34,34,34,34	0
2	FE	S	306	1/1	1.00	0.03	39,39,39,39	0
2	FE	S	307	1/1	1.00	0.04	46,46,46,46	0
2	FE	T	306	1/1	1.00	0.04	36,36,36,36	0
2	FE	T	307	1/1	1.00	0.04	37,37,37,37	0
2	FE	C	306	1/1	1.00	0.04	36,36,36,36	0
2	FE	C	307	1/1	1.00	0.04	31,31,31,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.