



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 12, 2024 – 12:39 PM EST

PDB ID : 3M1R
Title : The crystal structure of formimidoylglutamase from *Bacillus subtilis* subsp. *subtilis* str. 168
Authors : Tan, K.; Bigelow, L.; Trevino, D.; Buck, K.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2010-03-05
Resolution : 2.20 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

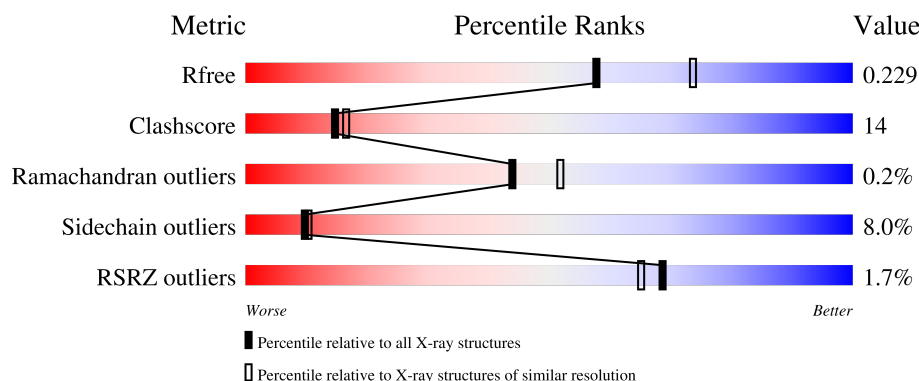
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



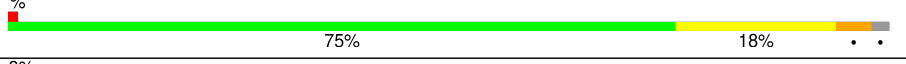


The reported resolution of this entry is 2.20 Å.

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}	164625	5791 (2.20-2.20)
Clashscore	180529	6634 (2.20-2.20)
Ramachandran outliers	177936	6560 (2.20-2.20)
Sidechain outliers	177891	6561 (2.20-2.20)
RSRZ outliers	164620	5791 (2.20-2.20)

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	322	
1	B	322	
1	C	322	
1	D	322	
1	E	322	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	322	<div> <div></div> <div>%</div> <div>74%</div> <div>22%</div> <div>..</div> </div>

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
2	CL	A	321	-	-	X	-
2	CL	B	321	-	-	X	-
4	PEG	A	325	-	-	X	-
4	PEG	A	326	-	-	X	-
4	PEG	B	324	-	-	X	-
4	PEG	D	323	-	-	X	-
4	PEG	E	324	-	-	X	-
4	PEG	F	328	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 15171 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 Formimidoylglutamase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	318	Total	C	N	O	S	Se	0	0	0
			2462	1558	421	474	1	8			
1	B	317	Total	C	N	O	S	Se	0	0	0
			2449	1549	419	472	1	8			
1	C	316	Total	C	N	O	S	Se	0	0	0
			2441	1544	418	471	1	7			
1	D	321	Total	C	N	O	S	Se	0	0	0
			2479	1568	424	478	1	8			
1	E	316	Total	C	N	O	S	Se	0	0	0
			2441	1544	418	471	1	7			
1	F	316	Total	C	N	O	S	Se	0	0	0
			2444	1549	418	469	1	7			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP P42068
A	-1	ASN	-	expression tag	UNP P42068
A	0	ALA	-	expression tag	UNP P42068
B	-2	SER	-	expression tag	UNP P42068
B	-1	ASN	-	expression tag	UNP P42068
B	0	ALA	-	expression tag	UNP P42068
C	-2	SER	-	expression tag	UNP P42068
C	-1	ASN	-	expression tag	UNP P42068
C	0	ALA	-	expression tag	UNP P42068
D	-2	SER	-	expression tag	UNP P42068
D	-1	ASN	-	expression tag	UNP P42068
D	0	ALA	-	expression tag	UNP P42068
E	-2	SER	-	expression tag	UNP P42068
E	-1	ASN	-	expression tag	UNP P42068
E	0	ALA	-	expression tag	UNP P42068
F	-2	SER	-	expression tag	UNP P42068
F	-1	ASN	-	expression tag	UNP P42068

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	0	ALA	-	expression tag	UNP P42068

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



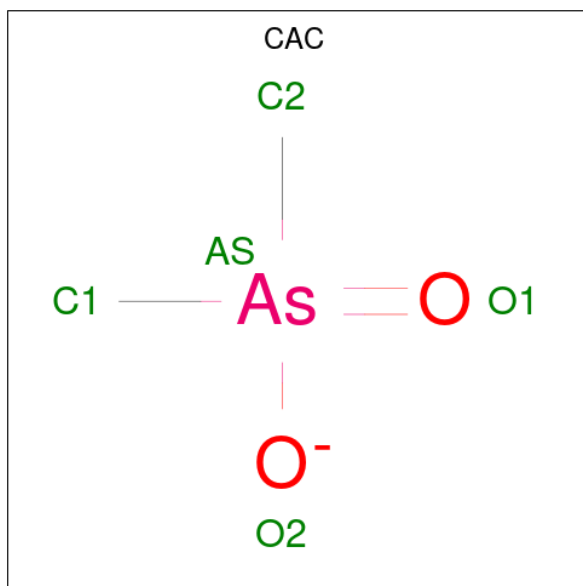
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			7	4	3		
4	A	1	Total	C	O	0	0
			7	4	3		
4	A	1	Total	C	O	0	0
			7	4	3		
4	B	1	Total	C	O	0	0
			7	4	3		
4	B	1	Total	C	O	0	0
			7	4	3		
4	C	1	Total	C	O	0	0
			7	4	3		
4	C	1	Total	C	O	0	0
			7	4	3		
4	C	1	Total	C	O	0	0
			7	4	3		
4	C	1	Total	C	O	0	0
			7	4	3		
4	C	1	Total	C	O	0	0
			7	4	3		
4	D	1	Total	C	O	0	0
			7	4	3		
4	D	1	Total	C	O	0	0
			7	4	3		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	E	1	Total C O 7 4 3	0	0
4	E	1	Total C O 7 4 3	0	0
4	E	1	Total C O 7 4 3	0	0
4	F	1	Total C O 7 4 3	0	0
4	F	1	Total C O 7 4 3	0	0
4	F	1	Total C O 7 4 3	0	0
4	F	1	Total C O 7 4 3	0	0
4	F	1	Total C O 7 4 3	0	0
4	F	1	Total C O 7 4 3	0	0

- Molecule 5 is CACODYLATE ION (three-letter code: CAC) (formula: $\text{C}_2\text{H}_6\text{AsO}_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	1	Total As C O 10 2 4 4	0	1
5	E	1	Total As C O 10 2 4 4	0	1

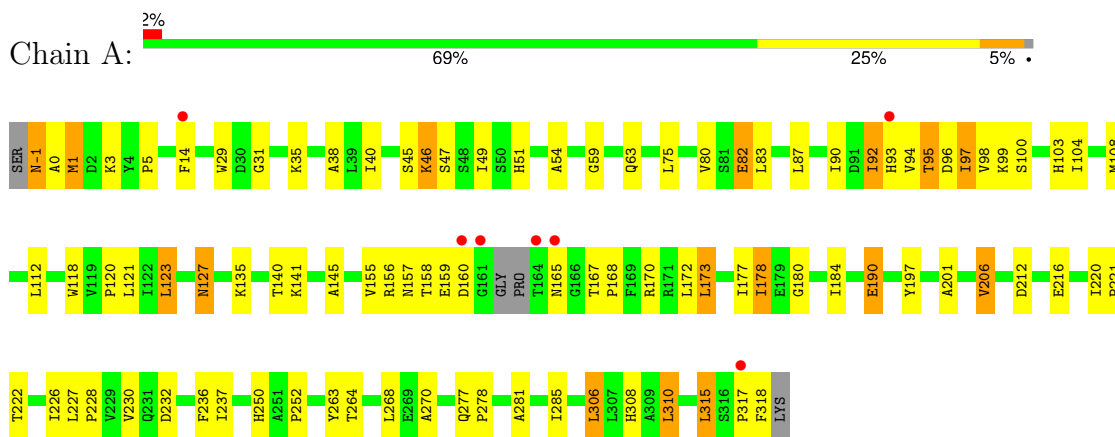
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	36	Total 36	O 36	0	0
6	B	36	Total 36	O 36	0	0
6	C	55	Total 55	O 55	0	0
6	D	46	Total 46	O 46	0	0
6	E	45	Total 45	O 45	0	0
6	F	35	Total 35	O 35	0	0

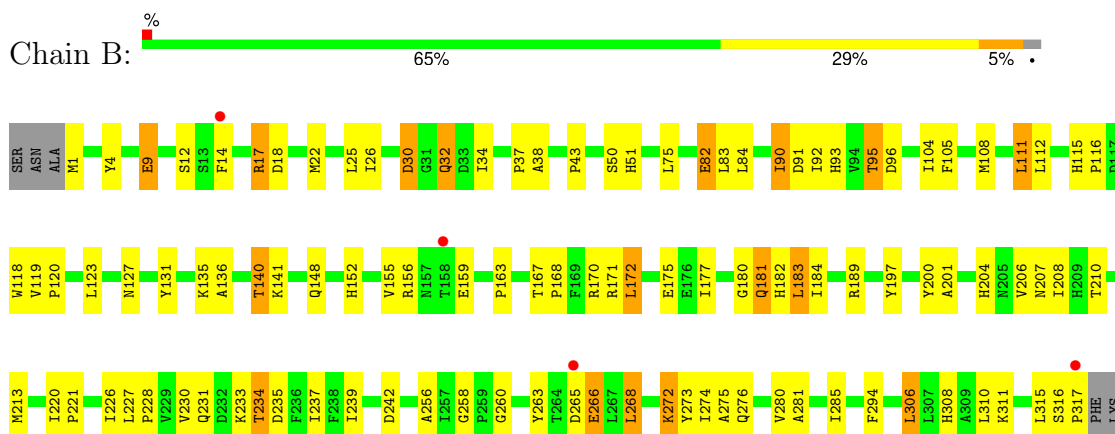
3 Residue-property plots [i](#)

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.

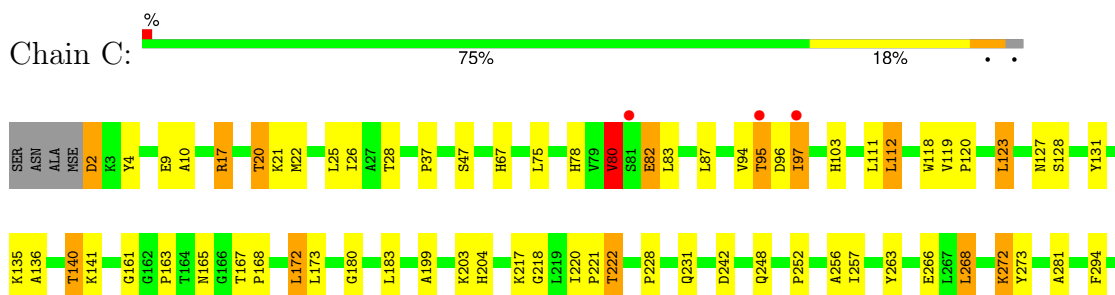
• Molecule 1: Formimidoylglutamase



• Molecule 1: Formimidoylglutamase

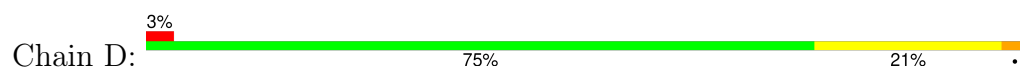


• Molecule 1: Formimidoylglutamase

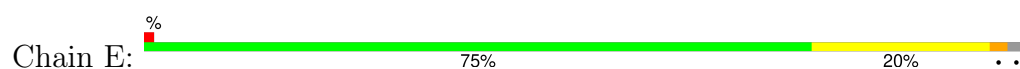




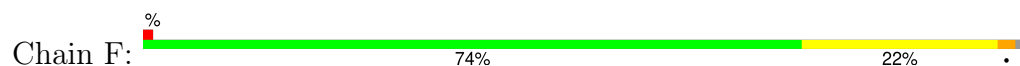
• Molecule 1: Formimidoylglutamase



• Molecule 1: Formimidoylglutamase



• Molecule 1: Formimidoylglutamase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	142.04Å 118.98Å 123.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.47 – 2.20 32.47 – 2.20	Depositor EDS
% Data completeness (in resolution range)	88.0 (32.47-2.20) 96.4 (32.47-2.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 2.20Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.176 , 0.230 0.181 , 0.229	Depositor DCC
R_{free} test set	5124 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	40.6	Xtriage
Anisotropy	0.433	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 63.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.003 for -h,l,k	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	15171	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.69% 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

5.1 Standard geometry

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

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	0.39	0/2507	0.56	0/3388
1	B	0.37	0/2496	0.56	0/3377
1	C	0.42	0/2488	0.60	1/3367 (0.0%)
1	D	0.40	0/2526	0.57	0/3416
1	E	0.41	0/2488	0.60	0/3367
1	F	0.38	0/2492	0.56	0/3372
All	All	0.39	0/14997	0.58	1/20287 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	242	ASP	CB-CG-OD1	6.19	123.87	118.30

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	2462	0	2432	82	0
1	B	2449	0	2423	101	0
1	C	2441	0	2411	56	0
1	D	2479	0	2448	64	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2441	0	2411	59	0
1	F	2444	0	2416	59	0
2	A	2	0	0	4	0
2	B	2	0	0	3	0
2	C	2	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
3	E	2	0	0	0	0
3	F	2	0	0	0	0
4	A	21	0	30	11	0
4	B	14	0	20	4	0
4	C	49	0	70	5	0
4	D	14	0	20	5	0
4	E	21	0	30	7	0
4	F	42	0	60	7	0
5	C	10	0	0	3	0
5	E	10	0	0	1	0
6	A	36	0	0	1	0
6	B	36	0	0	2	0
6	C	55	0	0	1	0
6	D	46	0	0	1	0
6	E	45	0	0	0	0
6	F	35	0	0	0	0
All	All	15171	0	14771	408	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 14.

The worst 5 of 408 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:D:152:HIS:HE2	4:D:323:PEG:H11	1.27	0.98
1:F:93:HIS:HD2	1:F:95:THR:H	1.12	0.96
1:D:93:HIS:HD2	1:D:95:THR:H	1.14	0.94
1:E:295:ARG:H	4:E:325:PEG:H21	1.33	0.93
1:F:135:LYS:HA	1:F:177:ILE:CD1	2.00	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	A	314/322 (98%)	297 (95%)	17 (5%)	0	100	100
1	B	315/322 (98%)	306 (97%)	7 (2%)	2 (1%)	22	23
1	C	314/322 (98%)	306 (98%)	7 (2%)	1 (0%)	37	42
1	D	319/322 (99%)	307 (96%)	12 (4%)	0	100	100
1	E	314/322 (98%)	301 (96%)	13 (4%)	0	100	100
1	F	314/322 (98%)	302 (96%)	11 (4%)	1 (0%)	37	42
All	All	1890/1932 (98%)	1819 (96%)	67 (4%)	4 (0%)	44	52

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	32	GLN
1	B	82	GLU
1	F	229	VAL
1	C	80	VAL

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	270/265 (102%)	243 (90%)	27 (10%)	6	6

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	269/265 (102%)	244 (91%)	25 (9%)	7	7
1	C	268/265 (101%)	245 (91%)	23 (9%)	8	9
1	D	272/265 (103%)	253 (93%)	19 (7%)	12	14
1	E	268/265 (101%)	251 (94%)	17 (6%)	15	17
1	F	268/265 (101%)	250 (93%)	18 (7%)	13	15
All	All	1615/1590 (102%)	1486 (92%)	129 (8%)	10	10

5 of 129 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	81	SER
1	F	106	GLN
1	B	272	LYS
1	B	268	LEU
1	F	121	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	276	GLN
1	F	231	GLN
1	D	101	HIS
1	F	304	HIS
1	E	250	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 48 ligands modelled in this entry, 21 are monoatomic - leaving 27 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	$\# Z > 2$
4	PEG	B	324	-	6,6,6	0.57	0	5,5,5	0.80	0
4	PEG	C	325	-	6,6,6	0.55	0	5,5,5	0.77	0
4	PEG	C	327	-	6,6,6	0.62	0	5,5,5	0.85	0
4	PEG	D	323	-	6,6,6	0.64	0	5,5,5	1.17	1 (20%)
4	PEG	C	331	-	6,6,6	0.59	0	5,5,5	0.73	0
4	PEG	F	327	-	6,6,6	0.56	0	5,5,5	0.73	0
4	PEG	D	324	-	6,6,6	0.57	0	5,5,5	0.61	0
4	PEG	C	329	-	6,6,6	0.56	0	5,5,5	0.70	0
4	PEG	A	325	-	6,6,6	0.59	0	5,5,5	0.66	0
4	PEG	A	326	-	6,6,6	0.55	0	5,5,5	0.95	1 (20%)
4	PEG	C	328	-	6,6,6	0.54	0	5,5,5	0.77	0
4	PEG	F	323	-	6,6,6	0.55	0	5,5,5	0.82	0
4	PEG	C	330	-	6,6,6	0.57	0	5,5,5	0.79	0
5	CAC	C	320[A]	-	2,4,4	0.73	0	2,6,6	0.27	0
4	PEG	C	326	-	6,6,6	0.57	0	5,5,5	0.72	0
4	PEG	F	325	-	6,6,6	0.57	0	5,5,5	0.74	0
5	CAC	E	320[A]	-	2,4,4	0.78	0	2,6,6	0.21	0
4	PEG	A	324	-	6,6,6	0.60	0	5,5,5	0.69	0
4	PEG	F	326	-	6,6,6	0.60	0	5,5,5	0.90	0
4	PEG	E	325	-	6,6,6	0.62	0	5,5,5	0.82	0
4	PEG	E	326	-	6,6,6	0.53	0	5,5,5	0.78	0
4	PEG	F	324	-	6,6,6	0.55	0	5,5,5	0.62	0
4	PEG	F	328	-	6,6,6	0.57	0	5,5,5	0.56	0
4	PEG	B	325	-	6,6,6	0.59	0	5,5,5	0.71	0
4	PEG	E	324	-	6,6,6	0.60	0	5,5,5	0.67	0
5	CAC	C	320[B]	-	2,4,4	0.76	0	2,6,6	0.25	0
5	CAC	E	320[B]	-	2,4,4	0.73	0	2,6,6	0.24	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
4	PEG	B	324	-	-	3/4/4/4	-
4	PEG	C	325	-	-	2/4/4/4	-
4	PEG	C	327	-	-	1/4/4/4	-
4	PEG	D	323	-	-	4/4/4/4	-
4	PEG	C	331	-	-	1/4/4/4	-
4	PEG	F	327	-	-	2/4/4/4	-
4	PEG	D	324	-	-	1/4/4/4	-
4	PEG	C	329	-	-	3/4/4/4	-
4	PEG	A	325	-	-	0/4/4/4	-
4	PEG	A	326	-	-	1/4/4/4	-
4	PEG	C	328	-	-	2/4/4/4	-
4	PEG	F	323	-	-	3/4/4/4	-
4	PEG	C	330	-	-	3/4/4/4	-
4	PEG	C	326	-	-	1/4/4/4	-
4	PEG	F	325	-	-	2/4/4/4	-
4	PEG	A	324	-	-	1/4/4/4	-
4	PEG	F	326	-	-	1/4/4/4	-
4	PEG	E	325	-	-	1/4/4/4	-
4	PEG	E	326	-	-	3/4/4/4	-
4	PEG	F	324	-	-	2/4/4/4	-
4	PEG	F	328	-	-	1/4/4/4	-
4	PEG	B	325	-	-	2/4/4/4	-
4	PEG	E	324	-	-	2/4/4/4	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	323	PEG	C3-O2-C2	2.46	124.04	113.26
4	A	326	PEG	C3-O2-C2	2.00	122.03	113.26

There are no chirality outliers.

5 of 42 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	323	PEG	C1-C2-O2-C3
4	A	324	PEG	C1-C2-O2-C3
4	F	326	PEG	O1-C1-C2-O2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
4	C	327	PEG	O1-C1-C2-O2
4	D	323	PEG	O1-C1-C2-O2

There are no ring outliers.

16 monomers are involved in 43 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	324	PEG	4	0
4	C	327	PEG	1	0
4	D	323	PEG	4	0
4	D	324	PEG	1	0
4	C	329	PEG	1	0
4	A	325	PEG	8	0
4	A	326	PEG	5	0
4	C	328	PEG	3	0
4	F	323	PEG	2	0
5	C	320[A]	CAC	2	0
5	E	320[A]	CAC	1	0
4	A	324	PEG	3	0
4	E	325	PEG	2	0
4	F	328	PEG	5	0
4	E	324	PEG	5	0
5	C	320[B]	CAC	1	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	310/322 (96%)	-0.05	7 (2%) 61 57	27, 52, 85, 148	0
1	B	309/322 (95%)	0.03	4 (1%) 74 71	25, 55, 92, 108	0
1	C	309/322 (95%)	-0.20	4 (1%) 74 71	25, 44, 71, 105	0
1	D	313/322 (97%)	-0.12	9 (2%) 54 51	24, 50, 81, 105	0
1	E	309/322 (95%)	-0.15	3 (0%) 79 76	24, 46, 81, 112	0
1	F	309/322 (95%)	-0.08	4 (1%) 74 71	25, 50, 83, 113	0
All	All	1859/1932 (96%)	-0.09	31 (1%) 69 65	24, 50, 84, 148	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	158	THR	4.9
1	A	161	GLY	3.7
1	A	164	THR	3.7
1	F	95	THR	3.7
1	B	14	PHE	3.6

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 monosaccharides in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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
4	PEG	F	327	7/7	0.54	0.17	91,93,95,95	0
4	PEG	F	326	7/7	0.71	0.15	71,77,78,78	0
4	PEG	A	326	7/7	0.77	0.16	69,70,76,77	0
4	PEG	C	330	7/7	0.80	0.17	69,75,86,87	0
4	PEG	A	324	7/7	0.81	0.16	37,56,62,62	0
4	PEG	B	325	7/7	0.83	0.14	76,81,86,87	0
4	PEG	E	325	7/7	0.83	0.14	67,70,74,76	0
3	CA	D	322	1/1	0.84	0.14	84,84,84,84	0
2	CL	C	322	1/1	0.84	0.15	89,89,89,89	0
4	PEG	C	329	7/7	0.85	0.13	86,87,89,90	0
4	PEG	C	327	7/7	0.85	0.18	39,51,55,57	0
4	PEG	D	323	7/7	0.85	0.15	43,51,63,66	0
4	PEG	C	326	7/7	0.86	0.11	57,68,76,77	0
4	PEG	C	331	7/7	0.86	0.17	86,89,91,92	0
4	PEG	B	324	7/7	0.87	0.13	37,46,59,59	0
2	CL	A	321	1/1	0.87	0.12	75,75,75,75	0
4	PEG	E	324	7/7	0.87	0.14	41,44,53,56	0
4	PEG	A	325	7/7	0.88	0.12	52,61,66,68	0
4	PEG	F	325	7/7	0.88	0.14	76,78,82,84	0
2	CL	B	321	1/1	0.89	0.11	58,58,58,58	0
3	CA	F	322	1/1	0.89	0.08	77,77,77,77	0
5	CAC	E	320[A]	5/5	0.89	0.17	26,31,59,106	5
5	CAC	E	320[B]	5/5	0.89	0.17	15,20,48,134	5
4	PEG	F	328	7/7	0.90	0.14	50,62,66,67	0
4	PEG	C	325	7/7	0.90	0.11	62,63,64,68	0
3	CA	A	323	1/1	0.90	0.12	69,69,69,69	0
4	PEG	C	328	7/7	0.91	0.10	43,57,67,68	0
4	PEG	F	323	7/7	0.91	0.09	46,55,61,67	0
3	CA	E	323	1/1	0.92	0.10	61,61,61,61	0
2	CL	A	320	1/1	0.92	0.08	49,49,49,49	0
3	CA	C	324	1/1	0.92	0.09	62,62,62,62	0
2	CL	D	320	1/1	0.92	0.09	53,53,53,53	0
4	PEG	F	324	7/7	0.93	0.10	48,59,71,77	0
4	PEG	D	324	7/7	0.94	0.09	52,62,77,80	0
4	PEG	E	326	7/7	0.95	0.08	50,60,71,72	0
3	CA	B	323	1/1	0.96	0.07	59,59,59,59	0
5	CAC	C	320[A]	5/5	0.96	0.14	15,30,57,125	5

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	CAC	C	320[B]	5/5	0.96	0.14	12,16,72,128	5
2	CL	F	320	1/1	0.96	0.06	48,48,48,48	0
2	CL	C	321	1/1	0.96	0.10	42,42,42,42	0
2	CL	B	320	1/1	0.97	0.09	35,35,35,35	0
3	CA	C	323	1/1	0.97	0.06	33,33,33,33	0
2	CL	E	321	1/1	0.97	0.13	34,34,34,34	0
3	CA	B	322	1/1	0.98	0.04	39,39,39,39	0
3	CA	F	321	1/1	0.98	0.06	39,39,39,39	0
3	CA	E	322	1/1	0.98	0.04	34,34,34,34	0
3	CA	A	322	1/1	0.99	0.06	35,35,35,35	0
3	CA	D	321	1/1	0.99	0.05	37,37,37,37	0

6.5 Other polymers ⓘ

There are no such residues in this entry.